91478

STIC-Biotech/ChemLib

From: Turner, Sharon
Sent: Monday, April 14, 2003 2:23 PM
To: STIC-Biotech/ChemLib
Subject: 09930871

Please search CDB and Interference files

Backtranslation of SEQ ID NO:12 standard and oligomer search
Standard and Oligomer search SEQ ID NO:11

[redacted]
USPTO
CM1-10B09
Mailroom 10B19
Biotechnology GAU 1647
(703) 308-0056

CRF

priority 60/225,999 8-16-00
file 8-15-01

POINT OF CONTACT:
PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

Searcher:_____
Phone:_____
Location:_____
Date Picked Up: 4/16
Date Completed: 4/24
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 23, 2003, 02:38:26 ; Search time 568 Seconds
(without alignments)
7965.255 Million cell updates/sec

Title: US-09-930-871-12
Perfect score: 2009
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Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4368727

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=oligop2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		2007	99.9	6030	24	AAD32844	Human ion channel
2		1970	98.1	5922	24	AAD32845	Human ion channel
3		1733	86.3	8378	22	AAH55763	Human adult form o
4		1545	76.9	6027	24	AAD27266	Human transporter
5		1447	72.0	8378	22	AAH55764	Human neonatal for
6		1444	71.9	4362	24	AAD32846	Human ion channel
7		1382	68.8	4179	24	AAD32847	Human ion channel
8		1332	66.3	4197	24	AAD32848	Human ion channel
9		1326	66.0	5997	24	AAD32839	Human ion channel
10		1289	64.2	5889	24	AAD32840	Human ion channel
11		947	47.1	8131	24	ABL39689	Human sodium chann
12		763	38.0	4329	24	AAD32841	Human ion channel
13		701	34.9	4146	24	AAD32842	Human ion channel
14		670	33.3	4164	24	AAD32843	Human ion channel
15	c	392	19.5	1992	22	AAK02861	Human brain expres
16	c	392	19.5	1992	22	AAI02784	Probe #2775 used t
17	c	385	19.2	1194	22	ABA48040	Human breast cell
18	c	385	19.2	1194	22	ABA65925	Human foetal liver
19	c	385	19.2	1194	22	ABA33014	Probe #11480 for g
20	c	385	19.2	1194	22	AAK14344	Human brain expres
21	c	385	19.2	1194	22	AAK40073	Human bone marrow
22	c	385	19.2	1194	22	AAI20854	Probe #10787 for g
23	c	385	19.2	1194	22	AAI46090	Probe #14776 used
24	c	385	19.2	1194	22	AAI06565	Probe #6556 used t
25	c	385	19.2	1194	24	ABS14151	Human genome-deriv
26	c	379	18.9	1178	22	AAK15629	Human brain expres
27	c	379	18.9	1178	22	AAI07805	Probe #7796 used t
28	c	322	16.0	969	22	ABA42912	Human breast cell
29	c	322	16.0	969	22	ABA53333	Human foetal liver
30	c	322	16.0	969	22	ABA23110	Probe #1576 for ge
31	c	322	16.0	969	22	AAK01598	Human brain expres
32	c	322	16.0	969	22	AAK27041	Human bone marrow
33	c	322	16.0	969	22	AAI11641	Probe #1574 for ge
34	c	322	16.0	969	22	AAI32938	Probe #1624 used t
35	c	322	16.0	969	22	AAI01568	Probe #1559 used t
36	c	322	16.0	969	24	ABS01620	Human genome-deriv
37		318	15.8	3403	22	AAH55792	Human SCN1A genomi
38		277	13.8	1456	22	ABA08320	Human Na channel p
39		139	6.9	8349	22	AAH55793	Human adult form o
40		139	6.9	8349	22	AAH55794	Human neonatal for
41		119	5.9	1425	23	AAS84262	DNA encoding novel
42		119	5.9	3700	22	AAH55822	Human SCN2A genomi
43		99	4.9	6822	24	ABK63697	Rat sequence diffe
44		96	4.8	965	22	AAH55777	Human SCN1A genomi
45		94	4.7	606	23	ABV58235	Human prostate exp

ALIGNMENTS

RESULT 1
AAD32844
ID AAD32844 standard; cDNA; 6030 BP.
XX
AC AAD32844;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #6.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..6030

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FT                   /product= "Human ion channel protein #6"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
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PN   WO200214498-A2.
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PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20515.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 2; Page 55-57; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other;

Alignment Scores:
Pred. No.:              0           Length:          6030
Score:                  2007.00     Matches:         2009
Percent Similarity:     100.00%     Conservative:    0
Best Local Similarity:  100.00%     Mismatches:      0
Query Match:            99.90%      Indels:          0
DB:                     24          Gaps:            0

US-09-930-871-12 (1-2009) x AAD32844 (1-6030)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

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Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

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Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

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Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

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Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027

RESULT 2
AAD32845
ID   AAD32845 standard; cDNA; 5922 BP.
XX
AC   AAD32845;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #7.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5922
FT                   /*tag= a
FT                   /product= "Human ion channel protein #7"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20516.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 62-64; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;

Alignment Scores:
Pred. No.:              0           Length:          5922
Score:                  1970.00     Matches:         1972
Percent Similarity:     100.00%     Conservative:    0
Best Local Similarity:  100.00%     Mismatches:      0
Query Match:            98.06%      Indels:          0
DB:                     24          Gaps:            0

US-09-930-871-12 (1-2009) x AAD32845 (1-5922)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
Db   4381 CTTTACTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
          ||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5916

RESULT 3
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AAH55763
ID   AAH55763 standard; cDNA; 8378 BP.
XX
AC   AAH55763;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99674.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 90-93; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:          8378
Score:                  1733.00        Matches:         2006
Percent Similarity:     99.75%         Conservative:    0
Best Local Similarity:  99.75%         Mismatches:      3
Query Match:            86.26%         Indels:          5
DB:                     22             Gaps:            0

US-09-930-871-12 (1-2009) x AAH55763 (1-8378)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385
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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db    386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db    446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db    506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db    566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db    626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db    686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db    746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db    806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db    866 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 925

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db    926 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db    986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db   1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db   1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db   1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db   1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db   1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db   1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db   1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db   1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
Db   2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   2186 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2245

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   2246 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2305

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   2306 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2365

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2366 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2425

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2426 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2485

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Db   2546 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2605

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2606 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2665

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2666 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2725

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2966 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3025

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAsnLe 1000
          |||||||||||||||||||||||||||||||||    |||||||||||||||||||||||
Db   3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACAACCT 3264

Qy   1000 uAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHi 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3265 TGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCA 3324

Qy   1020 sLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleAr 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3325 CAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAG 3384

Qy   1040 gLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSe 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3385 GAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAG 3444

Qy   1060 rCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspValA 1080
          ||||||||||||||||||    |||||||||||||||||||||||||||||||||||||||
Db   3445 TTGTATGTCCAATCATACAGC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAA 3503

Qy   1080 snGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluS 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3504 ATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAA 3563

Qy   1100 erAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValG 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3564 GTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAG 3623

Qy   1120 lyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3624 GAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAG 3683

Qy   1140 luSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3684 AAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCG 3743

Qy   1160 lyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaC 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3744 GCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTT 3803

Qy   1180 ysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3804 GTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCA 3863

Qy   1200 rgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpP 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3864 GAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGT 3923

Qy   1220 heGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspI 1240
          ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db   3924 TTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCG-GCATTTGAAGATA 3982

Qy   1240 leTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3983 TATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCA 4042

Qy   1260 hrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrP 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4043 CTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATT 4102

Qy   1280 heThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuT 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4103 TCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAA 4162

Qy   1300 hrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4163 CAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAG 4222

Qy   1320 laLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaL 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4223 CTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCC 4282

Qy   1340 euLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuI 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4283 TTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAA 4342

Qy   1360 lePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4343 TTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCA 4402

Qy   1380 hrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuI 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4403 CAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAA 4462

Qy   1400 leGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyP 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4463 TAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGAT 4522

Qy   1420 heGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4523 TTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATG 4582

Qy   1440 laAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetT 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4583 CAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGT 4642

Qy   1460 yrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleG 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4643 ATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTG 4702

Qy   1480 lyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheM 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4703 GTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTA 4762
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Qy   1500 etThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProG 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4763 TGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGC 4822

Qy   1520 lnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrA 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4823 AAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCA 4882

Qy   1540 rgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetV 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4883 GACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGG 4942

Qy   1560 alGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValP 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4943 TGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGT 5002

Qy   1580 heIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrP 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5003 TCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATT 5062

Qy   1600 heThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetP 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5063 TTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGT 5122

Qy   1620 heLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgL 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5123 TTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTC 5182

Qy   1640 euAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuL 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5183 TTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGC 5242

Qy   1660 euPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuV 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5243 TCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAG 5302

Qy   1680 alMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValG 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5303 TCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTG 5362

Qy   1700 lyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnI 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5363 GGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAA 5422

Qy   1720 leThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProA 1740
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Db   5423 TTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCG 5482

Qy   1740 spCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProS 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5483 ACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCAT 5542

Qy   1760 erValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnM 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5543 CTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACA 5602

Qy   1780 etTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProL 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5603 TGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTC 5662

Qy   1800 euSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaT 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5663 TGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAA 5722

Qy   1820 hrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuA 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5723 CTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCA 5782

Qy   1840 snLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5783 ATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTG 5842

Qy   1860 spArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerG 1880
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Db   5843 ACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTG 5902

Qy   1880 lyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerL 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5903 GAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCA 5962

Qy   1900 ysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaV 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5963 AGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTG 6022

Qy   1920 alIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerP 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6023 TCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCT 6082

Qy   1940 heThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetI 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6083 TTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGA 6142

Qy   1960 leIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6143 TAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTG 6202

Qy   1980 laAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnG 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6203 CAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAG 6262

Qy   2000 luGlyLysAspGluLysAlaLysGlyLys 2009
          ||||||||||||||||||||||||||||
Db   6263 AAGGCAAAGATGAAAAAGCCAAAGGGAAA 6291
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RESULT 4
AAD27266
ID   AAD27266 standard; cDNA; 6027 BP.
XX
AC   AAD27266;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human transporter and ion channel-13 (TRICH-13) cDNA.
XX
KW   Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW   nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW   antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW   Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW   amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW   Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW   cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW   bradyarrythmia; gene expression; drug screening; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..6027
FT                   /*tag= a
FT                   /product= "Human TRICH-13 protein"
FT                   /note= "CDS does not include stop codon"
FT                   /partial
XX
PN   WO200192304-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US17065.
XX
PR   26-MAY-2000; 2000US-208424P.
PR   01-JUN-2000; 2000US-209001P.
PR   08-JUN-2000; 2000US-210588P.
PR   16-JUN-2000; 2000US-212335P.
PR   22-JUN-2000; 2000US-213747P.
PR   29-JUN-2000; 2000US-215391P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
```

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XX
PI   Thornton M,  Walia NK,  Yue H,  Nguyen DB,  Lai P,  Gandhi AR;
PI   Tribouley CM,  Yao MG,  Ramkumar J,  Au-Young J,  Lu Y,  Tang YT;
PI   Azimzai Y,  Bruns CM,  Griffin JA,  Yang J,  Sanjanwala MS;
PI   Raumann BE,  Lee EA,  Hafalia A,  Baughn MR,  Green BD,  Khan FA;
PI   Kearney L,  Elliot VS,  Seilhamer JJ,  Policky JL,  Borowsky ML;
PI   Burford N,  Ding L,  Lu DAM,  Hillman JL;
XX
DR   WPI; 2002-122055/16.
DR   P-PSDB; AAE16776.
XX
PT   New human transporters and ion channels (TRICH) polypeptides useful for
PT   diagnosing, treating or preventing disorders associated with aberrant
PT   expression of TRICH  -
XX
PS   Claim 11; Page 196-197; 210pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH)
CC   polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC   sequences are useful in the diagnosis, treatment, and prevention of
CC   disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC   palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC   amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC   muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC   asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC   cardiac disease (angina, hypertension, or bradyarrythmia) and in the
CC   assessment of the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of transporters and ion channels.
CC   The polynucleotides may be used to detect and quantify gene expression
CC   in biopsied tissues in which TRICH expression may be correlated with a
CC   disease, to generate hybridization probes for mapping naturally occurring
CC   genomic sequence, and in drug screening. The present sequence is human
CC   TRICH-13 cDNA.
XX
SQ   Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          6027
Score:                    1545.00        Matches:         2004
Percent Similarity:       99.50%         Conservative:    0
Best Local Similarity:    99.50%         Mismatches:      5
Query Match:              76.90%         Indels:          10
DB:                       24             Gaps:            0

US-09-930-871-12 (1-2009) x AAD27266 (1-6027)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLys-ThrPheIleValLeuAsnLysGlyLysAlaIlePh 100
           ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGCA-GACTTTTATAGTATTGAATAAAGGGAAGGCCATCTT 299

Qy     100 eArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIl 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 CCGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAAT 359

Qy     120 eAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuTh 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 AGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGAC 419

Qy     140 rAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrTh 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 AAACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAGTACAC 479

Qy     160 rPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLe 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 CTTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTT 539

Qy     180 uGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPh 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 AGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATT 599

Qy     200 eAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVa 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 TGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGT 659

Qy     220 lLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLe 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 TCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCT 719

Qy     240 uIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVa 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 GATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGT 779

Qy     260 lPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 ATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATG 839

Qy     280 pProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTy 300
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Db     840 GCCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTA 899

Qy     300 rAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAs 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 TAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGA 959

Qy     320 pSerArg-TyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerS 340
           |   ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 TTC-AGGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCT 1018

Qy     340 erAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1019 CTGATGCAGGGCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATT 1078

Qy     360 yrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetT 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1079 ATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGA 1138

Qy     380 hrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrM 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1139 CTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACA 1198

Qy     400 etIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1199 TGATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGG 1258

Qy     420 laValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnL 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1259 CTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGA 1318

Qy     440 ysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnG 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1319 AAGAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGC 1378

Qy     460 lnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuS 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379 AGGCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCT 1438

Qy     480 erAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnA 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439 CAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATC 1498
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Qy    500 rgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluP 520
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Db   1499 GGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAAT 1558

Qy    520 heGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluG 540
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Db   1559 TCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAG 1618

Qy    540 lyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleA 560
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Db   1619 GGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCC 1678

Qy    560 rgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyA 580
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Db   1679 GTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGC 1738

Qy    580 rgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluA 600
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Db   1739 GAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGG 1798

Qy    600 spAsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnS 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1799 ATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACA 1858

Qy    620 erAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyL 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1859 GCAACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGA 1918

Qy    640 ysMetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValP 660
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Db   1919 AGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTC 1978

Qy    660 roThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspA 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1979 CTACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATG 2038

Qy    680 spAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValS 700
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Qy    700 erMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleL 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2099 CCATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTC 2158

Qy    720 euThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrL 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2159 TAACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATA 2218

Qy    740 ysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisV 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2219 AATTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATG 2278

Qy    760 alValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValL 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2279 TTGTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCT 2338

Qy    780 euAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValL 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2339 TAAATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGC 2398

Qy    800 euThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleI 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2399 TTACAGTAGGAAACTTGGTATTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTA 2458

Qy    820 leAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleV 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2459 TTGCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTG 2518

Qy    840 alThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgS 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2519 TGACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTT 2578

Qy    860 erPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuI 880
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2579 CATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAA 2638

Qy    880 leLysIleIleGlyAsnSerVal-GlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIle 899
          |||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db   2639 TAAAGATCATCGGCAATTCCGG-GGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATC 2697

Qy    900 IleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCys 919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2698 ATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGT 2757

Qy    920 ValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHis 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2758 GTCTGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCAC 2817

Qy    940 SerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCys 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2818 TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGT 2877

Qy    960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly 979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2878 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 2937

Qy    980 AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAs 999
          |||||||||||||||||||||||||||||||||||    |||||||||||||||||||||
Db   2938 AACCTAGTGGTACTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACAA 2996

Qy    999 nLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMe 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2997 CCTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGAT 3056

Qy   1019 tHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIl 1039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3057 GCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCAT 3116

Qy   1039 eArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAs 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3117 TAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGA 3176

Qy   1059 pSerCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspV 1079
          ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||||
Db   3177 CAGTTGTATGTCCAATCATACAGC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATG 3235

Qy   1079 alAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspG 1099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3236 TAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATG 3295

Qy   1099 luSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaV 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3296 AAAGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTG 3355

Qy   1119 alGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuG 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3356 TAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGG 3415

Qy   1139 luGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspI 1159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3416 AAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACA 3475

Qy   1159 leGlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluA 1179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3476 TCGGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAG 3535

Qy   1179 laCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3536 CTTGTTTCACTGAAGGTTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAG 3595

Qy   1199 lyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnT 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3596 GCAGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACT 3655

Qy   1219 rpPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluA 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3656 GGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAG 3715

Qy   1239 spIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValP 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3716 ATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTT 3775

Qy   1259 heThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrT 1279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3776 TCACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACAT 3835

Qy   1279 yrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerL 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3836 ATTTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTT 3895

Qy   1299 euThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3896 TAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAA 3955

Qy   1319 rgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnA 1339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3956 GAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTAGTTGTGAATG 4015

Qy   1339 laLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpL 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4016 CCCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGC 4075

Qy   1359 euIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnT 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4076 TAATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACA 4135

Qy   1379 hrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysL 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4136 CCACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAAC 4195

Qy   1399 euIleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4196 TAATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAG 4255

Qy   1419 lyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4256 GATTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGT 4315

Qy   1439 yrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrM 1459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4316 ATGCAGCAGTTGATTCCAGAAATGTAGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACA 4375

Qy   1459 etTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheI 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4376 TGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTA 4435

Qy   1479 leGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIleP 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4436 TTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCT 4495

Qy   1499 heMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysP 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4496 TTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAAC 4555

Qy   1519 roGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4556 CGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAA 4615

Qy   1539 hrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetM 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4616 CCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGA 4675

Qy   1559 etValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuV 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4676 TGGTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGG 4735

Qy   1579 alPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrT 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4736 TGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATT 4795
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Qy   1599 yrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyM 1619
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Db   4796 ATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTA 4855

Qy   1619 etPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleA 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4856 TGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCC 4915

Qy   1639 rgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrL 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4916 GTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGC 4975

Qy   1659 euLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheL 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4976 TGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCC 5035

Qy   1679 euValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluV 1699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5036 TAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAG 5095

Qy   1699 alGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheG 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5096 TTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCC 5155

Qy   1719 lnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProP 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5156 AAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCAC 5215

Qy   1739 roAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnP 1759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5216 CCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACC 5275

Qy   1759 roSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValA 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5276 CATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGA 5335

Qy   1779 snMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluP 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5336 ACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGC 5395

Qy   1799 roLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspA 1819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5396 CTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATG 5455

Qy   1819 laThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProL 1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5456 CAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTC 5515

Qy   1839 euAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5516 TCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTG 5575

Qy   1859 lyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluS 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5576 GTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGA 5635

Qy   1879 erGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProS 1899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5636 GTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTT 5695

Qy   1899 erLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerA 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5696 CCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTG 5755

Qy   1919 laValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaS 1939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5756 CTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTT 5815

Qy   1939 erPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspM 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5816 CCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACA 5875
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Qy   1959 etIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerT 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5876 TGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCA 5935

Qy   1979 hrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluG 1999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5936 CTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGC 5995

Qy   1999 lnGluGlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||||||||
Db   5996 AAGAAGGCAAAGATGAAAAAGCCAAAGGGAAA 6027

RESULT 5
AAH55764
ID   AAH55764 standard; cDNA; 8378 BP.
XX
AC   AAH55764;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99675.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 93-96; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Alignment Scores:
Pred. No.:              0           Length:          8378
Score:                  1447.00     Matches:         2002
Percent Similarity:     99.40%      Conservative:    0
Best Local Similarity:  99.40%      Mismatches:      7

Query Match:            72.03%      Indels:          12
DB:                     22          Gaps:            0

US-09-930-871-12 (1-2009) x AAH55764 (1-8378)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy    201 AlaTyr-ValThrGluPheValAsp-LeuGlyAsnVal-SerAlaLeuArgThrPheArg 219
          |||   ||||||||||||||||   |||||||||   ||||||||||||||||||||||
Db    866 GCGTT-TGTAACAGAATTTGTAAA-CCTAGGCAATTT-TTCAGCTCTTCGCACTTTCAGA 922

Qy    220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    923 GTCTTGAGAGCTTTGAAAACTATTTCGGTAATTCCAGGCCTGAAAACCATTGTGGGAGCC 982

Qy    240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    983 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 1042

Qy    260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 1102

Qy    280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsn 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1103 TGGCCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAAT 1162

Qy    300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 TATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAA 1222

Qy    320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1223 GATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGC 1282
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Qy    340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1283 TCTGATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAAT 1342

Qy    360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1343 TATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATG 1402

Qy    380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1403 ACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTAC 1462

Qy    400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1463 ATGATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTG 1522

Qy    420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1523 GCTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAG 1582

Qy    440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1583 AAAGAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAG 1642

Qy    460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeu 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1643 CAGGCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTC 1702

Qy    480 SerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsn 499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1703 TCAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAAT 1762

Qy    500 ArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGlu 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1763 CGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAA 1822

Qy    520 PheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlu 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1823 TTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAA 1882

Qy    540 GlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIle 559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1883 GGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATC 1942

Qy    560 ArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGly 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1943 CGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGG 2002

Qy    580 ArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGlu 599
          ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db   2003 CGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCC-AGCACCTTTGAG 2061

Qy    600 AspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsn 619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2062 GATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAAC 2121

Qy    620 SerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGly 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2122 AGCAACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGG 2181

Qy    640 LysMetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerVal 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2182 AAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTT 2241

Qy    660 ProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAsp 679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 CCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGAT 2301

Qy    680 AspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisVal 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2302 GACAATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTT 2361

Qy    700 SerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIle 719
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2362 TCCATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATT 2421

Qy    720 LeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyr 739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2422 CTAACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTAT 2481

Qy    740 LysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHis 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2482 AAATTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACAT 2541

Qy    760 ValValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleVal 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2542 GTTGTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTC 2601

Qy    780 LeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnVal 799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2602 TTAAATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTG 2661

Qy    800 LeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIle 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2662 CTTACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATT 2721

Qy    820 IleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIle 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 ATTGCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATT 2781

Qy    840 ValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArg 859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2782 GTGACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGT 2841

Qy    860 SerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeu 879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2842 TCATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTA 2901

Qy    880 IleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIle 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2902 ATAAAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATC 2961

Qy    900 IleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCys 919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2962 ATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGT 3021

Qy    920 ValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHis 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3022 GTCTGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCAC 3081

Qy    940 SerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCys 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3082 TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGT 3141

Qy    960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly 979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3142 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 3201

Qy    980 AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAs 999
          ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db   3202 AACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACAA 3260

Qy    999 nLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMe 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3261 CCTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGAT 3320

Qy   1019 tHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIl 1039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3321 GCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCAT 3380

Qy   1039 eArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAs 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3381 TAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGA 3440

Qy   1059 pSerCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspV 1079
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
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Db   3441 CAGTTGTATGTCCAATCATACAGC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATG 3499

Qy   1079 alAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspG 1099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3500 TAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATG 3559

Qy   1099 luSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaV 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3560 AAAGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTG 3619

Qy   1119 alGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuG 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3620 TAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGG 3679

Qy   1139 luGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspI 1159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3680 AAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACA 3739

Qy   1159 leGlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluA 1179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3740 TCGGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAG 3799

Qy   1179 laCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3800 CTTGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAG 3859

Qy   1199 lyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnT 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3860 GCAGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACT 3919

Qy   1219 rpPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluA 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3920 GGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAG 3979

Qy   1239 spIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValP 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3980 ATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTT 4039

Qy   1259 heThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrT 1279
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db   4040 TCACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAAA-T 4098

Qy   1279 yrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerL 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4099 ATTTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTT 4158

Qy   1299 euThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4159 TAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAA 4218

Qy   1319 rgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnA 1339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4219 GAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATG 4278

Qy   1339 laLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpL 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4279 CCCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGC 4338

Qy   1359 euIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnT 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4339 TAATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACA 4398

Qy   1379 hrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysL 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4399 CCACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAAC 4458

Qy   1399 euIleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValG 1419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4459 TAATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAG 4518

Qy   1419 lyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4519 GATTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGT 4578

Qy   1439 yrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrM 1459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4579 ATGCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACA 4638

Qy   1459 etTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheI 1479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4639 TGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTA 4698

Qy   1479 leGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIleP 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4699 TTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCT 4758

Qy   1499 heMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysP 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4759 TTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAAC 4818

Qy   1519 roGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValT 1539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4819 CGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAA 4878

Qy   1539 hrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetM 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4879 CCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGA 4938

Qy   1559 etValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuV 1579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4939 TGGTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGG 4998

Qy   1579 alPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrT 1599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4999 TGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATT 5058

Qy   1599 yrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyM 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5059 ATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTA 5118

Qy   1619 etPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleA 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5119 TGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCC 5178

Qy   1639 rgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrL 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5179 GTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGC 5238

Qy   1659 euLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheL 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5239 TGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCC 5298

Qy   1679 euValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluV 1699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5299 TAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAG 5358

Qy   1699 alGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheG 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5359 TTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCC 5418

Qy   1719 lnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProP 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5419 AAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCAC 5478

Qy   1739 roAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnP 1759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5479 CCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACC 5538

Qy   1759 roSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValA 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5539 CATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGA 5598

Qy   1779 snMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluP 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5599 ACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGC 5658
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Qy   1799 roLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspA 1819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5659 CTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATG 5718

Qy   1819 laThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProL 1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5719 CAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTC 5778

Qy   1839 euAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5779 TCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTG 5838

Qy   1859 lyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluS 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5839 GTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGA 5898

Qy   1879 erGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProS 1899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5899 GTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTT 5958

Qy   1899 erLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerA 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5959 CCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTG 6018

Qy   1919 laValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaS 1939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6019 CTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTT 6078

Qy   1939 erPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspM 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6079 CCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACA 6138

Qy   1959 etIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerT 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6139 TGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCA 6198

Qy   1979 hrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluG 1999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6199 CTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGC 6258

Qy   1999 lnGluGlyLysAspGluLysAlaLysGlyLys 2009
          ||||||||||||||||||||||||||||||
Db   6259 AAGAAGGCAAAGATGAAAAAGCCAAAGGGAAA 6290
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RESULT 6
AAD32846
ID   AAD32846 standard; cDNA; 4362 BP.
XX
AC   AAD32846;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #8.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4362
FT                   /*tag= a
FT                   /product= "Human ion channel protein #8"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20517.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 69-70; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4362 BP; 1300 A; 845 C; 995 G; 1219 T; 3 other;
```

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Alignment Scores:
Pred. No.:                0              Length:          4362
Score:                    1444.00        Matches:         1446
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              71.88%         Indels:          0
DB:                       24             Gaps:            0

US-09-930-871-12 (1-2009) x AAD32846 (1-4362)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240

Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440

Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsn 1446

Db   4321 GCAGTTGATTCCAGAAAT 4338
```

RESULT 7
AAD32847
ID AAD32847 standard; cDNA; 4179 BP.
XX
AC AAD32847;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #9.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..4179
FT   /*tag= a

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FT                   /product= "Human ion channel protein #9"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20518.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 73-75; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4179 BP; 1239 A; 815 C; 958 G; 1164 T; 3 other;

Alignment Scores:
Pred. No.:              0              Length:          4179
Score:                  1382.00        Matches:         1384
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            68.79%         Indels:          0
DB:                     24             Gaps:            0

US-09-930-871-12 (1-2009) x AAD32847 (1-4179)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
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Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArg 1384
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Db   4141 ACTGGTGACAGG 4152
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RESULT 8
AAD32848
ID   AAD32848 standard; cDNA; 4197 BP.
XX
AC   AAD32848;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #10.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= "Human ion channel protein #10"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20519.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 78-79; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;
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Alignment Scores:
Pred. No.:              0           Length:          4197
Score:                  1332.00     Matches:         1334
Percent Similarity:     100.00%     Conservative:    0
Best Local Similarity:  100.00%     Mismatches:      0
Query Match:            66.30%      Indels:          0
DB:                     24          Gaps:            0

US-09-930-871-12 (1-2009) x AAD32848 (1-4197)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu  80
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

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Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

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Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg 1334
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGG 4002
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RESULT 9
AAD32839
ID AAD32839 standard; cDNA; 5997 BP.
XX
AC AAD32839;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #1.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..5997
FT   /*tag= a
FT   /product= "Human ion channel protein #1"
FT   /transl_except= (pos:2941..2943, aa:Xaa)
FT   /transl_except= (pos:3166..3168, aa:Xaa)
FT   /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;

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XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20510.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 28-30; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5997 BP; 1773 A; 1185 C; 1338 G; 1698 T; 3 other;

Alignment Scores:
Pred. No.:                0          Length:          5997
Score:                    1326.00    Matches:         1992
Percent Similarity:       99.15%     Conservative:    0
Best Local Similarity:    99.15%     Mismatches:      17
Query Match:              66.00%     Indels:          17
DB:                       24         Gaps:            0

US-09-930-871-12 (1-2009) x AAD32839 (1-5997)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
           ||||||||||||
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627
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Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy    1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy    2001 GlyLysAspGluLysAlaLysGlyLys 2009
           |||||||||||||||||||||||||||
Db    5968 GGCAAAGATGAAAAAGCCAAAGGGAAA 5994

RESULT 10
AAD32840
ID   AAD32840 standard; cDNA; 5889 BP.
XX
AC   AAD32840;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5889
FT                   /*tag= a
FT                   /product= "Human ion channel protein #2"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20511.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 35-36; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;

Alignment Scores:
Pred. No.:                0          Length:          5889
Score:                    1289.00    Matches:         1955
Percent Similarity:       99.14%     Conservative:    0
Best Local Similarity:    99.14%     Mismatches:      17
Query Match:              64.16%     Indels:          17
DB:                       24         Gaps:            0

US-09-930-871-12 (1-2009) x AAD32840 (1-5889)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907
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Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db    5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy    1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
Db    5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy    1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
Db    5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy    1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
Db    5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy    1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
Db    5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy    1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
Db    5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy    1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
Db    5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy    1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
Db    5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy    1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
Db    5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy    1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
Db    5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy    1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
Db    5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy    1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db    5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy    1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5883

RESULT 11
ABL39689
ID   ABL39689 standard; cDNA; 8131 BP.
XX
AC   ABL39689;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.
XX
KW   Human; sodium channel; SCN1A; chromosome 2q24; gene; ss;
KW   familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             15..6018
FT                   /*tag= a
FT                   /product= "sodium channel SCN1A"
XX
PN   WO200196552-A1.
XX
PD   20-DEC-2001.
XX
PF   12-JUN-2001; 2001WO-JP04956.
XX
PR   13-JUN-2000; 2000JP-0177540.
PR   13-JUN-2000; 2000JP-0177544.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kanazawa I,  Goto J,  Jeong S;
XX
DR   WPI; 2002-098066/13.
DR   P-PSDB; ABB06026.
XX
PT   Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT   studying physiological mechanism in which excitant cells participate
PT   and causes of diseases and developing drugs for motor endplate disease
PT   -
XX
PS   Claim 5; Page 20-40; 88pp; Japanese.
XX
CC   The present invention describes human sodium channels SCN1A and SCN3A.
CC   The present sequence encodes the human sodium channel SCN1A. SCN1A and
CC   SCN3A have been located to the human chromosome 2 long arm, positions
CC   2q24 and 2q24-31 respectively. The sodium channel proteins are useful
CC   in studying the physiological mechanism in which excitant cells
CC   participate and cause human diseases, and in developing remedies for
CC   e.g. familial hypercalcaemic periodic paralysis of extremities and
CC   motor endplate disease.
XX
SQ   Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other;

Alignment Scores:
Pred. No.:                0              Length:          8131
Score:                    947.00         Matches:         1988
Percent Similarity:       98.61%         Conservative:    0
Best Local Similarity:    98.61%         Mismatches:      21
Query Match:              47.14%         Indels:          28
DB:                       24             Gaps:            0

US-09-930-871-12 (1-2009) x ABL39689 (1-8131)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
Db      19 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 78

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db      79 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 138

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db     139 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 198

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db     199 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 258

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db     259 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 318

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db     319 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 378

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db     379 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 438
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Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    439 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 498

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 558

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 618

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 798

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 858

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 918

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 978

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    979 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1038

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1098

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db   1099 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTCTGTCCTTGTTTCGACTAATGACT 1158

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1218

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1278

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1338

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1398

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1458

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1518

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1578

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1638

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1698

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGT 1758

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1818

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1878

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1938

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1998

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||
Db   1999 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2026

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2027 GG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2085

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2145

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2205

Qy    741 PheSerAsnIlePheLeu-IleTrpAspCysSerProTyrTrpLeuLysValLysHisVa 760
          |||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db   2206 TTTTCCAACATATT-CTCAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGT 2264

Qy    760 lValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLe 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2265 TGTCAACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTT 2324

Qy    780 uAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLe 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2325 AAATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCT 2384

Qy    800 uThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIl 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2385 TACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTAT 2444

Qy    820 eAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2445 TGCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGT 2504

Qy    840 lThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSe 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2505 GACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTC 2564

Qy    860 rPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIl 880
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Db   2565 ATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAAT 2624

Qy    880 eLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIl 900

Db   2625 AAAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCAT 2684

Qy    900 eValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVa 920

Db   2685 CGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGT 2744

Qy    920 lCysLysIleAlaSerAspCysGlnLeuPro---ArgTrpHisMetAsnAspPhePheHi 939

Db   2745 CTGCAAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCA 2804

Qy    939 sSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCy 959

Db   2805 CTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTG 2864

Qy    959 sMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGl 979

Db   2865 TATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGG 2924

Qy    979 yAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspA 999

Db   2925 AAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACA 2983

Qy    999 snLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgM 1019

Db   2984 ACCTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGA 3043

Qy   1019 etHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheI 1039

Db   3044 TGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCA 3103

Qy   1039 leArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysA 1059

Db   3104 TTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAG 3163

Qy   1059 spSerCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAsp 1078

Db   3164 ACAGTTGTATGTCCAATCATACAAC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGAT 3222

Qy   1079 ValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAsp 1098

Db   3223 GTAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGAT 3282

Qy   1099 GluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAla 1118

Db   3283 GAAAGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCT 3342

Qy   1119 ValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeu 1138

Db   3343 GTAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTG 3402

Qy   1139 GluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrVal-As 1158

Db   3403 GAAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGGA 3462

Qy   1158 pIleGlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGl 1178

Db   3463 CATCGGCGC-CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGA 3521

Qy   1178 uAlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGl 1198

Db   3522 AGCTTGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGA 3581

Qy   1198 uGlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAs 1218

Db   3582 AGGCAGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAA 3641

Qy   1218 nTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGl 1238

Db   3642 CTGGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGA 3701

Qy   1238 uAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysVa 1258

Db   3702 AGATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGT 3761

Qy   1258 lPheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnTh 1278

Db   3762 TTTCACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAAC 3821

Qy   1278 rTyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSe 1298

Db   3822 ATATTTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAG 3881

Qy   1298 rLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLe 1318

Db   3882 TTTAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACT 3941

Qy   1318 uArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAs 1338

Db   3942 AAGAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAA 4001

Qy   1338 nAlaLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTr 1358

Db   4002 TGCCCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTG 4061

Qy   1358 pLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAs 1378

Db   4062 GCTAATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAA 4121

Qy   1378 nThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLy 1398

Db   4122 CACCACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAA 4181

Qy   1398 sLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnVa 1418

Db   4182 ACTAATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGT 4241

Qy   1418 lGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMe 1438

Db   4242 AGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAAT 4301

Qy   1438 tTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTy 1458

Db   4302 GTATGCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTA 4361

Qy   1458 rMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPh 1478

Db   4362 CATGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTT 4421

Qy   1478 eIleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIl 1498

Db   4422 TATTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACAT 4481

Qy   1498 ePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLy 1518

Db   4482 CTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAA 4541

Qy   1518 sProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVa 1538

Db   4542 ACCGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGT 4601

Qy   1538 lThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMe 1558

Db   4602 AACCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAAT 4661

Qy   1558 tMetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLe 1578

Db   4662 GATGGTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCT 4721

Qy   1578 uValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTy 1598

Db   4722 GGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTA 4781
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Qy   1598 rTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGl 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4782 TTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGG 4841

Qy   1618 yMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIl 1638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4842 TATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGAT 4901

Qy   1638 eArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgTh 1658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4902 CCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCAC 4961

Qy   1658 rLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPh 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4962 GCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTT 5021

Qy   1678 eLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGl 1698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5022 CCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGA 5081

Qy   1698 uValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPh 1718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5082 AGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATT 5141

Qy   1718 eGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysPr 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5142 CCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCC 5201

Qy   1738 oProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAs 1758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5202 ACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAA 5261

Qy   1758 nProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValVa 1778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5262 CCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGT 5321

Qy   1778 lAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGl 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5322 GAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGA 5381

Qy   1798 uProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAs 1818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5382 GCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGA 5441

Qy   1818 pAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProPr 1838
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Db   5442 TGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCC 5501

Qy   1838 oLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSe 1858
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5502 TCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAG 5561

Qy   1858 rGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGl 1878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5562 TGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGA 5621

Qy   1878 uSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnPr 1898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5622 GAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCC 5681

Qy   1898 oSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSe 1918
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5682 TTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATC 5741

Qy   1918 rAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAl 1938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5742 TGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGC 5801

Qy   1938 aSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAs 1958
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5802 TTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGA 5861

Qy   1958 pMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSe 1978
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5862 CATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTC 5921

Qy   1978 rThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGl 1998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5922 CACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGA 5981

Qy   1998 uGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
          ||||||||||||||||||||||||||||||||
Db   5982 GCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAA 6015
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RESULT 12
AAD32841
ID AAD32841 standard; cDNA; 4329 BP.
XX
AC AAD32841;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #3.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4329
FT /*tag= a
FT /product= "Human ion channel protein #3"
FT /transl_except= (pos:2941..2943, aa:Xaa)
FT /transl_except= (pos:3166..3168, aa:Xaa)
FT /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20512.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders
XX
PS Claim 1; Page 41-42; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are

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CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4329 BP; 1287 A; 840 C; 988 G; 1211 T; 3 other;

Alignment Scores:
Pred. No.:                0              Length:          4329
Score:                    763.00         Matches:         1429
Percent Similarity:       98.82%         Conservative:    0
Best Local Similarity:    98.82%         Mismatches:      17
Query Match:              37.98%         Indels:          17
DB:                       24             Gaps:            0

US-09-930-871-12 (1-2009) x AAD32841 (1-4329)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Db    3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy    1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db    4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy    1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db    4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy    1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db    4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy    1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db    4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy    1441 AlaValAspSerArgAsn 1446
           |||||||||||||||||
Db    4288 GCAGTTGATTCCAGAAAT 4305
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RESULT 13
AAD32842

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ID   AAD32842 standard; cDNA; 4146 BP.
XX
AC   AAD32842;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #4.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4146
FT                   /*tag= a
FT                   /product= "Human ion channel protein #4"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20513.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 46-47; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;
```

Alignment Scores:

Pred. No.:	0	Length:	4146
Score:	701.00	Matches:	1367
Percent Similarity:	98.77%	Conservative:	0
Best Local Similarity:	98.77%	Mismatches:	17
Query Match:	34.89%	Indels:	17
DB:	24	Gaps:	0

US-09-930-871-12 (1-2009) x AAD32842 (1-4146)

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Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787
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Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
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Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

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Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArg 1384
          ||||||||||||
Db   4108 ACTGGTGACAGG 4119
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RESULT 14
AAD32843
ID AAD32843 standard; cDNA; 4164 BP.
XX
AC AAD32843;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #5.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4164
FT /*tag= a
FT /product= "Human ion channel protein #5"
FT /transl_except= (pos:2941..2943, aa:Xaa)
FT /transl_except= (pos:3166..3168, aa:Xaa)
FT /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20514.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders
XX
PS Claim 1; Page 51-52; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in

CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4164 BP; 1219 A; 816 C; 958 G; 1168 T; 3 other;

Alignment Scores:

Pred. No.:	0	Length:	4164
Score:	670.00	Matches:	1317
Percent Similarity:	98.73%	Conservative:	0
Best Local Similarity:	98.73%	Mismatches:	17
Query Match:	33.35%	Indels:	17
DB:	24	Gaps:	0

US-09-930-871-12 (1-2009) x AAD32843 (1-4164)

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Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg 1334
          ||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGG 3969

RESULT 15
AAK02861/c
ID   AAK02861 standard; DNA; 1992 BP.
XX
AC   AAK02861;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 2852.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 2852; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 1992 BP; 589 A; 399 C; 384 G; 620 T; 0 other;

Alignment Scores:
Pred. No.:                0             Length:          1992
Score:                    392.00        Matches:         392
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              19.51%        Indels:          0
DB:                       22            Gaps:            0

US-09-930-871-12 (1-2009) x AAK02861 (1-1992)

Qy   1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgVal 1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1445 GGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTG 1386

Qy   1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1385 ATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGC 1326

Qy   1658 ThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeu 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1325 ACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTC 1266

Qy   1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArg 1697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGG 1206

Qy   1698 GluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeu 1717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTA 1146

Qy   1718 PheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLys 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAG 1086

Qy   1738 ProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGly 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 CCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGG 1026

Qy   1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 AACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTG 966

Qy   1778 ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 GTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA 906

Qy   1798 GluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspPro 1817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 GAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCC 846

Qy   1818 AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluPro 1837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 GATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCG 786

Qy   1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 CCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTG 726

Qy   1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 AGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGA 666

Qy   1878 GluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 GAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAAT 606

Qy   1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluVal 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 CCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTA 546

Qy   1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937
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Qy   1938 AlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGlu 1957
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Db    485 GCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAA 426

Qy   1958 AspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMet 1977
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Qy   1978 SerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHis 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1998 GluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
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Db    305 GAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAA 270
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Search completed: April 23, 2003, 05:07:08
Job time : 909 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 14:05:09 ; Search time 127 Seconds
(without alignments)
14561.109 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	104	1.7	930	3	US-08-605-284B-1	Sequence 1, Appli
	2	104	1.7	930	3	US-08-605-284B-2	Sequence 2, Appli
	3	104	1.7	930	3	US-08-605-284B-21	Sequence 21, Appl
	4	79	1.3	6371	3	US-08-836-325-13	Sequence 13, Appl
	5	79	1.3	6404	3	US-08-836-325-14	Sequence 14, Appl
	6	53	0.9	930	3	US-08-605-284B-3	Sequence 3, Appli
	7	44	0.7	3033	3	US-08-836-325-1	Sequence 1, Appli
	8	44	0.7	6452	3	US-08-836-325-9	Sequence 9, Appli
	9	29	0.5	5977	3	US-09-024-020B-1	Sequence 1, Appli
	10	29	0.5	5977	4	US-09-425-043-1	Sequence 1, Appli
	11	29	0.5	6007	3	US-09-024-020B-2	Sequence 2, Appli
	12	29	0.5	6007	4	US-09-425-043-2	Sequence 2, Appli
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	15	29	0.5	6586	3	US-09-024-020B-43	Sequence 43, Appl
	16	29	0.5	6586	4	US-09-425-043-43	Sequence 43, Appl
	17	29	0.5	6826	3	US-09-024-020B-8	Sequence 8, Appli
	18	29	0.5	6826	4	US-09-425-043-8	Sequence 8, Appli
	19	26	0.4	6048	4	US-09-634-920-3	Sequence 3, Appli
	20	26	0.4	6315	2	US-08-808-793-2	Sequence 2, Appli
	21	26	0.4	6315	3	US-08-772-512A-2	Sequence 2, Appli
	22	26	0.4	6318	2	US-08-808-793-1	Sequence 1, Appli
	23	26	0.4	6318	3	US-08-772-512A-1	Sequence 1, Appli
	24	22	0.4	696	3	US-09-024-020B-5	Sequence 5, Appli
	25	22	0.4	696	4	US-09-425-043-5	Sequence 5, Appli
	26	20	0.3	702	4	US-08-843-417-3	Sequence 3, Appli
	27	20	0.3	2508	1	US-07-959-943-10	Sequence 10, Appl
	28	20	0.3	2573	4	US-08-669-656A-3	Sequence 3, Appli
	29	20	0.3	6344	4	US-08-843-417-1	Sequence 1, Appli
	30	20	0.3	6524	4	US-08-669-656A-1	Sequence 1, Appli
	31	20	0.3	6527	4	US-08-669-656A-7	Sequence 7, Appli
	32	20	0.3	7052	4	US-08-669-656A-5	Sequence 5, Appli
c	33	19	0.3	944	2	US-08-786-606-4	Sequence 4, Appli
c	34	19	0.3	987	6	5240847-19	Patent No. 5240847
c	35	19	0.3	1032	6	5240847-25	Patent No. 5240847
c	36	19	0.3	1112	2	US-08-933-750C-97	Sequence 97, Appl
c	37	19	0.3	1112	3	US-09-234-613-97	Sequence 97, Appl
c	38	19	0.3	1120	1	US-08-188-582-8	Sequence 8, Appli
c	39	19	0.3	1120	1	US-08-646-715-8	Sequence 8, Appli
c	40	19	0.3	1314	4	US-09-134-001C-1070	Sequence 1070, Ap
	41	19	0.3	5874	4	US-08-843-417-9	Sequence 9, Appli
c	42	19	0.3	8252	1	US-08-046-585-15	Sequence 15, Appl
c	43	19	0.3	8252	1	US-08-393-703-15	Sequence 15, Appl
c	44	19	0.3	8252	5	PCT-US93-11721-15	Sequence 15, Appl
	45	18	0.3	189	1	US-08-248-474-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1
US-08-605-284B-1
; Sequence 1, Application US/08605284B
; Patent No. 6060271
; GENERAL INFORMATION:
; APPLICANT: WALEWSKI, JOSE L.
; APPLICANT: RECIO-PINTO, ESPERANZA
; TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
; TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,284B
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 930 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-605-284B-1

Query Match 1.7%; Score 104; DB 3; Length 930;
Best Local Similarity 100.0%; Pred. No. 1.1e-39;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4924 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4983
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Db 487 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 546

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Qy   4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 5027
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Db    547 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 590


RESULT 2
US-08-605-284B-2
; Sequence 2, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-605-284B-2

  Query Match             1.7%;  Score 104;  DB 3;  Length 930;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-39;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4924 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4983
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Db    487 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 546

Qy   4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 5027
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Db    547 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 590


RESULT 3
US-08-605-284B-21
; Sequence 21, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-605-284B-21

  Query Match             1.7%;  Score 104;  DB 3;  Length 930;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-39;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    487 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 546

Qy   4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 5027
          ||||||||||||||||||||||||||||||||||||||||||||
Db    547 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 590


RESULT 4
US-08-836-325-13
; Sequence 13, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Usin
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6371 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  DNA (genomic)
US-08-836-325-13

  Query Match             1.3%;  Score 79;  DB 3;  Length 6371;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-28;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy   5009 TGTTTAACATCGGCCTCCT 5027
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Db   4946 TGTTTAACATCGGCCTCCT 4964


RESULT 5
US-08-836-325-14
; Sequence 14, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;     APPLICANT:  Mandel, Gail
;     APPLICANT:  Halegoua, Simon
;     APPLICANT:  Borden, Laurence A.
;     TITLE OF INVENTION:  Peripheral Nervous System Specific
;     TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;     TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;     TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;     TITLE OF INVENTION:  Thereof
;     NUMBER OF SEQUENCES:  19
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;       STREET:  1100 New York Ave., N. W., Suite 600
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20005-3934
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/836,325
;       FILING DATE:  2-MAY-1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/14251
;       FILING DATE:  02-NOV-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/482,401
;       FILING DATE:  07-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/334,029
;       FILING DATE:  02-NOV-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ludwig, Steven R.
;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6404 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  DNA (genomic)
US-08-836-325-14

  Query Match             1.3%;  Score 79;  DB 3;  Length 6404;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-28;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   4919 TCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGT 4978

Qy   5009 TGTTTAACATCGGCCTCCT 5027
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Db   4979 TGTTTAACATCGGCCTCCT 4997


RESULT 6
US-08-605-284B-3
; Sequence 3, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;     APPLICANT:  WALEWSKI, JOSE L.
;     APPLICANT:  RECIO-PINTO, ESPERANZA
;     TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;     TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;       STREET:  CLINTON SQUARE, P.O. BOX 1051
;       CITY:  ROCHESTER
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  14603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/605,284B
;       FILING DATE:  09-FEB-1996
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BRAMAN, SUSAN J.
;       REGISTRATION NUMBER:  34,103
;       REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  716-263-1636
;       TELEFAX:  716-263-1600
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  930 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-605-284B-3
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  Query Match             0.9%;  Score 53;  DB 3;  Length 930;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-15;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCT 590


RESULT 7
US-08-836-325-1
; Sequence 1, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3033 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..3033
US-08-836-325-1

  Query Match             0.7%;  Score 44;  DB 3;  Length 3033;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4492 ATCTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAA 4535
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Db   1549 ATCTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAA 1592


RESULT 8
US-08-836-325-9
; Sequence 9, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Usin
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6452 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  326..6277
US-08-836-325-9

  Query Match             0.7%;  Score 44;  DB 3;  Length 6452;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   44;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4492 ATCTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAA 4535
          ||||||||||||||||||||||||||||||||||||||||||||
Db   4733 ATCTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAA 4776


RESULT 9
US-09-024-020B-1
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; Sequence 1, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
;   APPLICANT: DELGADO, STEPHEN G.
;   APPLICANT: DIETRICH, PAUL S.
;   APPLICANT: FISH, LINDA M.
;   APPLICANT: HERMAN, RONALD C.
;   APPLICANT: SANGAMESWARAN, LAKSHMI
;   TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
;   TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: JANET PAULINE CLARK
;     STREET: 3401 HILLVIEW AVENUE, MS A2-250
;     CITY: PALO ALTO
;     STATE: CA
;     COUNTRY: U.S.A.
;     ZIP: 94304-1397
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/024,020B
;     FILING DATE: 16-FEB-1998
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/039,447
;     FILING DATE: 26-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: CLARK, JANET P.
;     REGISTRATION NUMBER: 34,799
;     REFERENCE/DOCKET NUMBER: R0020B-REG
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (650) 852-3097
;     TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5977 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-024-020B-1

  Query Match             0.5%;  Score 29;  DB 3;  Length 5977;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           |||||||||||||||||||||||||||||
Db     643 ACAGAGTTTGTGGACCTGGGCAATGTCTC 671


RESULT 10
US-09-425-043-1
; Sequence 1, Application US/09425043
; Patent No. 6335172
; GENERAL INFORMATION:
;   APPLICANT: DELGADO, STEPHEN G.
;   APPLICANT: DIETRICH, PAUL S.
;   APPLICANT: FISH, LINDA M.
;   APPLICANT: HERMAN, RONALD C.
;   APPLICANT: SANGAMESWARAN, LAKSHMI
;   TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
;   TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: JANET PAULINE CLARK
;     STREET: 3401 HILLVIEW AVENUE, MS A2-250
;     CITY: PALO ALTO
;     STATE: CA
;     COUNTRY: U.S.A.
;     ZIP: 94304-1397
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/425,043
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 09/024,020
;     FILING DATE: 16-FEB-1998
;     APPLICATION NUMBER: US 60/039,447
;     FILING DATE: 26-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: CLARK, JANET P.
;     REGISTRATION NUMBER: 34,799
;     REFERENCE/DOCKET NUMBER: R0020B-REG
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (650) 852-3097
;     TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 5977 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-425-043-1

  Query Match             0.5%;  Score 29;  DB 4;  Length 5977;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           |||||||||||||||||||||||||||||
Db     643 ACAGAGTTTGTGGACCTGGGCAATGTCTC 671


RESULT 11
US-09-024-020B-2
; Sequence 2, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
;   APPLICANT: DELGADO, STEPHEN G.
;   APPLICANT: DIETRICH, PAUL S.
;   APPLICANT: FISH, LINDA M.
;   APPLICANT: HERMAN, RONALD C.
;   APPLICANT: SANGAMESWARAN, LAKSHMI
;   TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
;   TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: JANET PAULINE CLARK
;     STREET: 3401 HILLVIEW AVENUE, MS A2-250
;     CITY: PALO ALTO
;     STATE: CA
;     COUNTRY: U.S.A.
;     ZIP: 94304-1397
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/024,020B
;     FILING DATE: 16-FEB-1998
;     CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 60/039,447
;     FILING DATE: 26-FEB-1997
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-2

  Query Match             0.5%;  Score 29;  DB 3;  Length 6007;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           |||||||||||||||||||||||||||||
Db     643 ACAGAGTTTGTGGACCTGGGCAATGTCTC 671


RESULT 12
US-09-425-043-2
; Sequence 2, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-2

  Query Match             0.5%;  Score 29;  DB 4;  Length 6007;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           |||||||||||||||||||||||||||||
Db     643 ACAGAGTTTGTGGACCTGGGCAATGTCTC 671


RESULT 13
US-09-024-020B-7
; Sequence 7, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-7

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  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
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Db     790 ACAGAGTTTGTGGACCTGGGCAATGTCTC 818


RESULT 14
US-09-425-043-7
; Sequence 7, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-7

  Query Match             0.5%;  Score 29;  DB 4;  Length 6556;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           ||||||||||||||||||||||||||||||
Db     790 ACAGAGTTTGTGGACCTGGGCAATGTCTC 818


RESULT 15
US-09-024-020B-43
; Sequence 43, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6586 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-43

  Query Match             0.5%;  Score 29;  DB 3;  Length 6586;
  Best Local Similarity   100.0%;  Pred. No. 0.00063;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     610 ACAGAGTTTGTGGACCTGGGCAATGTCTC 638
           ||||||||||||||||||||||||||||||
Db     790 ACAGAGTTTGTGGACCTGGGCAATGTCTC 818


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Job time : 178 secs
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 17:24:10 ; Search time 379 Seconds
(without alignments)
17312.444 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 709820 seqs, 544064369 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	6030	100.0	6030	10	US-09-930-871-11	Sequence 11, Appl
	2	5917	98.1	5922	10	US-09-930-871-13	Sequence 13, Appl
	3	4338	71.9	4362	10	US-09-930-871-15	Sequence 15, Appl
	4	4152	68.9	4179	10	US-09-930-871-17	Sequence 17, Appl
	5	4003	66.4	4197	10	US-09-930-871-19	Sequence 19, Appl
	6	3987	66.1	5997	10	US-09-930-871-1	Sequence 1, Appli
	7	3874	64.2	5889	10	US-09-930-871-3	Sequence 3, Appli
	8	2295	38.1	4329	10	US-09-930-871-5	Sequence 5, Appli
	9	2109	35.0	4146	10	US-09-930-871-7	Sequence 7, Appli
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c	12	1157	19.2	1194	10	US-09-864-761-18334	Sequence 18334, A
c	13	1141	18.9	1178	10	US-09-864-761-26829	Sequence 26829, A
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	15	268	4.4	347	10	US-09-864-761-31970	Sequence 31970, A
	16	264	4.4	490	10	US-09-864-761-10615	Sequence 10615, A
	17	262	4.3	487	10	US-09-864-761-15573	Sequence 15573, A
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	20	249	4.1	249	10	US-09-864-761-32083	Sequence 32083, A
	21	243	4.0	249	10	US-09-864-761-27066	Sequence 27066, A
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	24	138	2.3	473	10	US-09-864-761-13959	Sequence 13959, A
	25	114	1.9	142	10	US-09-864-761-20706	Sequence 20706, A
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	45	19	0.3	335	9	US-09-902-941-372	Sequence 372, App

ALIGNMENTS

RESULT 1
US-09-930-871-11
; Sequence 11, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-11

Query Match 100.0%; Score 6030; DB 10; Length 6030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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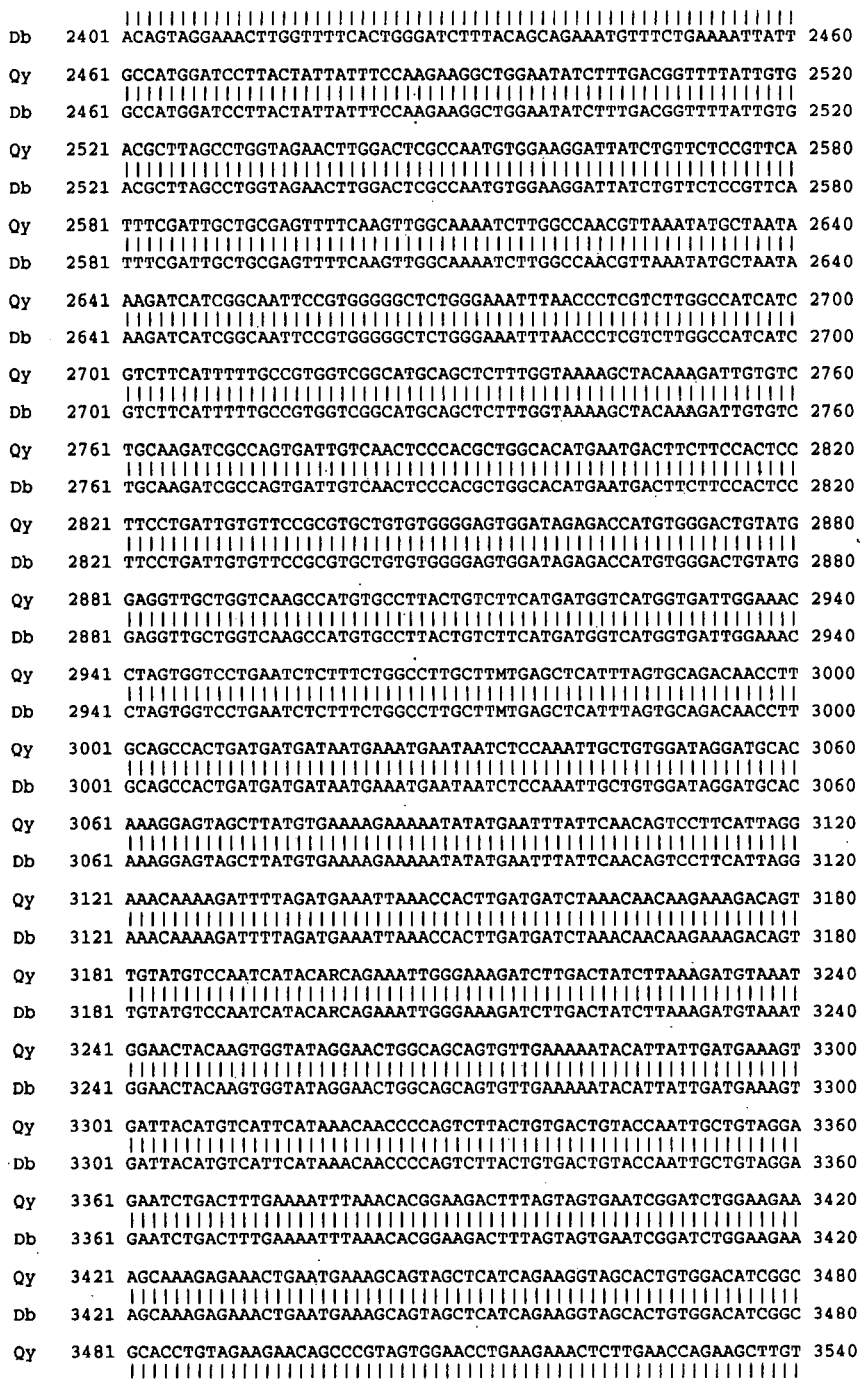
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Db 3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Qy 4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db 4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Qy 4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Db 4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Qy 4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Db 4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Qy 4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Db 4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Qy 4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Db 4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Qy 4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Db 4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Qy 4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Db 4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Qy 4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Db 4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Qy 4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
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Qy 4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Db 4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
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Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
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Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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RESULT 2
US-09-930-871-13
; Sequence 13, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucle
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5922
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-13

Query Match 98.1%; Score 5917; DB 10; Length 5922;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

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Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

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Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

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Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

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Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
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Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

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Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

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Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917

Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
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RESULT 3
US-09-930-871-15
; Sequence 15, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 4362
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-15

Query Match 71.9%; Score 4338; DB 10; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

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Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

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Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
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Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAAT 4338
          |||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAAT 4338


RESULT 4
US-09-930-871-17
; Sequence 17, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 4179
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-17

  Query Match             68.9%;  Score 4152;  DB 10;  Length 4179;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
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Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGG 4152
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Db   4141 ACTGGTGACAGG 4152
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RESULT 5
US-09-930-871-19
; Sequence 19, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19

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;   LENGTH: 4197
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-19

  Query Match             66.4%;  Score 4003;  DB 10;  Length 4197;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4003;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

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Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

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Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

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Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

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Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

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Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGG 4003

Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGG 4003
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RESULT 6
US-09-930-871-1
; Sequence 1, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989

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;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5997
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-1

  Query Match             66.1%;  Score 3987;  DB 10;  Length 5997;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
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Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
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Db   2071 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2130

Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
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Db   2131 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2190

Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
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Db   2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
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Db   2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
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Db   2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
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Db   2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430

Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
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Db   2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
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Db   2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Db   2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
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Db   2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
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Db   2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730

Qy   2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
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Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
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Db   2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850

Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
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Db   2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910

Qy   2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970

Qy   3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030

Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
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Db   3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090

Qy   3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150

Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210

Qy   3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270

Qy   3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
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Db   3271 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3330

Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
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Db   3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390

Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
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Db   3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510

Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
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Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

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Db   3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630

Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
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Db   3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690

Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
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Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
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Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
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Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990

Qy   4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
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Qy   5284 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5343

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RESULT 7
US-09-930-871-3
; Sequence 3, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
;  TITLE OF INVENTION:  Same
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;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 5889
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-3

  Query Match           64.2%;  Score 3874;  DB 10;  Length 5889;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3874;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
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Db   2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430

Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730

Qy   2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850

Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910

Qy   2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970

Qy   3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030

Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
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Db   3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090

Qy   3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150

Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210

Qy   3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270

Qy   3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3271 TACATGTCATTCATAAACAACCCCAGTCTTAGTGTGACTGTACCAATTGCTGTAGGAGAA 3330

Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
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Db   3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390

Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
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Db   3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450

Qy   3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510

Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

Qy   3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630

Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690

Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
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Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
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Db   3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870

Qy   3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
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Qy    4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy    4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
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Db    4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110

Qy    4144 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4203
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4111 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4170

Qy    4204 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4263
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4171 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4230

Qy    4264 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4323
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4231 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4290

Qy    4324 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4291 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4350

Qy    4384 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4443
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Db    4351 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4410

Qy    4444 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4411 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4470

Qy    4504 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4563
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Db    4471 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4530

Qy    4564 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4531 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4590

Qy    4624 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4683
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Db    4591 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4650

Qy    4684 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4743
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Db    4651 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4710

Qy    4744 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4803
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4711 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4770

Qy    4804 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4771 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4830

Qy    4864 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4923
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Db    4831 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4890

Qy    4924 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4891 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4950

Qy    4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5043
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Db    4951 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5010

Qy    5044 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5011 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5070

Qy    5104 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5071 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5130

Qy    5164 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5223
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Db    5131 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5190

Qy    5224 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5191 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5250

Qy    5284 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5251 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5310

Qy    5344 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5311 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5370

Qy    5404 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5371 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5430

Qy    5464 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5431 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5490

Qy    5524 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5491 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5550

Qy    5584 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5643
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Db    5551 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5610

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Qy    5704 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5763
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Db    5671 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5730

Qy    5764 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5731 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5790

Qy    5824 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5791 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5850

Qy    5884 GACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
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Db    5851 GACAGAATAAATGAAAACTCTATTACAGAAAAAA 5884


RESULT 8
US-09-930-871-5
; Sequence 5, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
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;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;    LENGTH: 4329
;    TYPE: DNA
;    ORGANISM: homo sapiens
US-09-930-871-5

  Query Match             38.1%;  Score 2295;  DB 10;  Length 4329;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2295;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
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Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
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Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2190

Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
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Db   2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
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Db   2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430

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Db   2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
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Db   2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730

Qy   2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850

Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910

Qy   2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
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Db   2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970

Qy   3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030

Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
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Db   3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090

Qy   3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150

Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
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Db   3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210

Qy   3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270

Qy   3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3271 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3330

Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390

Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450

Qy   3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510

Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

Qy   3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630

Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690

Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870

Qy   3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990

Qy   4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
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Db   3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy   4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143

Db   4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110

Qy   4144 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4203

Db   4111 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4170

Qy   4204 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4263

Db   4171 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4230

Qy   4264 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4323

Db   4231 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4290

Qy   4324 GTTGATTCCAGAAAT 4338

Db   4291 GTTGATTCCAGAAAT 4305


RESULT 9
US-09-930-871-7
; Sequence 7, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 4146
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-7

  Query Match             35.0%;  Score 2109;  DB 10;  Length 4146;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103

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Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163

Db   2071 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2130

Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223

Db   2131 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2190

Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283

Db   2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343

Db   2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403

Db   2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463

Db   2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430

Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523

Db   2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583

Db   2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643

Db   2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703

Db   2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763

Db   2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730

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Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883

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Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943

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Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423

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Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483

Db   3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450
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Qy   3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510

Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

Qy   3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630

Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690

Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870

Qy   3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
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Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990

Qy   4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy   4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110

Qy   4144 GGTGACAGG 4152
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Db   4111 GGTGACAGG 4119
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RESULT 10
US-09-930-871-9
; Sequence 9, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 4164
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-9
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  Query Match             33.3%;  Score 2011;  DB 10;  Length 4164;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2011;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
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Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGG 2011
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Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGG 2011


RESULT 11
US-09-864-761-10189/c
; Sequence 10189, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10189
;   LENGTH: 1992
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-10189

  Query Match           19.6%;  Score 1181;  DB 10;  Length 1992;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    4850 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 4909
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Db    1447 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 1388

Qy    4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 1328

Qy    4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
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Db    1327 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 1268
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Qy   5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
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Db   1267 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 1208

Qy   5090 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 5149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 1148

Qy   5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
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Db   1147 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 1088

Qy   5210 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 5269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 1028

Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 968

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 908

Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
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Db    907 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 848

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 788

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 728

Qy   5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 668

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 608

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
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Db    607 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 548

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Db    547 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 488

Qy   5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
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Db    487 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 428

Qy   5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 368

Qy   5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
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Db    367 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 308

Qy   5990 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db    307 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 267


RESULT 12
US-09-864-761-18334/c
; Sequence 18334, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18334
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
;   OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
US-09-864-761-18334

 Query Match             19.2%;  Score 1157;  DB 10;  Length 1194;
 Best Local Similarity   100.0%;  Pred. No. 0;
 Matches 1157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy   4850 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 4909
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Db   1157 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 1098

Qy   4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
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Db   1097 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 1038

Qy   4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
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Db   1037 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 978

Qy   5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
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Db    977 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 918

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Db    917 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 858

Qy   5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
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Db    857 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 798

Qy   5210 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 5269
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Db    797 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 738

Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
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Db    737 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 678

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
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Db    677 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 618

Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
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Db    617 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 558

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
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Db    557 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 498

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
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Db    497 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 438

Qy   5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
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Db    437 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 378

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
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Db    377 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 318

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
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Db    317 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 258

Qy   5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
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Db    257 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 198

Qy   5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
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Db    197 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 138

Qy   5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
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Db    137 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 78

Qy   5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
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Db     77 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 18

Qy   5990 ATGAGCAAGAAGGCAAA 6006
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Db     17 ATGAGCAAGAAGGCAAA 1
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RESULT 13
US-09-864-761-26829/c
; Sequence 26829, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26829
; LENGTH: 1178
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010127.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
; OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
US-09-864-761-26829

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Db   1141 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 1082

Qy   4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
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Db   1081 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 1022

Qy   4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 962

Qy   5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
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Db    961 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 902

Qy   5090 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 5149
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Qy   5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
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Db    841 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 782

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Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 662

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
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Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
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Db    601 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 542

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
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Db    541 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 482

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
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Db    421 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 362

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
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Db    361 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 302

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
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Db    241 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 182

Qy   5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
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Db    181 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 122

Qy   5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
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Db    121 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 62

Qy   5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
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RESULT 14
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; Sequence 1576, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1576
;   LENGTH: 969
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
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;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
US-09-864-761-1576

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  Matches  969;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    789 CATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGT 730

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Qy   5436 GGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGC 5495
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Db    489 AGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCAT 430

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Qy   5976 AATTGTGGA 5984
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; Sequence 31970, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
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;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31970
;   LENGTH: 347
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL =   5
;   OTHER INFORMATION: EST_HUMAN HIT: AA912739.1, EVALUE 1.00e-119
;   OTHER INFORMATION: NT HIT: M22253.1, EVALUE 1.00e-103
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US-09-864-761-31970
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Qy   3215 ATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTG 3274
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GenCore version 5.1.4_p5_4578
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10393	100.0	6030	6	AX391140	AX391140 Sequence
2	10367	99.7	8378	6	AX164171	AX164171 Sequence
3	10321.5	99.3	6046	9	AY043484	AY043484 Homo sapi
4	10321	99.3	8378	6	AX164172	AX164172 Sequence
5	10320.5	99.3	5997	6	AX391130	AX391130 Sequence
6	10273	98.8	8131	9	AF225985	AF225985 Homo sapi
7	10253	98.6	8398	10	RNSCPIR	X03638 Rat brain m
8	10253	98.6	8399	10	RATNACHI	M22253 Rattus norv
9	10197	98.1	5922	6	AX391142	AX391142 Sequence
10	10124.5	97.4	5889	6	AX391132	AX391132 Sequence
11	9025.5	86.8	8349	6	AX164203	AX164203 Sequence
12	9025.5	86.8	8349	6	AX164204	AX164204 Sequence
13	9022.5	86.8	6328	9	HUMHBAX	M94055 Human volta
14	9000.5	86.6	8553	10	RNSCPIIR	X03639 Rat brain m
15	8967.5	86.3	8552	10	RATNACHII	M22254 Rattus norv
16	8664	83.3	9123	9	AF225987	AF225987 Homo sapi
17	8488.5	81.6	6599	9	HSA251507	AJ251507 Homo sapi
18	8468.5	81.5	9112	6	AX164235	AX164235 Sequence
19	8462.5	81.4	9112	6	AX164236	AX164236 Sequence
20	8453.5	81.3	8976	9	AF225986	AF225986 Homo sapi
21	8448.5	81.3	6822	6	AX401928	AX401928 Sequence
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23	8344.5	80.3	8378	5	AF123593	AF123593 Cynops py
24	7913	76.1	6404	6	AR107906	AR107906 Sequence
25	7877	75.8	6452	6	AR107904	AR107904 Sequence
26	7876	75.8	5952	10	RNU79568	U79568 Rattus norv
27	7876	75.8	9316	10	AF000368	AF000368 Rattus no
28	7861.5	75.6	6371	6	AR107905	AR107905 Sequence
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34	7736.5	74.4	5937	10	AF049617	AF049617 Mus muscu
35	7720.5	74.3	5977	6	AR181335	AR181335 Sequence
36	7720.5	74.3	6556	6	AR181338	AR181338 Sequence
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38	7712.5	74.2	6586	6	AR181360	AR181360 Sequence
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44	7525.5	72.4	6826	10	RATSCP6A	L39018 Rattus norv
45	7511	72.2	4362	6	AX391144	AX391144 Sequence

ALIGNMENTS

RESULT 1

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LOCUS       AX391140               6030 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 11 from Patent WO0214498.
ACCESSION   AX391140
VERSION     AX391140.1  GI:19584237
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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  JOURNAL   Patent: WO 0214498-A 11 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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BASE COUNT     1786 a   1190 c   1345 g   1706 t      3 others
ORIGIN

Alignment Scores:
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Score:                  10393.00        Matches:        2009
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            99.96%         Indels:         0
DB:                     6              Gaps:           0

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Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

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Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

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Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027

RESULT 2
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AX164171
LOCUS       AX164171               8378 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0138564.
ACCESSION   AX164171
VERSION     AX164171.1  GI:14545110
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 1 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8378
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2496 a   1575 c   1782 g   2525 t
ORIGIN

Alignment Scores:
Pred. No.:                0          Length:          8378
Score:                10367.00        Matches:         2006
Percent Similarity:      99.85%       Conservative:    0
Best Local Similarity:   99.85%       Mismatches:      3
Query Match:             99.71%       Indels:          1
DB:                      6            Gaps:            0

US-09-930-871-12 (1-2009) x AX164171 (1-8378)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db     326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db     386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db     446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Db     506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db     566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Db     746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db     806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db     866 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 925

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db     926 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Db    1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db    1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db    1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db    1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Db    1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db    1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db    1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
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Db   2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db   3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db   3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3265

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   3266 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3325

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3386 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3445

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3446 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3505

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
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Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3626 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3685

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3686 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3745

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3746 GCACCTGTAGAAGAACAGCCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3805

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3866 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3925

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   3926 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCG-GCATTTGAAGATATA 3984

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 4104

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db  4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164

Qy  1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Qy  1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Qy  1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Qy  1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Qy  1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db  4465 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4524

Qy  1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Qy  1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db  4585 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4644

Qy  1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db  4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704

Qy  1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db  4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764

Qy  1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Qy  1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Qy  1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Qy  1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Db  5065 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 5124

Qy  1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Qy  1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Qy  1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Qy  1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Qy  1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db  5365 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5424

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Qy  1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Qy  1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Qy  1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Qy  1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Qy  1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Db  6025 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 6084

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Db  6145 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6204

Qy  1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Qy  2001 GlyLysAspGluLysAlaLysGlyLys 2009
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RESULT 3
AY043484
LOCUS       AY043484               6046 bp    mRNA    linear   PRI 24-APR-2002
DEFINITION  Homo sapiens voltage-gated sodium channel type I mRNA, complete
            cds.
ACCESSION   AY043484
VERSION     AY043484.1  GI:15421161
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimomura,J.,
            Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa,K.
  TITLE     Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy
  JOURNAL   Neurology 58 (7), 1122-1124 (2002)
  MEDLINE   21938587
   PUBMED   11940708
REFERENCE   2  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
            mRNA
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,
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BASE COUNT     1808 a   1188 c   1345 g   1704 t      1 others
ORIGIN
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Alignment Scores:

Pred. No.:	0	Length:	6046
Score:	10321.50	Matches:	1996
Percent Similarity:	99.35%	Conservative:	0
Best Local Similarity:	99.35%	Mismatches:	2
Query Match:	99.27%	Indels:	11
DB:	9	Gaps:	1

US-09-930-871-12 (1-2009) x AY043484 (1-6046)

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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGARTACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTGGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTGGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          |||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACAACAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACAGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGCCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCTTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187
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Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Db   5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
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Db   5968 GGCAAAGATGAAAAAGCCAAAGGGAAA 5994

RESULT 4
AX164172
LOCUS       AX164172                8378 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138564.
ACCESSION   AX164172
VERSION     AX164172.1  GI:14545111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 2 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8378
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2498 a   1571 c   1775 g   2534 t
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          8378
Score:                    10321.00        Matches:         2002
Percent Similarity:       99.75%         Conservative:    2
Best Local Similarity:    99.65%         Mismatches:      5
Query Match:              99.27%         Indels:          2
DB:                       6              Gaps:            0

US-09-930-871-12 (1-2009) x AX164172 (1-8378)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          |||:::|||||||||||||||:::||||||||||  ||||||||||||||||||||||||
Db    866 GCGTTTGTAACAGAATTTGTAAACCTAGGCAATTTTTCAGCTCTTCGCACTTTCAGAGTC 925

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    926 TTGAGAGCTTTGAAAACTATTTCGGTAATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105
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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db   1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db   1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db   1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db   1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db   1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db   1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db   1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCC-AGCACCTTTGAGGAT 2064

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   2065 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2124

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
Db   2125 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2184

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   2185 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2244

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   2245 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2304

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2365 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2424

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2425 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2484

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2485 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2544

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2545 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2604

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2605 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2664

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2665 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2724

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2785 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2844

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2845 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2904

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2965 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3024

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   3025 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3084

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   3085 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3144

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   3145 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3204

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3385 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3444

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Db   3445 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3504

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Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

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Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

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Db   3925 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3984

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAAA-TATTTC 4103

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

Db   4104 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4163

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

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Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

Db   4224 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4283

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   4284 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4343

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db   4344 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4403

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

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Db   5484 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5543

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Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   6084 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 6143

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Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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RESULT 5
AX391130
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DEFINITION  Sequence 1 from Patent WO0214498.
ACCESSION   AX391130
VERSION     AX391130.1  GI:19584232
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 1 21-FEB-2002;

            Lexicon Genetics Incorporated (US)
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                     /db_xref="taxon:9606"
BASE COUNT     1773 a   1185 c   1338 g   1698 t      3 others
ORIGIN

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Score:                    10320.50        Matches:         1998
Percent Similarity:       99.45%         Conservative:    0
Best Local Similarity:    99.45%         Mismatches:      0
Query Match:              99.26%         Indels:          11
DB:                       6              Gaps:            1

US-09-930-871-12 (1-2009) x AX391130 (1-5997)

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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

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Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

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Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

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Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

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Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

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Qy    1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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RESULT 6
AF225985
LOCUS       AF225985               8131 bp    mRNA    linear   PRI 01-FEB-2001
DEFINITION  Homo sapiens voltage-gated sodium channel alpha subunit SCN1A
            (SCN1A) mRNA, complete cds.
ACCESSION   AF225985
VERSION     AF225985.1  GI:12642269
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Cloning of cDNA for human voltage-gated sodium channel alpha
            subunit, SCN1A
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Department of Neurology, University of
            Tokyo, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo
            113-8655, Japan
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BASE COUNT     2453 a    1530 c    1719 g    2422 t      7 others
ORIGIN

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Score:                    10273.00        Matches:         1990
Percent Similarity:       99.00%         Conservative:    0
Best Local Similarity:    99.00%         Mismatches:      8
Query Match:              98.81%         Indels:          12
DB:                       9              Gaps:            2

US-09-930-871-12 (1-2009) x AF225985 (1-8131)

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Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1279 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1338

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1339 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1398

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1459 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1518

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1519 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1578

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1579 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1638

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1759 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1818

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1819 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1878

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1999 ACATCGCCTGTTGGACAGCTTCTGCCA---------------------------------- 2025

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2146 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2205

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Db   2446 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2505

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

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Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2626 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2685

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2686 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2745

Qy    921 CysLysIleAlaSerAspCysGlnLeuPro---ArgTrpHisMetAsnAspPhePheHis 939

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Qy   1040 ArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAsp 1059

Db   3106 AGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGAC 3165

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Qy   1100 SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal 1119

Db   3286 AGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTA 3345

Qy   1120 GlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139

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Qy   1160 GlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAla 1179

Db   3466 CGGCGCCCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCT 3525

Qy   1180 CysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGly 1199

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Qy   1200 ArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrp 1219

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Qy   1320 AlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAla 1339

Db   3946 GCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCC 4005

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Db   4006 CTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTA 4065

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Qy   1420 PheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyr 1439

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Qy   1440 AlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMet 1459

Db   4306 GCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATG 4365

Qy   1460 TyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1479

Db   4366 TATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATT 4425
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Qy   1480 GlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePhe 1499
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Qy   1500 MetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPro 1519
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Qy   1580 PheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyr 1599
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Qy   1680 ValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVal 1699
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RESULT 7
RNSCPIR
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DEFINITION  Rat brain mRNA for sodium channel protein I.
ACCESSION   X03638
VERSION     X03638.1  GI:57216
KEYWORDS    glycoprotein; sodium channel.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8398)
  AUTHORS   Noda,M., Ikeda,T., Kayano,T., Suzuki,H., Takeshima,H., Kurasaki,M.,
            Takahashi,H. and Numa,S.
  TITLE     Existence of distinct sodium channel messenger RNAs in rat brain
  JOURNAL   Nature 320 (6058), 188-192 (1986)
  MEDLINE   86146901
   PUBMED   3754035
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                     ALFNIGLLLFLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQITTSAGW
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                     ILENFSVATEESAEPLSEDDFEMFYEVWEKFDPDATQFMEFEKLSQFAAALEPPLNLP
                     QPNKLQLIAMDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSK
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     misc_feature    882. .890
                     /note="pot. glycosylation site"
     misc_feature    1101. .1109
                     /note="pot. glycosylation site"
     misc_feature    1152. .1160
                     /note="pot. glycosylation site"
     misc_feature    1263. .1271
                     /note="pot. glycosyaltion site"
     variation       1629. .1694
                     /note="GAU (Asp) is AAU (Asn) in variant clone"
     variation       2031. .2033
                     /note="GAG (Glu) is AAG (Lys) in variant clone"
     variation       2262. .2294
                     /note="seq. deleted in variant clone (11 aa's)"
     variation       2718. .2720
                     /note="GAC (Asp) is AAC (Asn) in varian clone"
     misc_feature    2925. .2933
                     /note="pot. glycosylation site"
     misc_feature    4383. .4391
                     /note="pot. glycosylation site"
     misc_feature    4425. .4433
                     /note="pot. glycosylation site"
     misc_feature    8376. .8381
                     /note="put. polyA signal"
     polyA_site      8398
                     /note="polyA site"
BASE COUNT     2370 a   1798 c   1918 g   2312 t
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:          8398
Score:                  10253.00        Matches:         1971
Percent Similarity:     99.30%         Conservative:    24
Best Local Similarity:  98.11%         Mismatches:      14
Query Match:            98.61%         Indels:          0
DB:                     10             Gaps:            0

US-09-930-871-12 (1-2009) x RNSCPIR (1-8398)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 311

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     312 TCTCTTGCAGCTATTGAAAGGCGCATTGCAGAAGAAAAAGCTAAGAATCCCAAGCCAGAC 371

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 AAAAAAGATGATGATGAAAATGGCCCAAAGCCGAACAGTGACTTGGAAGCTGGGAAGAAC 431

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 CTTCCATTTATCTATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTG 491

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     492 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 551

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     552 CGGTTCAGTGCCACTTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 611

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     612 GCTATTAAGATTTTGGTACACTCATTATTCAGCATGTTAATTATGTGCACTATTTTGACG 671

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 AACTGTGTATTTATGACAATGAGTAACCCTCCTGACTGGACAAAGAATGTAGAGTACACC 731

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     732 TTCACAGGAATATATACCTTTGAATCACTAATAAAAATTATTGCAAGGGGCTTCTGTTTA 791

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     792 GAAGATTTTACTTTCCTTCGTGACCCATGGAACTGGCTGGACTTCACTGTCATTACATTC 851

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     852 GCATATGTGACGGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTT 911

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 CTTCGAGCATTGAAAACAATATCAGTCATTCCAGGCCTGAAGACCATCGTGGGGGCCCTG 971

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 ATCCAGTCTGTGAAGAAGCTCTCTGACGTCATGATCCTCACCGTGTTCTGTCTCAGTGTG 1031

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db    1032 TTTGCTCTAATCGGGTTGCAGCTTTTCATGGGCAACCTGAGGAATAAGTGTGTACAGTGG 1091

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||:::|||   :::|||
Db    1092 CCCCCCACCAACGCTTCCCTTGAGGAACATAGCATAGAGAAGAATGTAACTACGGATTAC 1151

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db    1152 AACGGCACACTTGTAAATGAAACCGTGTTTGAATTTGACTGGAAATCATACATTCAAGAC 1211

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db    1212 TCAAGATATCATTATTTCCTGGAGGGTGTTTTAGATGCACTACTGTGTGGAAATAGCTCT 1271

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1272 GATGCAGGCCAATGTCCAGAAGGTTACATGTGTGTAAAAGCTGGCAGAAACCCTAACTAT 1331

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1332 GGTTACACAAGCTTTGACACCTTCAGCTGGGCATTTCTGTCCCTGTTTCGACTGATGACT 1391

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1392 CAGGACTTCTGGGAAAATCTTTACCAACTGACATTGCGTGCTGCCGGGAAAACATACATG 1451
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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db   1452 ATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTACCTGATAAACTTGATCCTGGCT 1511

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1512 GTGGTGGCCATGGCCTATGAGGAACAGAACCAGGCCACATTGGAGGAGGCTGAACAGAAG 1571

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1572 GAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAGCAGCAGGAAGCCGCACAGCAG 1631

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1632 GCGGCGGCAGCAACAGCATCAGAACATTCCAGGGAGCCCAGTGCAGCGGGCAGGCTCTCA 1691

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1692 GATAGCTCTTCAGAAGCCTCCAAGTTGAGTTCAAAGAGCGCTAAAGAAAGGCGGAATCGG 1751

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1752 AGGAAAAAAAGAAAACAGAAAGAGCAGTCTGGAGGGAAGAGAAAGATGATGATGAATTC 1811

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1812 CACAAATCCGAGTCCGAAGATAGCATCAGGAGGAAGGGCTTCCGCTTCTCCATAGAAGGG 1871

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1872 AACAGACTGACCTATGAAAAGAGGTACTCTTCCCCACATCAGTCTCTGTTGAGCATTCGC 1931

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1932 GGCTCACTGTTTTCCCCGAGACGCAATAGCAGAACAAGTCTTTTCAGCTTCAGAGGGCGA 1991

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1992 GCGAAGGACGTGGGGTCTGAGAATGATTTTGCGGACGATGAGCACAGCACCTTCGAGGAC 2051

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   2052 AATGAGAGCAGGAGAGACTCTCTGTTTGTTCCCCGAAGACATGGAGAGCGACGCAACAGT 2111

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
Db   2112 AACCTCAGCCAAACCAGCAGATCCTCCCGAATGCTGGCGGGGCTTCCAGCAAACGGGAAG 2171

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   2172 ATGCACAGCACAGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGCGGACCCTCGGTTCCG 2231

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   2232 ACATCGCCAGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2291

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   2292 AATGGAACAACTACTGAAACTGAGATGAGAAAGAGGAGGTCAAGTTCTTTCCATGTTTCC 2351

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2352 ATGGACTTTCTTGAGGATCCTTCCCAGAGGCAAAGGCAATGAGCATTGCCAGCATCTTA 2411

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2412 ACAAATACAGTAGAAGAACTAGAAGAATCCAGACAGAAATGTCCACCCTGTTGGTATAAA 2471

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2472 TTTTCCAACATATTTTTAATTTGGGACTGTTCTCCATATTGGCTAAAAGTTAAACATATT 2531

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2532 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCAATTACTATCTGTATTGTGTTA 2591

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2592 AATACCCTTTTCATGGCCATGGAGCACTACCCCATGACTGAACATTTCAATCATGTACTT 2651

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2652 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTCACAGCAGAAATGTTCCTGAAAATCATT 2711

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2712 GCCATGGACCCTTACTATTATTTCCAAGAGGGCTGGAATATCTTTGATGGTTTCATTGTG 2771

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2772 ACACTCAGCCTGGTAGAACTTGGCCTTGCCAATGTGGAAGGGTTATCAGTTCTCCGTTCA 2831

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2832 TTCCGACTGCTCCGAGTCTTCAAGTTGGCAAAGTCCTGGCCCACACTGAACATGCTCATT 2891

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2892 AAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTGGTGCTGGCCATCATC 2951

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2952 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTCGGCAAAAGTTACAAAGATTGTGTC 3011

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   3012 TGCAAAATTGCCACTGACTGCAAACTCCCGCGCTGGCACATGAACGACTTCTTCCACTCC 3071

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   3072 TTCCTGATCGTGTTCCGAGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGCATG 3131

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   3132 GAGGTCGCGGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTAGGAAC 3191

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   3192 CTTGTGGTCCTGAACCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3251

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   3252 GCAGCCACTGACGATGACAACGAAATGAACAACCTTCAAATTGCTGTGGACAGGATGCAC 3311

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3312 AAAGGAGTAGCTTATGTAAAAAGAAAAATATATGAGTTTATTCAACAGTCCTTTGTTAGG 3371

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db   3372 AAACAGAAGATCCTAGATGAAATTAAGCCACTTGATGATCTAAACAACAGAAAAGACAAT 3431

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
Db   3432 TGTACATCTAACCACACGACAGAGATTGGGAAAGATCTGGACTGTCTGAAAGATGTGAAT 3491

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
Db   3492 GGAACCACGAGTGGCATAGGGACCGGCAGCAGTGTGGAAAAGTACATCATTGATGAGAGT 3551

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
Db   3552 GACTACATGTCATTCATAAACAACCCCAGCCTCACCGTGACTGTGCCCATTGCTGTGGGA 3611

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3612 GAGTCTGACTTTGAAAACTTAAACACAGAGGACTTTAGCAGTGAATCAGATCTAGAAGAA 3671

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3672 AGCAAAGAGAAACTCAACGAAAGCAGTAGTTCCTCAGAAGGAAGCACAGTAGACATCGGG 3731

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||   ||||||||||||||:::||||||||||||||||||||||||||||||||||
Db   3732 GCGCCTGCGGAGGAACAGCCTGTCATGGAACCAGAAGAAACCCTTGAGCCCGAAGCTTGC 3791

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db   3792 TTCACTGAAGGCTGTGTGCAGAGATTCAAGTGCTGTCAAATCAGTGTGGAAGAAGGAAGA 3851

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3852 GGAAAACAGTGGTGGAACCTTCGGAGAACGTGCTTCCGAATAGTTGAGCACAACTGGTTT 3911

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3912 GAGACCTTCATTGTGTTCATGATTCTCCTCAGTAGTGGTGCCCTGGCCTTTGAGGATATA 3971

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3972 TACATTGATCAGCGAAAGACAATCAAGACCATGCTGGAGTATGCAGACAAGGTTTTCACT 4031

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db   4032 TACATTTTTATCCTGGAGATGCTCCTCAAATGGGTAGCCTACGGCTATCAAACGTATTTC 4091

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   4092 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4151

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   4152 GCAAATGCCTTGGGTTACTCTGAACTTGGGGCCATCAAGTCCCTAAGGACACTAAGAGCT 4211

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db   4212 CTGAGACCCCTAAGAGCCTTATCACGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTG 4271

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Db   4272 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGCCTTATATTCTGGCTAATT 4331

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4332 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTGTTAACACCACA 4391

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4392 ACTGGTGACACATTTGAGATCACCGAAGTCAATAATCATTCTGATTGCCTAAAACTAATA 4451

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db   4452 GAAAGAAATGAGACTGCCCGGTGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4511

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4512 GGGTATCTTTCTTTGCTTCAAGTTGCGACGTTTAAGGGTTGGATGGATATCATGTATGCA 4571

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4572 GCAGTTGATTCCAGAAATGTGGAACTGCAGCCTAAGTATGAGGAAAGCCTGTACATGTAC 4631

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4632 CTGTACTTCGTCATCTTCATCATCTTCGGCTCGTTCTTCACTCTAAATCTATTCATCGGT 4691

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db   4692 GTCATCATAGACAACTTCAACCAGCAGAAGAAGAAGTTTGGAGGTCAAGACATCTTTATG 4751

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4752 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAGAAATTAGGATCAAAAAAGCCACAA 4811

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4812 AAGCCTATCCCTCGACCTGGAAACAAATTTCAAGGAATGGTCTTTGACTTTGTAACCAGA 4871

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4872 CAAGTGTTTGACATCAGCATCATGATCCTCATCTGTCTGAACATGGTGACCATGATGGTG 4931

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||:::|||||||||:::||||||||||||||||||||||||||||
Db   4932 GAAACGGATGACCAGAGCGATTATGTGACAAGCATTTTGTCACGTATCAACCTGGTGTTC 4991

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4992 ATTGTGCTGTTCACCGGCGAGTGCGTGCTGAAGCTCATCTCCCTCCGCCATTATTATTTC 5051

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   5052 ACCATTGGCTGGAATATTTTCGATTTTGTGGTGGTCATCCTCTCCATTGTAGGAATGTTT 5111

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   5112 CTTGCGGAGCTGATAGAGAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTCATCCGCCTG 5171

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   5172 GCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGCACTCTGCTC 5231

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5232 TTTGCTCTGATGATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCTGGTC 5291

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5292 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGA 5351

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5352 ATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCCTGTTCCAAATC 5411

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5412 ACCACCTCTGCGGGCTGGGACGGACTGCTGGCCCCCATCCTCAACAGCAAACCCCCTGAC 5471

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5472 TGTGACCCTAATAAAGTTAACCCCGGAAGCTCGGTGAAGGGGGACTGTGGGAACCCATCC 5531

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5532 GTGGGGATTTTCTTTTTTGTCAGCTACATCATCATATCCTTCCTGGTGGTGGTGAACATG 5591

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5592 TACATCGCTGTCATCCTGGAGAACTTCAGCGTTGCCACCGAAGAAAGTGCAGAGCCCCTG 5651

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5652 AGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACCCTGACGCCACT 5711

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5832 CGCATCCACTGCCTGGACATCTTGTTTGCTTTTACAAAGCGGGTCTTGGGCGAGAGTGGA 5891

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5892 GAGATGGACGCTCTTCGAATCCAGATGGAAGAAAGGTTCATGGCTTCCAACCCCTCCAAG 5951

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5952 GTCTCCTATCAGCCAATCACTACAACGTTAAAACGAAAGCAAGAGGAGGTGTCAGCCGTT 6011

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db   6012 ATCATTCAGCGCGCTTACAGGCGCCACCTTTTGAAGCGAACAGTAAAACAAGCTTCATTC 6071

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   6072 ACATACAATAAGAACAAACTCAAGGGCGGGGCTAATCTTCTTGTAAAAGAAGACATGATC 6131

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6132 ATTGACAGGATAAATGAAAACTCTATTACAGAGAAAACTGACCTGACGATGTCCACTGCA 6191

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6192 GCTTGTCCGCCCTCCTACGACCGGGTGACAAAGCCAATCGTGGAGAAACACGAGCAGGAA 6251

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   6252 GGAAAAGATGAGAAAGCCAAAGGGAAA 6278
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RESULT 8
RATNACHI
LOCUS       RATNACHI                8399 bp    mRNA    linear   ROD 26-OCT-1995
DEFINITION  Rattus norvegicus sodium channel I mRNA, complete cds.
ACCESSION   M22253
VERSION     M22253.1  GI:1041088
KEYWORDS    Na+ channel; sodium channel.
SOURCE      Rattus norvegicus cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8399)
  AUTHORS   Noda,M. and Numa,S.
  TITLE     Structure and function of sodium channel
  JOURNAL   J. Recept. Res. 7 (1-4), 467-497 (1987)
  MEDLINE   87311395
   PUBMED   2442385
COMMENT     On Oct 27, 1995 this sequence version replaced gi:340711.
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                     /codon_start=1
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                     /protein_id="AAA79965.1"
                     /db_xref="GI:1041089"
                     /translation="MEQTVLVPPGPDSFNFFTRESLAAIERRIAEEKAKNPKPDKKDD
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                     FTGIYTFESLIKIIARGFCLEDFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTF
                     RVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNK
                     CVQWPPTNASLEEHSIEKNVTTDYNGTLVNETVFEFDWKSYIQDSRYHYFLEGVLDAL
                     LCGNSSDAGQCPEGYMCVKAGRNPNYGYTSFDTFSWAFLSLFRLMTQDFWENLYQLTL
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                     LKKQQEAAQQAAAATASEHSREPSAAGRLSDSSSEASKLSSKSAKERRNRRKKRKQKE
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                     RRNSRTSLFSFRGRAKDVGSENDFADDEHSTFEDNESRRDSLFVPRRHGERRNSNLSQ
                     TSRSSRMLAGLPANGKMHSTVDCNGVVSLVGGPSVPTSPVGQLLPEVIIDKPATDDNG
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                     FSNIFLIWDCSPYWLKVKHIVNLVVMDPFVDLAITICIVLNTLFMAMEHYPMTEHFNH
                     VLTVGNLVFTGIFTAEMFLKIIAMDPYYYFQEGWNIFDGFIVTLSLVELGLANVEGLS
                     VLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGK
                     SYKDCVCKIATDCKLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQAMCLTVF
                     MMVMVIRNLVVLNLFLALLLSSFSADNLAATDDDNEMNNLQIAVDRMHKGVAYVKRKI
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BASE COUNT     2371 a   1798 c   1918 g   2312 t
ORIGIN
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Alignment Scores:
Pred. No.:                0                Length:          8399
Score:                    10253.00          Matches:         1971
Percent Similarity:       99.30%           Conservative:    24
Best Local Similarity:    98.11%           Mismatches:      14
Query Match:              98.61%           Indels:          0
DB:                       10               Gaps:            0

US-09-930-871-12 (1-2009) x RATNACHI (1-8399)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 311

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db    312 TCTCTTGCAGCTATTGAAAGGCGCATTGCAGAAGAAAAAGCTAAGAATCCCAAGCCAGAC 371

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 AAAAAAGATGATGATGAAAATGGCCCAAAGCCGAACAGTGACTTGGAAGCTGGGAAGAAC 431

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 CTTCCATTTATCTATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTG 491

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 551

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 CGGTTCAGTGCCACTTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 611

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GCTATTAAGATTTTGGTACACTCATTATTCAGCATGTTAATTATGTGCACTATTTTGACG 671

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 AACTGTGTATTTATGACAATGAGTAACCCTCCTGACTGGACAAAGAATGTAGAGTACACC 731

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    732 TTCACAGGAATATATACCTTTGAATCACTAATAAAAATTATTGCAAGGGGCTTCTGTTTA 791

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    792 GAAGATTTTACTTTCCTTCGTGACCCATGGAACTGGCTGGACTTCACTGTCATTACATTC 851

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220

Db    852 GCATATGTGACGGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTT 911

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240

Db    912 CTTCGAGCATTGAAAACAATATCAGTCATTCCAGGCCTGAAGACCATCGTGGGGGCCCTG 971

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db    972 ATCCAGTCTGTGAAGAAGCTCTCTGACGTCATGATCCTCACCGTGTTCTGTCTCAGTGTG 1031

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db   1032 TTTGCTCTAATCGGGTTGCAGCTTTTCATGGGCAACCTGAGGAATAAGTGTGTACAGTGG 1091

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db   1092 CCCCCCACCAACGCTTCCCTTGAGGAACATAGCATAGAGAAGAATGTAACTACGGATTAC 1151

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db   1152 AACGGCACACTTGTAAATGAAACCGTGTTTGAATTTGACTGGAAATCATACATTCAAGAC 1211

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

Db   1212 TCAAGATATCATTATTTCCTGGAGGGTGTTTTAGATGCACTACTGTGTGGAAATAGCTCT 1271

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

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Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db   1572 GAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAGCAGCAGGAAGCCGCACAGCAG 1631

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1632 GCGGCGGCAGCAACAGCATCAGAACATTCCAGGGAGCCCAGTGCAGCGGGCAGGCTCTCA 1691

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db   1692 GATAGCTCTTCAGAAGCCTCCAAGTTGAGTTCAAAGAGCGCTAAAGAAAGGCGGAATCGG 1751

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

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Db   1872 AACAGACTGACCTATGAAAAGAGGTACTCTTCCCCACATCAGTCTCTGTTGAGCATTCGC 1931

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1932 GGCTCACTGTTTTCCCCGAGACGCAATAGCAGAACAAGTCTTTTCAGCTTCAGAGGGCGA 1991

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1992 GCGAAGGACGTGGGGTCTGAGAATGATTTTGCGGACGATGAGCACAGCACCTTCGAGGAC 2051

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   2052 AATGAGAGCAGGAGAGACTCTCTGTTTGTTCCCCGAAGACATGGAGAGCGACGCAACAGT 2111

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

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Db   2292 AATGGAACAACTACTGAAACTGAGATGAGAAAGAGGAGGTCAAGTTCTTTCCATGTTTCC 2351

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2352 ATGGACTTTCTTGAGGATCCTTCCCAGAGGCAAAGGGCAATGAGCATTGCCAGCATCTTA 2411

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

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Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2592 AATACCCTTTTCATGGCCATGGAGCACTACCCCATGACTGAACATTTCAATCATGTACTT 2651

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2652 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTCACAGCAGAAATGTTCCTGAAAATCATT 2711

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2712 GCCATGGACCCTTACTATTATTTCCAAGAGGGCTGGAATATCTTTGATGGTTTCATTGTG 2771

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2772 ACACTCAGCCTGGTAGAACTTGGCCTTGCCAATGTGGAAGGGTTATCAGTTCTCCGTTCA 2831

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2832 TTCCGACTGCTCCGAGTCTTCAAGTTGGCAAAGTCCTGGCCCACACTGAACATGCTCATT 2891

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2892 AAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTGGTGCTGGCCATCATC 2951

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2952 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTCGGCAAAAGTTACAAAGATTGTGTC 3011
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Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   3012 TGCAAAATTGCCACTGACTGCAAACTCCCGCGCTGGCACATGAACGACTTCTTCCACTCC 3071

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   3072 TTCCTGATCGTGTTCCGAGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGCATG 3131

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   3132 GAGGTCGCGGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTAGGAAC 3191

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   3192 CTTGTGGTCCTGAACCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3251

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   3252 GCAGCCACTGACGATGACAACGAAATGAACAACCTTCAAATTGCTGTGGACAGGATGCAC 3311

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db   3852 GGAAAACAGTGGTGGAACCTTCGGAGAACGTGCTTCCGAATAGTTGAGCACAACTGGTTT 3911

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Db   3912 GAGACCTTCATTGTGTTCATGATTCTCCTCAGTAGTGGTGCCCTGGCCTTTGAGGATATA 3971

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VERSION     AX391142.1  GI:19584238
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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                     /db_xref="taxon:9606"
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Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            98.08%         Indels:          0
DB:                     6              Gaps:            0

US-09-930-871-12 (1-2009) x AX391142 (1-5922)

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Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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RESULT 10
AX391132
LOCUS       AX391132                5889 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 3 from Patent WO0214498.
ACCESSION   AX391132
VERSION     AX391132.1  GI:19584233
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 3 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1733 a   1161 c   1313 g   1679 t      3 others
ORIGIN

Alignment Scores:
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Score:                    10124.50        Matches:         1961
Percent Similarity:       99.44%         Conservative:    0
Best Local Similarity:    99.44%         Mismatches:      0
Query Match:              97.38%         Indels:          11
DB:                       6              Gaps:            1

US-09-930-871-12 (1-2009) x AX391132 (1-5889)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010
Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067
Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127
Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187
Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247
Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307
Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367
Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427
Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487
Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547
Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607
Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667
Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727
Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787
Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847
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Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
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RESULT 3
AAH55763
ID AAH55763 standard; cDNA; 8378 BP.
XX
AC AAH55763;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99674.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 90-93; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	8378
Score:	10367.00	Matches:	2006
Percent Similarity:	99.85%	Conservative:	0
Best Local Similarity:	99.85%	Mismatches:	3

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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2641 AAGATCATCGGCAATTCCGGGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

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Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2941 CTAGTGGTACTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3181 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3541 TTCACTGAAGGTTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

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Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

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Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440

Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460

Db   4321 GCAGTTGATTCCAGAAATGTAGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480

Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500

Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520

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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

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Db   4621 CAAGTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580

Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600

Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAGTACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAGGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Db   1021 GATGCAGGGCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db   1201 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Db    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy    1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Qy    1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Qy    1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy    1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Db    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy    2001 GlyLysAspGluLysAlaLysGlyLys 2009
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Db    6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027

RESULT 2
AAD27266
ID   AAD27266 standard; cDNA; 6027 BP.
XX
AC   AAD27266;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human transporter and ion channel-13 (TRICH-13) cDNA.
XX
KW   Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW   nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW   antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW   Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW   amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW   Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW   cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW   bradyarrythmia; gene expression; drug screening; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Human TRICH-13 protein"
FT                   /note= "CDS does not include stop codon"
FT                   /partial
XX
PN   WO200192304-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US17065.
XX
PR   26-MAY-2000; 2000US-208424P.
PR   01-JUN-2000; 2000US-209001P.
PR   08-JUN-2000; 2000US-210588P.
PR   16-JUN-2000; 2000US-212335P.
PR   22-JUN-2000; 2000US-213747P.
PR   29-JUN-2000; 2000US-215391P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Thornton M, Walia NK, Yue H, Nguyen DB, Lai P, Gandhi AR;
PI   Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT;
PI   Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS;
PI   Raumann BE, Lee EA, Hafalia A, Baughn MR, Green BD, Khan FA;
PI   Kearney L, Elliot VS, Seilhamer JJ, Policky JL, Borowsky ML;
PI   Burford N, Ding L, Lu DAM, Hillman JL;
XX
DR   WPI; 2002-122055/16.
DR   P-PSDB; AAE16776.
XX
PT   New human transporters and ion channels (TRICH) polypeptides useful for
PT   diagnosing, treating or preventing disorders associated with aberrant
PT   expression of TRICH -
XX
PS   Claim 11; Page 196-197; 210pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH)
CC   polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC   sequences are useful in the diagnosis, treatment, and prevention of
CC   disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC   palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC   amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC   muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC   asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC   cardiac disease (angina, hypertension, or bradyarrythmia) and in the
CC   assessment of the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of transporters and ion channels.
CC   The polynucleotides may be used to detect and quantify gene expression
CC   in biopsied tissues in which TRICH expression may be correlated with a
CC   disease, to generate hybridization probes for mapping naturally occurring
CC   genomic sequence, and in drug screening. The present sequence is human
CC   TRICH-13 cDNA.
XX
SQ   Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;

Alignment Scores:
Pred. No.:              0              Length:          6027
Score:                  10376.00        Matches:         2004
Percent Similarity:     99.80%         Conservative:    1
Best Local Similarity:  99.75%         Mismatches:      4
Query Match:            99.80%         Indels:          0
DB:                     24             Gaps:            0

US-09-930-871-12 (1-2009) x AAD27266 (1-6027)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGCAGACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db  1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

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Db  1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

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Qy   501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db  1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

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Qy   541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db  1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db  1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

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Qy   601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db  1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

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Qy   641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

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Qy   701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

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Qy   801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

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Qy   821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

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Qy   861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

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Qy   881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

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Qy   901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

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Qy   961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

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Qy   981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

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Qy  1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy  1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

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Db  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy  1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy  1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

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FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
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PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20515.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 2; Page 55-57; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other;
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Alignment Scores:

Pred. No.:	0	Length:	6030
Score:	10393.00	Matches:	2009
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.96%	Indels:	0
DB:	24	Gaps:	0

US-09-930-871-12 (1-2009) x AAD32844 (1-6030)

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Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2003, 18:36:20 ; Search time 568 Seconds
(without alignments)
7965.255 Million cell updates/sec

Title: US-09-930-871-12
Perfect score: 10397
Sequence: 1 MEQTVLVPPGPDSFNFFTRE.....TKPIVEKHEQEGKDEKAKGK 2009

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09930871/runat_16042003_114837_8447/app_query.fasta_1.2183
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10393	100.0	6030	24	AAD32844	Human ion channel
2	10376	99.8	6027	24	AAD27266	Human transporter
3	10367	99.7	8378	22	AAH55763	Human adult form o
4	10321	99.3	8378	22	AAH55764	Human neonatal for
5	10320.5	99.3	5997	24	AAD32839	Human ion channel
6	10273	98.8	8131	24	ABL39689	Human sodium chann
7	10197	98.1	5922	24	AAD32845	Human ion channel
8	10124.5	97.4	5889	24	AAD32840	Human ion channel
9	9025.5	86.8	8349	22	AAH55793	Human adult form o
10	9025.5	86.8	8349	22	AAH55794	Human neonatal for
11	8664	83.3	9123	24	ABL39690	Human sodium chann
12	8468.5	81.5	9112	22	AAH55823	Human adult form o
13	8462.5	81.4	9112	22	AAH55824	Human neonatal for
14	8448.5	81.3	6822	24	ABK63697	Rat sequence diffe
15	7903	76.0	6404	17	AAT30195	Peripheral nervous
16	7861.5	75.6	6371	17	AAT30194	Peripheral nervous
17	7826	75.3	6452	17	AAT30193	Peripheral nervous
18	7755.5	74.6	6007	19	AAV58421	Tetrodotoxin-sensi
19	7720.5	74.3	5977	19	AAV58420	Tetrodotoxin-sensi
20	7720.5	74.3	6556	19	AAV58419	PN4 sodium channel
21	7712.5	74.2	6586	19	AAV58423	PN4 sodium channel
22	7685.5	73.9	7053	21	AAA93791	Human cDNA encodin
23	7685.5	73.9	7053	24	AAL42751	Human sodium chann
24	7511	72.2	4362	24	AAD32846	Human ion channel
25	7438.5	71.5	4329	24	AAD32841	Human ion channel
26	7181	69.1	4179	24	AAD32847	Human ion channel
27	7108.5	68.4	4146	24	AAD32842	Human ion channel
28	7105.5	68.3	4197	24	AAD32848	Human ion channel
29	7033	67.6	4164	24	AAD32843	Human ion channel
30	6348	61.1	6021	24	ABL42420	Rat voltage gated
31	6312	60.7	6048	22	AAF30825	Human SCN5A gene.
32	6310	60.7	6048	19	AAV09029	Human hH1 sodium c
33	6257.5	60.2	7555	16	AAQ81328	Cardiac sodium cha
34	6230.5	59.9	7555	11	AAQ05831	Cardiac sodium cha
35	6160	59.2	8530	22	AAS31089	Human diagnostic a
36	5555	53.4	5874	22	AAI66961	Human SNS1 ion cha
37	5555	53.4	5874	22	AAF57016	Human hPN3 cDNA se
38	5493	52.8	6606	20	AAX60872	NaNG polypeptide e
39	5456.5	52.5	6373	22	AAI66960	Mouse SNS1 ion cha
40	5437.5	52.3	6344	22	AAI66959	Rat SNS1 ion chann
41	5437.5	52.3	6344	22	AAF57009	Rat PN3 cDNA seque
42	5426	52.2	6527	18	AAT77806	cDNA encoding vari
43	5404	52.0	6524	18	AAT77803	cDNA encoding wild
44	5372.5	51.7	7052	18	AAT77805	cDNA encoding vari
45	4522	43.5	5822	22	AAF30103	Mouse sodium chann

ALIGNMENTS

RESULT 1
AAD32844
ID AAD32844 standard; cDNA; 6030 BP.
XX
AC AAD32844;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #6.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..6030

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Db    5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy    1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
Db    5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy    1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
Db    5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy    1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
Db    5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy    1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
Db    5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy    1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
Db    5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy    1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
Db    5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy    1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
Db    5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy    1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
Db    5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy    1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
Db    5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy    1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
Db    5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy    1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
Db    5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy    1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db    5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy    1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5883

RESULT 11
AX164203
LOCUS       AX164203               8349 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 33 from Patent WO0138564.
ACCESSION   AX164203
VERSION     AX164203.1  GI:14545141
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8349)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 33 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2496 a   1591 c   1775 g   2487 t
ORIGIN

Alignment Scores:
Pred. No.:                0          Length:          8349
Score:                    9025.50    Matches:         1759
Percent Similarity:       92.63%     Conservative:    113
Best Local Similarity:    87.04%     Mismatches:      114
Query Match:              86.81%     Indels:          35
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US-09-930-871-12 (1-2009) x AX164203 (1-8349)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy      41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
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Qy      60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
Db     286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy      80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
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Qy     100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119
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Qy     120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139
Db     466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525

Qy     140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159
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Qy     160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
Db     586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy     180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
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Qy     200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
Db     706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765

Qy     220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
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Qy     240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
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Qy   1729 LeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnPro 1748
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5320 GGAAGCTCAGTTAAAGGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGT 5379

Qy   1769 TyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsn 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5380 TACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAAC 5439

Qy   1789 PheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPhe 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5440 TTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTC 5499

Qy   1809 TyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeu 1828
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Db   5500 TATGAGGTTTGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTTGCCAAACTT 5559

Qy   1829 SerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGln 1848
          |||   ||||||   ||||||:::|||||||||   :::   :::|||||||||:::|||
Db   5560 TCTGATTTTGCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAG 5619

Qy   1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 CTCATTGCCATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATCTTA 5679

Qy   1869 PheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGln 1888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTTGCTTTTACAAAGCGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAG 5739

Qy   1889 MetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrThr 1908
          ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db   5740 ATGGAAGAGCGATTCATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCCATTACGACC 5799

Qy   1909 ThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArg 1928
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Db   5800 ACGTTGAAACGCAAACAAGAGGAGGTGTCTGCTATTATTATCCAGAGGGCTTACAGACGC 5859

Qy   1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948
          :::|||||||||:::   ||||||:::   |||      |||   |||:::|||   |||
Db   5860 TACCTCTTGAAGCAAAAAGTTAAAAAGGTATCAAGTATATACAAGAAAGACAAAGGCAAA 5919

Qy   1949 GlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSer 1968
                    ||||||||||||   :::|||||||:::::|||||||||||||
Db   5920 GAATGTGATGGAACACCCATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAATTCA 5979

Qy   1969 IleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988
               ||||||||||:::|||   ||||||  :::   |||||||||||||||
Db   5980 ACTCCAGAGAAAACCGATATGACGCCTTCCACCACGTCT---CCACCCTCGTATGATAGT 6036

Qy   1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
          ||||||||||||      ||||||   |||::::::      :::::::.::   ||||||
Db   6037 GTGACCAAACCAGAAAAAGAAAAATTTGAAAAAGACAAATCAGAAAAGGAAGACAAAGGG 6096

Qy   2009 Lys 2009
          |||
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RESULT 12
AX164204
LOCUS       AX164204               8349 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 34 from Patent WO0138564.
ACCESSION   AX164204
VERSION     AX164204.1  GI:14545142
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8349)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 34 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2496 a   1591 c   1775 g   2487 t
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          8349
Score:                    9025.50        Matches:         1759
Percent Similarity:       92.63%         Conservative:    113
Best Local Similarity:    87.04%         Mismatches:      114
Query Match:              86.81%         Indels:          35
DB:                       6              Gaps:            13

US-09-930-871-12 (1-2009) x AX164204 (1-8349)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||   |||:::|||||||||||||||||||||||||||||||   ||||||||||||||
Db    106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||:::|||||||||||||||||||||||||   ||||||   :::
Db    166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

Qy     41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
          :::||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy     60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
          :::||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy     80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy    100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119
          ||||||||||||||||   |||||||||||||||||||||||||||:::||||||
Db    406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy    120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139
          :::||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
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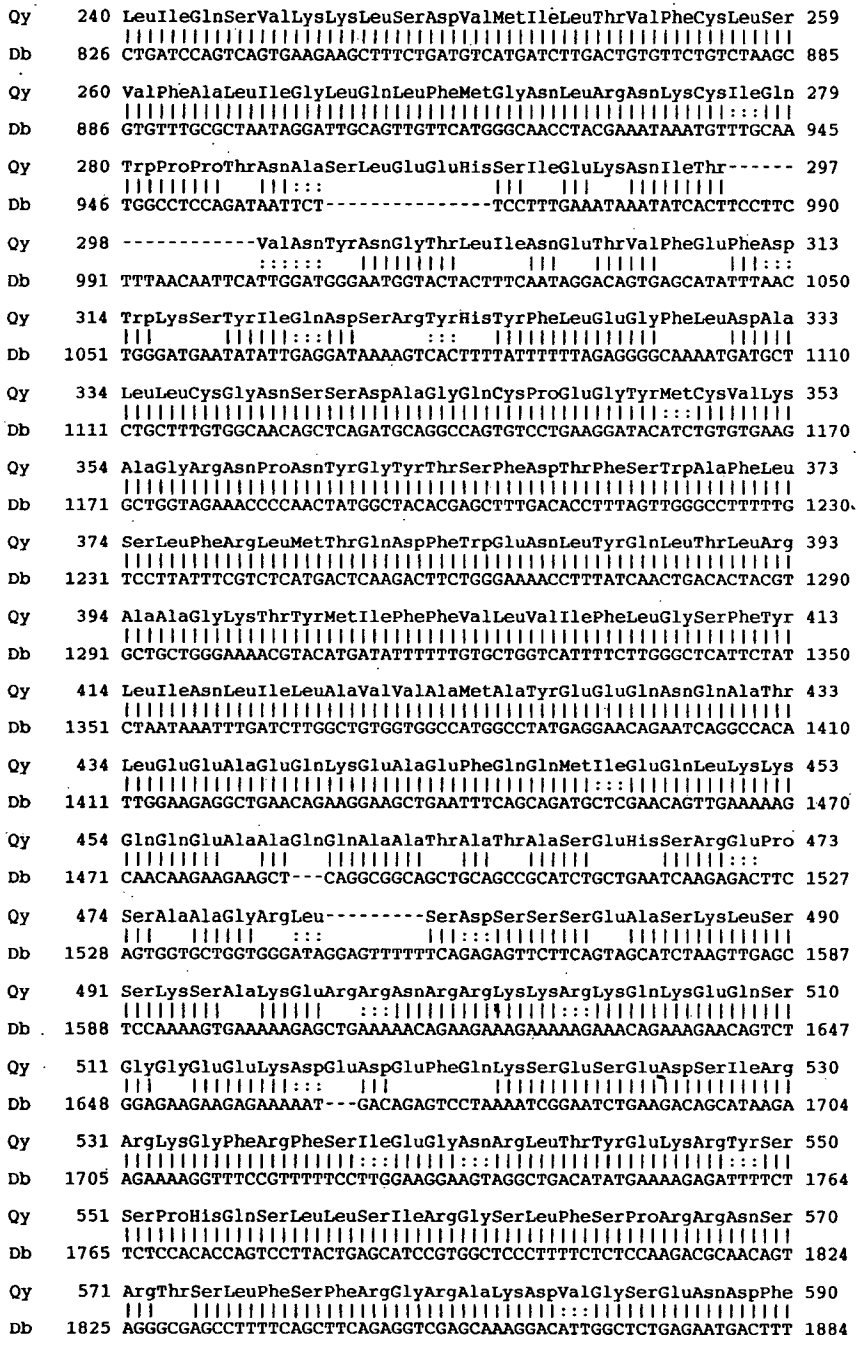
Qy    140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159
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Db    526 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 585

Qy    160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
          ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy    180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 705

Qy    200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765

Qy    220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825
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Qy 240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
Db 826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885
Qy 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
Db 886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945
Qy 280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr------ 297
Db 946 TGGCCTCCAGATAATTCT--------------TCCTTTGAAATAAATATCACTTCCTTC 990
Qy 298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
Db 991 TTTAACAATTCATTGGATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAAC 1050
Qy 314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAla 333
Db 1051 TGGGATGAATATATTGAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCT 1110
Qy 334 LeuLeuCysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353
Db 1111 CTGCTTTGTGGCAACAGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAG 1170
Qy 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373
Db 1171 GCTGGTAGAAACCCCAACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTG 1230
Qy 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393
Db 1231 TCCTTATTTCGTCTCATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGT 1290
Qy 394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413
Db 1291 GCTGCTGGGAAAACGTACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTAT 1350
Qy 414 LeuIleAsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433
Db 1351 CTAATAAATTTGATCTTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACA 1410
Qy 434 LeuGluGluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLys 453
Db 1411 TTGGAAGAGGCTGAACAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAG 1470
Qy 454 GlnGlnGluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluPro 473
Db 1471 CAACAAGAAGAAGCT---CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTC 1527
Qy 474 SerAlaAlaGlyArgLeu---------SerAspSerSerSerGluAlaSerLysLeuSer 490
Db 1528 AGTGGTGCTGGTGGGATAGGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGC 1587
Qy 491 SerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSer 510
Db 1588 TCCAAAAGTGAAAAAGAGCTGAAAAACAGAAGAAAGAAAAAGAAACAGAAAGAACAGTCT 1647
Qy 511 GlyGlyGluGluLysAspGluAspGluPheGlnLysSerGluSerGluAspSerIleArg 530
Db 1648 GGAGAAGAAGAGAAAAAT---GACAGAGTCCTAAAATCGGAATCTGAAGACAGCATAAGA 1704
Qy 531 ArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSer 550
Db 1705 AGAAAAGGTTTCCGTTTTTCCTTGGAAGGAAGTAGGCTGACATATGAAAAGAGATTTTCT 1764
Qy 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570
Db 1765 TCTCCACACCAGTCCTTACTGAGCATCCGTGGCTCCCTTTTCTCTCCAAGACGCAACAGT 1824
Qy 571 ArgThrSerLeuPheSerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPhe 590
Db 1825 AGGGCGAGCCTTTTCAGCTTCAGAGGTCGAGCAAAGGACATTGGCTCTGAGAATGACTTT 1884
Qy 591 AlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal 610
Db 1885 GCTGATGATGAGCACAGCACCTTTGAGGACAATGACAGCCGAAGAGACTCTCTGTTCGTG 1944
Qy 611 ProArgArgHisGlyGluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg 630
Db 1945 CCGCACAGACATGGAGAACGGCGCCACAGCAATGTCAGCCAGGCCAGCCGTGCCTCCAGG 2004
Qy 631 MetLeuAlaValProProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyVal 650
Db 2005 GTGCTCCCCATCCTGCCCATGAATGGGAAGATGCATAGCGCTGTGGACTGCAATGGTGTG 2064
Qy 651 ValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGlu 670
Db 2065 GTCTCCCTGGTCGGGGGCCCTTCTACCCTCACATCT---GCTGGGCAGCTCCTACCAGAG 2121
Qy 671 ValIleIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArg 690
Db 2122 --------------------------------GGCACAACTACTGAAACAGAAATAAGA 2148
Qy 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710
Db 2149 AAGAGACGGTCCAGTTCTTATCATGTTTCCATGGATTTATTGGAAGATCCTACATCAAGG 2208
Qy 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSer 730
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Qy 731 ArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCys 750
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Db 2389 GACCTGGCCATCACCATCTGCATTGTCTTAAATACACTCTTCATGGCTATGGAGCACTAT 2448
Qy 791 ProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIle 810
Db 2449 CCCATGACGGAGCAGTTCAGCAGTGTACTGTCTGTTGGAAACCTGGTCTTCACAGGGATC 2508
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Qy 831 GlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAla 850
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Qy 851 AsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 870
Db 2629 AATGTGGAAGGATTGTCAGTTCTCCGATCATTCCGGCTGCTCCGAGTTTTCAAGTTGGCA 2688
Qy 871 LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu 890
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Db 2809 CTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATTTCCAATGATTGTGAACTCCCA 2868
Qy 931 ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGly 950
Db 2869 CGCTGGCACATGCATGACTTTTTCCACTCCTTCCTGATCGTGTTCCGCGTGCTGTGTGGA 2928
Qy 951 GluTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr 970

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Qy    991 Leu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsn 1010

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Qy   1011 AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrValLysArgLysIle 1030

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Qy   1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050

Db   3169 CGTGAATTTATTCAGAAAGCCTTTGTTAGGAAGCAGAAAGCTTTAGATGAAATTAAACCG 3228

Qy   1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***---GluIle 1069

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Qy   1070 GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089

Db   3289 GGCAAAGACCTCAATTATCTCAAAGACGGAAATGGAACTACTAGTGGCATA------GGC 3342

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Db   3343 AGCAGTGTAGAAAAATATGTCGTGGATGAAAGTGATTACATGTCATTTATAAACAACCCT 3402

Qy   1110 SerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr 1129

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Qy   1130 GluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSer 1149

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Qy   1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168

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Qy   1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248

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Qy   1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288

Db   3880 CTAAAGTGGGTTGCATATGGTTTTCAAGTGTATTTTACCAATGCCTGGTGCTGGCTAGAC 3939

Qy   1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308

Db   3940 TTCCTGATTGTTGATGTCTCACTGGTTAGCTTAACTGCAAATGCCTTGGGTTACTCAGAA 3999

Qy   1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328

Db   4000 CTTGGTGCCATCAAATCCCTCAGAACACTAAGAGCTCTGAGGCCACTGAGAGCTTTGTCC 4059

Qy   1329 ArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348

Db   4060 CGGTTTGAAGGAATGAGGGCTGTTGTAAATGCTCTTTTAGGAGCCATTCCATCTATCATG 4119

Qy   1349 AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu 1368

Db   4120 AATGTACTTCTGGTTTGTCTGATCTTTTGGCTAATATTCAGTATCATGGGAGTGAATCTC 4179

Qy   1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388

Db   4180 TTTGCTGGCAAGTTTTACCATTGTATTAATTACACCACTGGAGAGATGTTTGATGTAAGC 4239

Qy   1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408

Db   4240 GTGGTCAACAACTACAGTGAGTGCAAAGCTCTCATTGAGAGCAATCAAACTGCCAGGTGG 4299

Qy   1409 LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnVal 1428

Db   4300 AAAAATGTGAAAGTAAACTTTGATAACGTAGGACTTGGATATCTGTCTCTACTTCAAGTA 4359

Qy   1429 AlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGlu 1448

Db   4360 GCCACGTTTAAGGGATGGATGGATATTATGTATGCAGCTGTTGATTCACGAAATGTAGAA 4419

Qy   1449 LeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468

Db   4420 TTACAACCCAAGTATGAAGACAACCTGTACATGTATCTTTATTTTGTCATCTTTATTATT 4479

Qy   1469 PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln 1488

Db   4480 TTTGGTTCATTCTTTACCTTGAATCTTTTCATTGGTGTCATCATAGATAACTTCAACCAA 4539

Qy   1489 GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyr 1508

Db   4540 CAGAAAAAGAAGTTTGGAGGTCAAGACATTTTTATGACAGAAGAACAGAAGAAATACTAC 4599

Qy   1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528

Db   4600 AATGCAATGAAAAAACTGGGTTCAAAGAAACCACAAAAACCCATACCTCGACCTGCTAAC 4659

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Db   4660 AAATTCCAAGGAATGGTCTTTGATTTTGTAACCAAACAAGTCTTTGATATCAGCATCATG 4719

Qy   1549 IleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyr 1568

Db   4720 ATCCTCATCTGCCTTAACATGGTCACCATGATGGTGGAAACCGATGACCAGAGTCAAGAA 4779

Qy   1569 ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCys 1588

Db   4780 ATGACAAACATTCTGTACTGGATTAATCTGGTGTTTATTGTTCTGTTCACTGGAGAATGT 4839

Qy   1589 ValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAsp 1608

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Qy   1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
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Qy   2009 Lys 2009
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RESULT 13
HUMHBAX
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DEFINITION  Human voltage-gated sodium channel mRNA, complete cds.
ACCESSION   M94055
VERSION     M94055.1  GI:456678
KEYWORDS    sodium channel alpha subunit; voltage-sensitive sodium channel.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6328)
  AUTHORS   Ahmed,C.M., Ware,D.H., Lee,S.C., Patten,C.D., Ferrer-Montiel,A.V.,
            Schinder,A.F., McPherson,J.D., Wagner-McPherson,C.B., Wasmuth,J.J.,
            Evans,G.A. and Montal,M.
  TITLE     Primary structure, chromosomal localization, and functional
            expression of a voltage-gated sodium channel from human brain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (17), 8220-8224 (1992)
  MEDLINE   92390418
   PUBMED   1325650
REFERENCE   2  (bases 1 to 6328)
  AUTHORS   Sun,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1992) William Sun, Biology Department, 9500
            Gilman Drive, University of California, San Diego, La Jolla, CA
            92093-0357, USA
COMMENT     On Feb 25, 1994 this sequence version replaced gi:183806.
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     CDS             106. .6123
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BASE COUNT     1847 a   1257 c   1433 g   1791 t
ORIGIN
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Alignment Scores:

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Percent Similarity:	92.63%	Conservative:	114
Best Local Similarity:	86.99%	Mismatches:	114
Query Match:	86.78%	Indels:	35
DB:	9	Gaps:	13

US-09-930-871-12 (1-2009) x HUMHBAX (1-6328)

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Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy    260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
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Qy    298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
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Qy   1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050
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Db   3343 AGCAGTGTAGAAAAATATGTCGTGGATGAAAGTGATTACATGTCATTTATAAACAACCCT 3402

Qy   1110 SerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr 1129
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Qy   1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168
Db   3520 AGTTCATCTGAAGGCAGCACGGTTGATATTGGAGCTCCCGCCGAGGGAGAACAGCCTGAG 3579

Qy   1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188
Db   3580 GTTGAACCTGAGGAATCCCTTGAACCTGAAGCCTGTTTTACAGAAGACTGTGTACGGAAG 3639

Qy   1189 PheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg 1208
Db   3640 TTCAAGTGTTGTCAGATAAGCATAGAAGAAGGCAAAGGGAAACTCTGGTGGAATTTGAGG 3699

Qy   1209 ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle 1228
Db   3700 AAAACATGCTATAAGATAGTGGAGCACAATTGGTTCGAAACCTTCATTGTCTTCATGATT 3759

Qy   1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248
Db   3760 CTGCTGAGCAGTGGGGCTCTGGCCTTTGAAGATATATACATTGAGCAGCGAAAAACCATT 3819

Qy   1249 LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeu 1268
Db   3820 AAGACCATGTTAGAATATGCTGACAAGGTTTTCACTTACATATTCATTCTGGAAATGCTG 3879

Qy   1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288
Db   3880 CTAAAGTGGGTTGCATATGGTTTTCAAGTGTATTTTACCAATGCCTGGTGCTGGCTAGAC 3939

Qy   1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308
Db   3940 TTCCTGATTGTTGATGTCTCACTGGTTAGCTTAACTGCAAATGCCTTGGGTTACTCAGAA 3999

Qy   1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328
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Qy   1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388
Db   4180 TTTGCTGGCAAGTTTTACCATTGTATTAATTACACCACTGGAGAGATGTTTGATGTAAGC 4239

Qy   1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408
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Qy   1449 LeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468
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Qy   1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528
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Qy   1649 LeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuPro 1668
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Qy   1689 MetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGlu 1708
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Qy   1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868
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Qy   1949 GlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSer 1968
Db   5920 GAATGTGATGGAACACCCATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAATTCA 5979

Qy   1969 IleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988
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Qy   1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
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Qy   2009 Lys 2009
Db   6097 AAA 6099
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RESULT 14
RNSCPIIR
LOCUS       RNSCPIIR                8553 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat brain mRNA for sodium channel protein II.
ACCESSION   X03639
VERSION     X03639.1  GI:57214
KEYWORDS    glycoprotein; sodium channel.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8553)
  AUTHORS   Noda,M., Ikeda,T., Kayano,T., Suzuki,H., Takeshima,H., Kurasaki,M.,
            Takahashi,H. and Numa,S.
  TITLE     Existence of distinct sodium channel messenger RNAs in rat brain
  JOURNAL   Nature 320 (6058), 188-192 (1986)
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BASE COUNT     2378 a   1883 c   1951 g   2341 t
ORIGIN

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Score:                  9000.50        Matches:         1751
Percent Similarity:     92.63%         Conservative:    121
Best Local Similarity:  86.64%         Mismatches:      114
Query Match:            86.57%         Indels:          35
DB:                     10             Gaps:            13

US-09-930-871-12 (1-2009) x RNSCPIIR (1-8553)

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Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy     80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
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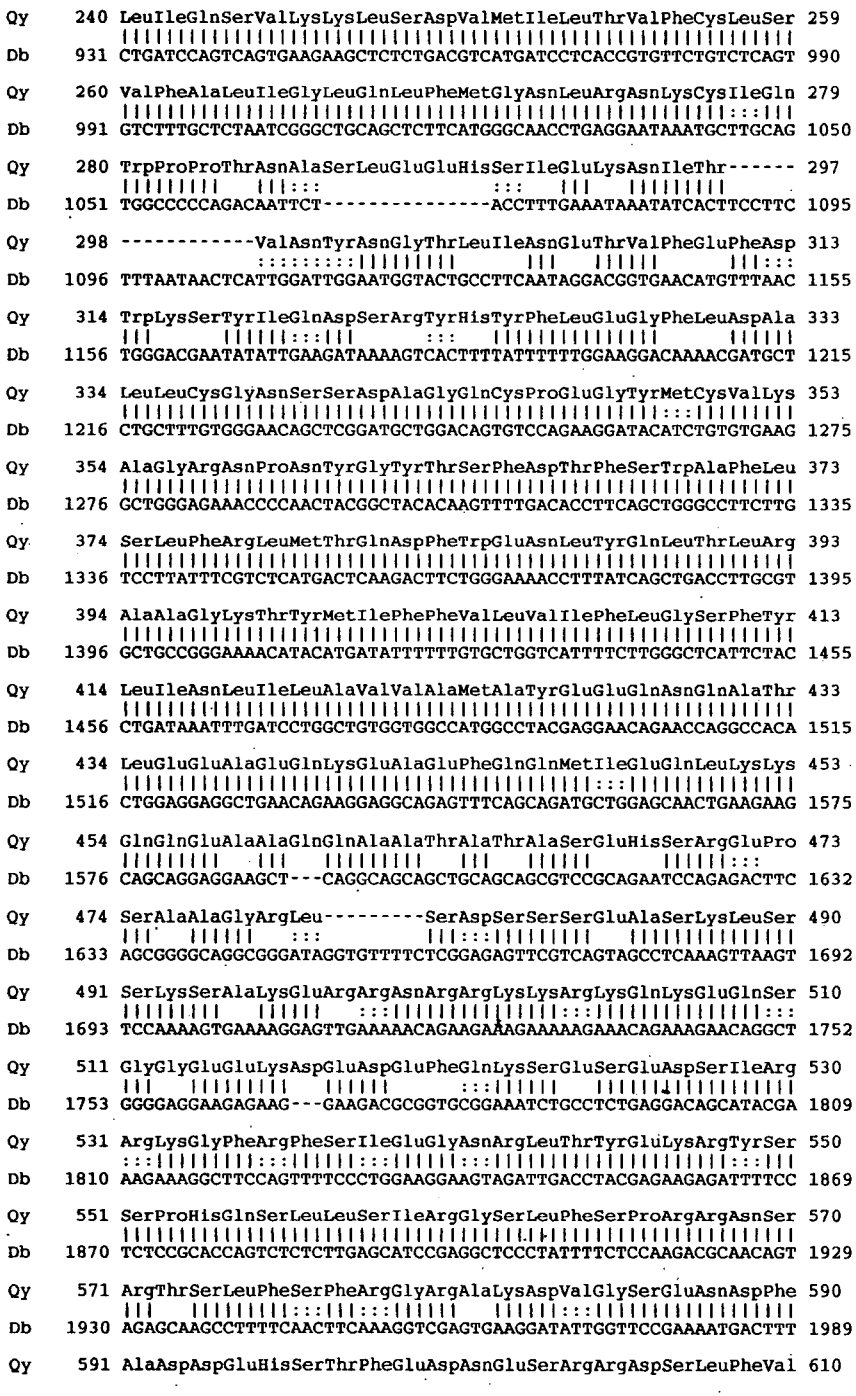
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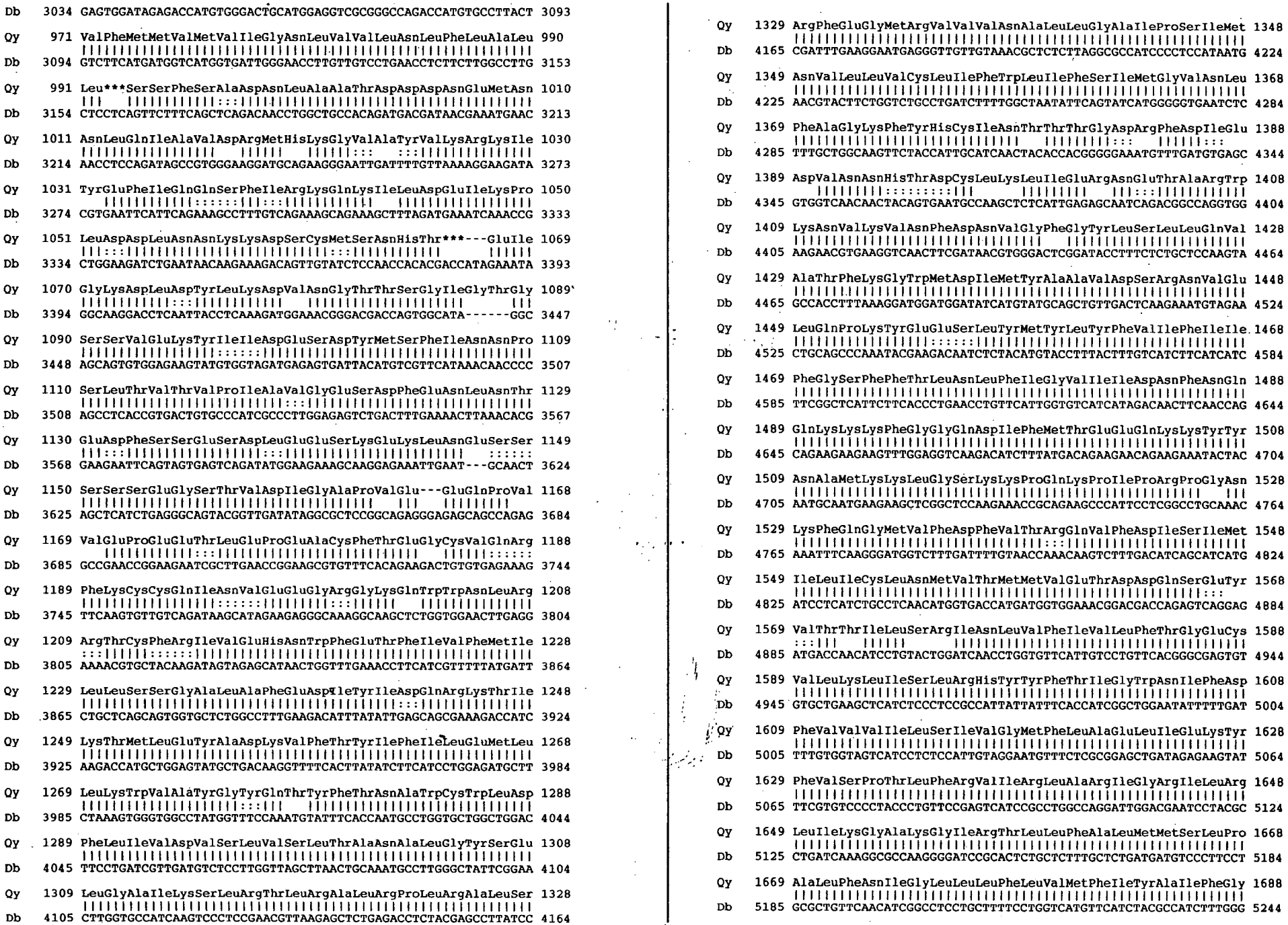
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Qy    220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
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Db 1576 CAGCAGGAGGAAGCT---CAGGCAGCAGCTGCAGCAGCGTCCGCAGAATCCAGAGACTTC 1632
Qy 474 SerAlaAlaGlyArgLeu---------SerAspSerSerSerGluAlaSerLysLeuSer 490
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Qy 511 GlyGlyGluGluLysAspGluAspGluPheGlnLysSerGluSerGluAspSerIleArg 530
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Qy 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570
Db 1870 TCTCCGCACCAGTCTCTCTTGAGCATCCGAGGCTCCCTATTTTCTCCAAGACGCAACAGT 1929
Qy 571 ArgThrSerLeuPheSerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPhe 590
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Qy 591 AlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal 610
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Qy 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSer 730
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Qy 731 ArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCys 750
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Qy 751 SerProTyrTrpLeuLysValLysHisValValAsnLeuValValMetAspProPheVal 770
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Qy 871 LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu 890
Db 2794 AAGTCCTGGCCCACACTGAACATGCTCATTAAGATCATCGGCAACTCGGTGGGTGCACTG 2853
Qy 891 GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGln 910
Db 2854 GGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAG 2913
Qy 911 LeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuPro 930
Db 2914 CTGTTTGGAAAGAGCTACAAGGAGTGTGTCTGTAAGATTTCCAATGATTGTGAGCTCCCG 2973
Qy 931 ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGly 950
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Qy 1011 AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrValLysArgLysIle 1030
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Qy 1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***---GluIle 1069
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Qy 1070 GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089
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Qy 1349 AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu 1368
Db 4225 AACGTACTTCTGGTCTGCCTGATCTTTTGGCTAATATTCAGTATCATGGGGGTGAATCTC 4284
Qy 1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388
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Db   5365 CTGCTGGCCCCTATACTAAATAGCGGACCTCCTGACTGTGACCCTGAAAAAGATCACCCT 5424

Qy   1749 GlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSer 1768
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Db   5425 GGAAGCTCGGTGAAGGGGGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGC 5484

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Db   5485 TACATCATCATATCCTTCCTGGTGGTGGTGAACATGTACATCGCTGTCATCCTGGAGAAC 5544

Qy   1789 PheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPhe 1808
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Qy   1809 TyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeu 1828
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Db   5665 TCTGACTTTGCAGCTGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACAAAGTCCAG 5724

Qy   1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868
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Qy   1869 PheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGln 1888
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Db   5785 TTTGCTTTTACAAAGCGGGTCCTGGGCGAGAGTGGAGAGATGGACGCTCTTCGAATCCAG 5844

Qy   1889 MetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrThr 1908
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Qy   1909 ThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArg 1928
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Qy   1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948
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Qy   1949 GlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSer 1968
                    ||||||||||||||:::|||   |||::::::|||||||||||||||
Db   6025 GAAGACGAGGGAACGCCCATCAAAGAAGACATCATCACAGATAAACTGAACGAGAATTCA 6084

Qy   1969 IleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988
               ||||||||||||:::|||   ||||||   :::   |||||||||||||||
Db   6085 ACTCCAGAGAAGACTGATGTGACACCTTCCACAACTTCT---CCACCTTCCTACGATAGC 6141

Qy   1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
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Db   6142 GTGACGAAACCGGAGAAGGAAAAATTTGAAAAGGACAAATCAGAAAAAGAGGACAAAGGG 6201

Qy   2009 Lys 2009
          |||
Db   6202 AAA 6204

RESULT 15
RATNACHII
LOCUS       RATNACHII              8552 bp    mRNA    linear   ROD 26-OCT-1995
DEFINITION  Rattus norvegicus sodium channel II mRNA.
ACCESSION   M22254
VERSION     M22254.1  GI:1041090
KEYWORDS    Na+ channel; sodium channel.
SOURCE      Rattus norvegicus cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8552)
  AUTHORS   Noda,M. and Numa,S.
  TITLE     Structure and function of sodium channel
  JOURNAL   J. Recept. Res. 7 (1-4), 467-497 (1987)
  MEDLINE   87311395
   PUBMED   2442385
COMMENT     On Oct 27, 1995 this sequence version replaced gi:340712.
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                     /db_xref="taxon:10116"
     misc_feature    2982. .6227
                     /product="Na+ channel"
                     /standard_name="sodium channel II"
                     /note="suspected CDS--internal stop codons preclude
                     translation"
BASE COUNT     2378 a   1880 c   1953 g   2341 t
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          8552
Score:                    8967.50        Matches:         1749
Percent Similarity:       92.53%         Conservative:    121
Best Local Similarity:    86.54%         Mismatches:      116
Query Match:              86.25%         Indels:          36
DB:                       10             Gaps:            13

US-09-930-871-12 (1-2009) x RATNACHII (1-8552)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||   ::::::|||||||||||||||||||||||||||||||   ||||||||||||||
Db    211 ATGGCACGGTCAGTGCTGGTACCTCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 270

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy     41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
          :::||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CGCAAGGACGAAGACGATGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCAGGAAAA 390

Qy     60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
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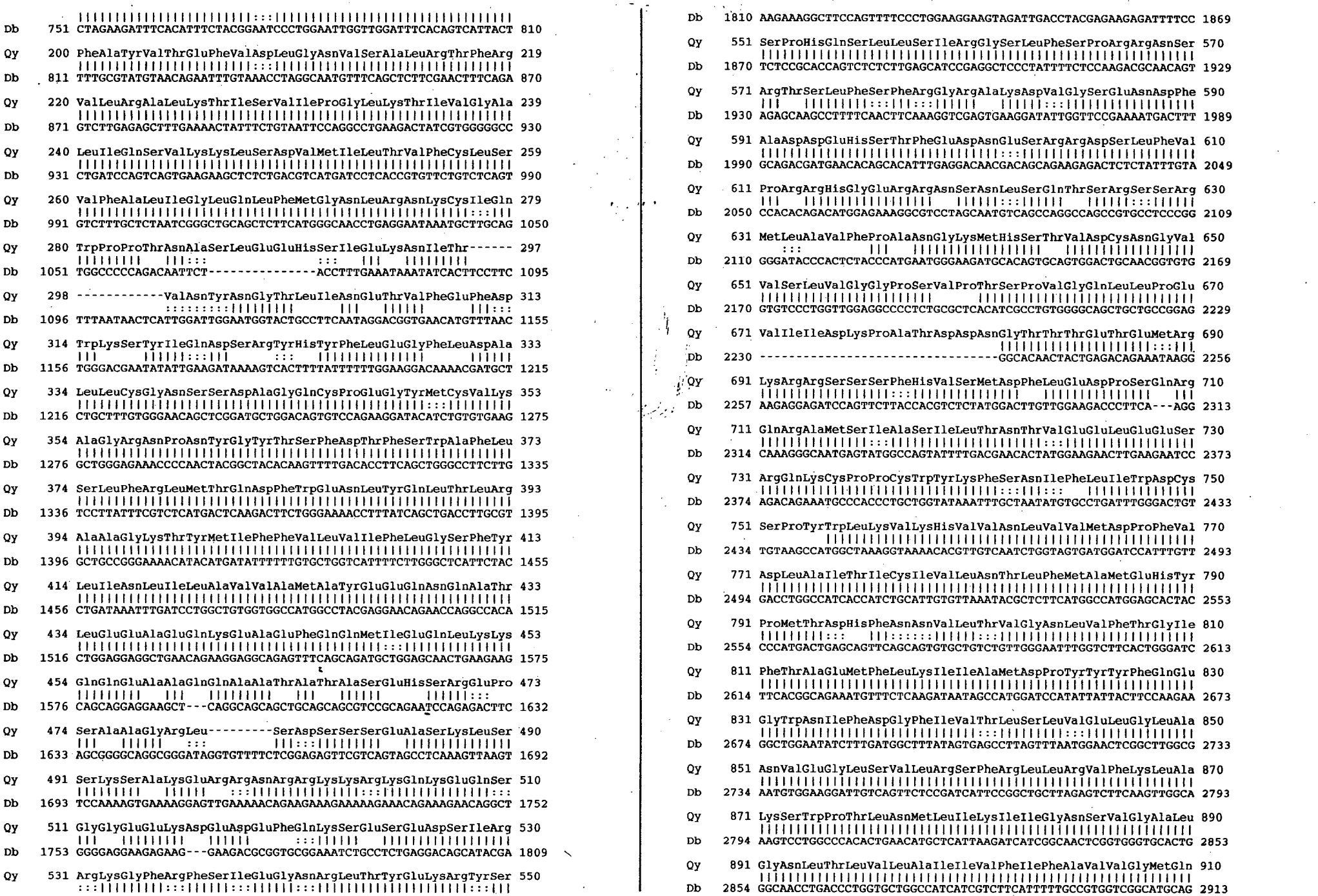
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Qy    160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
          ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    691 ACTTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATCCTTGCAAGGGGCTTTTGT 750

Qy    180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
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Db 751 CTAGAAGATTTCACATTTCTACGGAATCCCTGGAATTGGTTGGATTTCACAGTCATTACT 810
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Qy 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
Db 991 GTCTTTGCTCTAATCGGGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTTGCAG 1050
Qy 280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr------ 297
Db 1051 TGGCCCCCAGACAATTCT----------ACCTTTGAAATAAATATCACTTCCTTC 1095
Qy 298 ----------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
Db 1096 TTTAATAACTCATTGGATTGGAATGGTACTGCCTTCAATAGGACGGTGAACATGTTTAAC 1155
Qy 314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAla 333
Db 1156 TGGGACGAATATATTGAAGATAAAAGTCACTTTTATTTTTTGGAAGGACAAAACGATGCT 1215
Qy 334 LeuLeuCysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353
Db 1216 CTGCTTTGTGGGAACAGCTCGGATGCTGGACAGTGTCCAGAAGGATACATCTGTGTGAAG 1275
Qy 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373
Db 1276 GCTGGGAGAAACCCCAACTACGGCTACACAAGTTTTGACACCTTCAGCTGGGCCTTCTTG 1335
Qy 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393
Db 1336 TCCTTATTTCGTCTCATGACTCAAGACTTCTGGGAAAACCTTTATCAGCTGACCTTGCGT 1395
Qy 394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413
Db 1396 GCTGCCGGGAAAACATACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTAC 1455
Qy 414 LeuIleAsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433
Db 1456 CTGATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAGAACCAGGCCACA 1515
Qy 434 LeuGluGluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLys 453
Db 1516 CTGGAGGAGGCTGAACAGAAGGAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAG 1575
Qy 454 GlnGlnGluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluPro 473
Db 1576 CAGCAGGAGGAAGCT---CAGGCAGCAGCTGCAGCAGCGTCCGCAGAATCCAGAGACTTC 1632
Qy 474 SerAlaAlaGlyArgLeu---------SerAspSerSerSerGluAlaSerLysLeuSer 490
Db 1633 AGCGGGGCAGGCGGGATAGGTGTTTTCTCGGAGAGTTCGTCAGTAGCCTCAAAGTTAAGT 1692
Qy 491 SerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSer 510
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Qy 511 GlyGlyGluGluLysAspGluAspGluPheGlnLysSerGluSerGluAspSerIleArg 530
Db 1753 GGGGAGGAAGAGAAG---GAAGACGCGGTGCGGAAATCTGCCTCTGAGGACAGCATACGA 1809
Qy 531 ArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSer 550
Db 1810 AAGAAAGGCTTCCAGTTTTCCCTGGAAGGAAGTAGATTGACCTACGAGAAGAGATTTTCC 1869
Qy 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570
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Qy 571 ArgThrSerLeuPheSerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPhe 590
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Qy 591 AlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal 610
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Qy 611 ProArgArgHisGlyGluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg 630
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Qy 631 MetLeuAlaValProProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyVal 650
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Qy 651 ValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGlu 670
Db 2170 GTGTCCCTGGTTGGAGGCCCCTCTGCGCTCACATCGCCTGTGGGGCAGCTGCTGCCGGAG 2229
Qy 671 ValIleIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArg 690
Db 2230 ----------GGCACAACTACTGAGACAGAAATAAGG 2256
Qy 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710
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Qy 771 AspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyr 790
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Db 2614 TTCACGGCAGAAATGTTTCTCAAGATAATAGCCATGGATCCATATTATTACTTCCAAGAA 2673
Qy 831 GlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAla 850
Db 2674 GGCTGGAATATCTTTGATGGCTTTATAGTGAGCCTTAGTTTAATGGAACTCGGCTTGGCG 2733
Qy 851 AsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 870
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Qy 891 GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGln 910
Db 2854 GGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAG 2913

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Qy    911 LeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuPro 930
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Db   2914 CTGTTTGGAAG-AGCTACAAGGAGTGTGTCTGTAAGATTTCCAATGATTGTGAGCTCCCG 2972

Qy    931 ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGly 950
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Db   2973 CGCTGGCACATGCACGACTTCTTCCACTCCTTCCTGATCGTGTTTCGAGTGCTGTGTGGG 3032

Qy    951 GluTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr 970
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Db   3033 GAGTGGATAGAGACCATGTGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTACT 3092

Qy    971 ValPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeu 990
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Db   3093 GTCTTCATGATGGTCATGGTGATTGGGAACCTTGTTGTCCTGAACCTCTTCTTGGCCTTG 3152

Qy    991 Leu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsn 1010
          |||   ||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db   3153 CTCCTCAGTTCTTTCAGCTCAGACAACCTGGCTGCCACAGATGACGATAACGAAATGAAC 3212

Qy   1011 AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrValLysArgLysIle 1030
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Db   3213 AACCTCCAGATAGCCGTGGGAAGGATGCAGAAGGGAATTGATTTTGTTAAAAGGAAGATA 3272

Qy   1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050
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Db   3273 CGTGAATTCATTCAGAAAGCCTTTGTCAGAAAGCAGAAAGCTTTAGATGAAATCAAACCG 3332

Qy   1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***---GluIle 1069
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Qy   1070 GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089
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Qy   1090 SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro 1109
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Qy   1110 SerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr 1129
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Qy   1130 GluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSer 1149
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Qy   1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168
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Db   3624 AGCTCATCTGAGGGCAGTACGGTTGATATAGGCACTGCGGCAGAGGGAGAGCAGCCAGAG 3683

Qy   1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188
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Db   3684 GCCGAACCGGAAGAATCGCTTGAACCGGAAGCGTGTTTCACAGAAGACTGTGTGAGAAAG 3743

Qy   1189 PheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg 1208
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Qy   1209 ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle 1228
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Db   3804 AAAACGTGCTACAAGATAGTAGAGCATAACTGGTTTGAAACCTTCATCGTTTTTATGATT 3863

Qy   1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248
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Db   3864 CTGCTCAGCAGTGGTGCTCTGGCCTTTGAAGACATTTATATTGAGCAGCGAAAGACCATC 3923

Qy   1249 LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeu 1268
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Db   3924 AAGACCATGCTGGAGTATGCTGACAAGGTTTTCACTTATATCTTCATCCTGGAGATGCTT 3983

Qy   1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288
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Db   3984 CTAAAGTGGGTGGCCTATGGTTTCCAAATGTATTTCACCAATGCCTGGTGCTGGCTGGAC 4043

Qy   1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308
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Db   4044 TTCCTGATCGTTGATGTCTCCTTGGTTAGCTTAACTGCAAATGCCTTGGGCTATTCGGAA 4103

Qy   1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328
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Db   4104 CTTGGTGCCATCAAGTCCCTCCGAACGTTAAGAGCTCTGAGACCTCTACGAGCCTTATCC 4163

Qy   1329 ArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348
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Qy   1349 AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu 1368
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Qy   1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388
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Db   4284 TTTGCTGGCAAGTTCTACCATTGCATCAACTACACCACGGGGGAAATGTTTGATGTGAGC 4343

Qy   1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408
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Qy   1409 LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnVal 1428
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Qy   1429 AlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGlu 1448
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Db   4464 GCCACCTTTAAAGGATGGATGGATATCATGTATGCAGCTGTTGACTCAAGAAATGTAGAA 4523

Qy   1449 LeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468
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Db   4524 CTGCAGCCCAAATACGAAGACAATCTCTACATGTACCTTTACTTTGTCATCTTCATCATC 4583

Qy   1469 PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln 1488
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Db   4584 TTCGGCTCATTCTTCACCCTGAACCTGTTCATTGGTGTCATCATAGACAACTTCAACCAG 4643

Qy   1489 GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyr 1508
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Qy   1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528
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Qy   1589 ValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAsp 1608
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Qy   1609 PheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyr 1628
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Qy   1629 PheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArg 1648
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Db    5064 TTCGTGTCCCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGC 5123

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Db    5124 CTGATCAAAGGCGCCAAGGGGATCCGCACTCTGCTCTTTGCTCTGATGATGTCCCTTCCT 5183

Qy    1669 AlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGly 1688

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Db    5364 CTGCTGGCCCCTATACTAAATAGCGGACCTCCTGACTGTGACCCTGAAAAAGATCACCCT 5423

Qy    1749 GlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSer 1768

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Qy    1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868

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Qy    1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948

Db    5964 TATCTCCTGAAGCAGAAAGTTAAGAAAGTTTCGTCTATCTATAAAAAAGACAAAGGTAAA 6023

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Db    6084 ACTCCAGAGAAGACTGATGTGACACCTTCCACAACTTCT---CCACCTTCCTACGATAGC 6140

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Qy    2009 Lys 2009

Db    6201 AAA 6203
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Search completed: April 23, 2003, 01:44:23
Job time : 8079 secs

Query Match: 99.71% Indels: 1
DB: 22 Gaps: 0

US-09-930-871-12 (1-2009) x AAH55763 (1-8378)

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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db     506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db     626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db     686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db     746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db     806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db     866 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 925

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db     926 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db     986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db    1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db    1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db    1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db    1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db    1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db    1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db    1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db    1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db    1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db    1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db    1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db    1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db    1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db    1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db    1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db    2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db    2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
Db    2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db    2186 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2245

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db    2246 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2305

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db    2306 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2365

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2366 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2425

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2426 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2485

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2546 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2605

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2606 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2665

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2666 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2725

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2966 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3025

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3265

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3266 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3325

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3326 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3385

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3386 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3445

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3446 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3505

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3506 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3565

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3566 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3625

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3626 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3685

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

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Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3746 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3805

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3806 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3865

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3866 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3925

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240

Db   3926 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCG-GCATTTGAAGATATA 3984

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 4104

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

Db   4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

Db   4165 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4224

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

Db   4225 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4284

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   4285 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4344

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db   4345 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4404

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

Db   4405 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4464

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db   4465 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4524

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440

Db   4525 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4584
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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4585 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4644

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4765 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4824

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4825 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4884

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4885 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4944

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4945 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5004

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5005 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 5064

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   5065 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 5124

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5125 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 5184

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   5185 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 5244

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5245 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5304

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5305 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5364

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5365 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5424

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5425 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5484

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5485 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5544

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5545 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5604

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Db   5605 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5664

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5665 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5724

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Db   5725 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5784

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5785 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5844

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5845 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5904

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Db   5905 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5964

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5965 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 6024

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6025 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 6084

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6085 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 6144

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db   6145 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6204

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6205 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6264

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   6265 GGCAAAGATGAAAAAGCCAAAGGGAAA 6291
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RESULT 4
AAH55764
ID AAH55764 standard; cDNA; 8378 BP.
XX
AC AAH55764;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.

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DR   P-PSDB; AAB99675.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 93-96; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Alignment Scores:
Pred. No.:                0              Length:          8378
Score:                    10321.00       Matches:         2002
Percent Similarity:       99.75%         Conservative:    2
Best Local Similarity:    99.65%         Mismatches:      5
Query Match:              99.27%         Indels:          2
DB:                       22             Gaps:            0

US-09-930-871-12 (1-2009) x AAH55764 (1-8378)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db     326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db     386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db     446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db     506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db     566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db     626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db     686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db     746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db     806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db     866 GCGTTTGTAACAGAATTTGTAAACCTAGGCAATTTTTCAGCTCTTCGCACTTTCAGAGTC 925

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db     926 TTGAGAGCTTTGAAAACTATTTCGGTAATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db     986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db    1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db    1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db    1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db    1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db    1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db    1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db    1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db    1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db    1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db    1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db    1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db    1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db    1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCC-AGCACCTTTGAGGAT 2064

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   2065 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2124

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

Db   2125 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2184

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   2185 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2244

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   2245 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2304

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2305 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2364

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2365 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2424

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2425 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2484

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2485 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2544

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2545 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2604

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2605 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2664

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2665 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2724

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2725 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2784

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2785 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2844

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2845 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2904

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2905 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2964

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2965 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3024

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940

Db   3025 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3084

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   3085 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3144

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   3145 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3204

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   3205 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3264

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3265 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3324

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3325 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3384

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3385 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3444

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3445 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3504

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3505 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3564

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3565 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3624

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3625 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3684

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3685 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3744

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3745 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3804

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3805 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3864

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3865 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3924

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240

Db   3925 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3984

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAAA-TATTTC 4103
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Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4104 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4163

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4164 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4223

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4224 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4283

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4284 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4343

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4344 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4403

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4404 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4463

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4464 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4523

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4524 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4583

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4584 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4643

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4644 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4703

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4704 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4763

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4764 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4823

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4824 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4883

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4884 CAAGTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4943

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4944 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5003

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5004 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 5063

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5064 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 5123

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5124 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 5183
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Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   5184 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 5243

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   5244 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5303

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5304 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5363

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5364 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5423

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5424 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5483

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5484 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5543

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5544 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5603

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5604 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5663

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5664 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5723

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5724 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5783

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5784 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5843

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5844 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5903

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5904 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5963

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5964 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 6023

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6024 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 6083

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6084 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 6143

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6144 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6203

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6204 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6263

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
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          ||||||||||||||||||||||||||
Db    6264 GGCAAAGATGAAAAAGCCAAAGGGAAA 6290

RESULT 5
AAD32839
ID   AAD32839 standard; cDNA; 5997 BP.
XX
AC   AAD32839;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #1.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5997
FT                   /*tag= a
FT                   /product= "Human ion channel protein #1"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20510.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 28-30; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5997 BP; 1773 A; 1185 C; 1338 G; 1698 T; 3 other;

Alignment Scores:
Pred. No.:              0              Length:          5997
Score:                  10320.50       Matches:         1998
Percent Similarity:     99.45%         Conservative:    0
Best Local Similarity:  99.45%         Mismatches:      0
Query Match:            99.26%         Indels:          11
DB:                     24             Gaps:            1

US-09-930-871-12 (1-2009) x AAD32839 (1-5997)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy.   681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrVal*GluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247
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Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   5968 GGCAAAGATGAAAAAGCCAAAGGGAAA 5994

RESULT 6
ABL39689
ID   ABL39689 standard; cDNA; 8131 BP.
XX
AC   ABL39689;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.
XX
KW   Human; sodium channel; SCN1A; chromosome 2q24; gene; ss;
KW   familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             15..6018
FT                   /*tag= a
FT                   /product= "sodium channel SCN1A"
XX
PN   WO200196552-A1.
XX
PD   20-DEC-2001.
XX
PF   12-JUN-2001; 2001WO-JP04956.
XX
PR   13-JUN-2000; 2000JP-0177540.
PR   13-JUN-2000; 2000JP-0177544.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kanazawa I,  Goto J,  Jeong S;
XX
DR   WPI; 2002-098066/13.
DR   P-PSDB; ABB06026.
XX
PT   Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT   studying physiological mechanism in which excitant cells participate
PT   and causes of diseases and developing drugs for motor endplate disease
PT   -
XX
PS   Claim 5; Page 20-40; 88pp; Japanese.
XX
CC   The present invention describes human sodium channels SCN1A and SCN3A.
CC   The present sequence encodes the human sodium channel SCN1A. SCN1A and
CC   SCN3A have been located to the human chromosome 2 long arm, positions
CC   2q24 and 2q24-31 respectively. The sodium channel proteins are useful
CC   in studying the physiological mechanism in which excitant cells
CC   participate and cause human diseases, and in developing remedies for
CC   e.g. familial hypercalcaemic periodic paralysis of extremities and
CC   motor endplate disease.
XX
SQ   Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other;

Alignment Scores:
Pred. No.:                0          Length:          8131
Score:                    10273.00    Matches:         1990
Percent Similarity:       99.00%     Conservative:    0
Best Local Similarity:    99.00%     Mismatches:      8
Query Match:              98.81%     Indels:          12
DB:                       24         Gaps:            2

US-09-930-871-12 (1-2009) x ABL39689 (1-8131)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     19 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 78

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 138

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    139 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 198

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    199 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 258

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    259 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 318

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    319 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 378

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    379 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 438

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    439 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 498

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    499 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 558

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    559 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 618

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 798

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    799 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 858

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    859 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 918

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    919 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 978

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    979 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1038

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1039 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1098

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1099 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTCTGTCCTTGTTTCGACTAATGACT 1158

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1218

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1278

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1338

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1398

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1458

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1518

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1578

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1638

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1698

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGT 1758

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1818

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1878

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1938

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1998

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||
Db   1999 ACATCGCCTGTTGGACAGCTTCTGCCA------------------------------- 2025

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2026 GGGGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2085

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2145

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2205

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   2206 TTTTCCAACATATTCTCAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2265

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 GTCAACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2325

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2385

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2445

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2505

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2565

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2625
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Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2626 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2685

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2686 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2745

Qy    921 CysLysIleAlaSerAspCysGlnLeuPro---ArgTrpHisMetAsnAspPhePheHis 939
Db   2746 TGCAAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCAC 2805

Qy    940 SerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCys 959
Db   2806 TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGT 2865

Qy    960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly 979
Db   2866 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 2925

Qy    980 AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsn 999
Db   2926 AACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAAC 2985

Qy   1000 LeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMet 1019
Db   2986 CTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATG 3045

Qy   1020 HisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIle 1039
Db   3046 CACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATT 3105

Qy   1040 ArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAsp 1059
Db   3106 AGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGAC 3165

Qy   1060 SerCysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspVal 1079
Db   3166 AGTTGTATGTCCAATCATACAACAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTA 3225

Qy   1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGlu 1099
Db   3226 AATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAA 3285

Qy   1100 SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal 1119
Db   3286 AGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTA 3345

Qy   1120 GlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139
Db   3346 GGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAA 3405

Qy   1140 GluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIle 1159
Db   3406 GAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGGACAT 3465

Qy   1160 GlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAla 1179
Db   3466 CGGCGCCCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCT 3525

Qy   1180 CysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGly 1199
Db   3526 TGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGC 3585

Qy   1200 ArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrp 1219
Db   3586 AGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGG 3645

Qy   1220 PheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAsp 1239
Db   3646 TTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGAT 3705

Qy   1240 IleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPhe 1259
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Db   3706 ATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTC 3765

Qy   1260 ThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyr 1279
Db   3766 ACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATAT 3825

Qy   1280 PheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeu 1299
Db   3826 TTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTA 3885

Qy   1300 ThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArg 1319
Db   3886 ACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGA 3945

Qy   1320 AlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAla 1339
Db   3946 GCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCC 4005

Qy   1340 LeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeu 1359
Db   4006 CTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTA 4065

Qy   1360 IlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThr 1379
Db   4066 ATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACC 4125

Qy   1380 ThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeu 1399
Db   4126 ACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTA 4185

Qy   1400 IleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGly 1419
Db   4186 ATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGA 4245

Qy   1420 PheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyr 1439
Db   4246 TTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTAT 4305

Qy   1440 AlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMet 1459
Db   4306 GCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATG 4365

Qy   1460 TyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1479
Db   4366 TATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATT 4425

Qy   1480 GlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePhe 1499
Db   4426 GGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTT 4485

Qy   1500 MetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPro 1519
Db   4486 ATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCG 4545

Qy   1520 GlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThr 1539
Db   4546 CAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACC 4605

Qy   1540 ArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMet 1559
Db   4606 AGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATG 4665

Qy   1560 ValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuVal 1579
Db   4666 GTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTG 4725

Qy   1580 PheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyr 1599
Db   4726 TTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTAT 4785

Qy   1600 PheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMet 1619
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Db   4786 TTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATG 4845

Qy   1620 PheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArg 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4846 TTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGT 4905

Qy   1640 LeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeu 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4906 CTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTG 4965

Qy   1660 LeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeu 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4966 CTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTA 5025

Qy   1680 ValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVal 1699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5026 GTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTT 5085

Qy   1700 GlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGln 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5086 GGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAA 5145

Qy   1720 IleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProPro 1739
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Db   5146 ATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCC 5205

Qy   1740 AspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPro 1759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5206 GACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCA 5265

Qy   1760 SerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsn 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5266 TCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAAC 5325

Qy   1780 MetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPro 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5326 ATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCT 5385

Qy   1800 LeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAla 1819
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Db   5386 CTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCA 5445

Qy   1820 ThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeu 1839
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Db   5446 ACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTC 5505

Qy   1840 AsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGly 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5506 AATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGT 5565

Qy   1860 AspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSer 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5566 GACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGT 5625

Qy   1880 GlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSer 1899
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Db   5626 GGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCC 5685

Qy   1900 LysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAla 1919
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Db   5686 AAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCT 5745

Qy   1920 ValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSer 1939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5746 GTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCC 5805

Qy   1940 PheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMet 1959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5806 TTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATG 5865

Qy   1960 IleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThr 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5866 ATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACT 5925
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Qy   1980 AlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGln 1999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5926 GCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAA 5985

Qy   2000 GluGlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||||||
Db   5986 GAAGGCAAAGATGAAAAAGCCAAAGGGAAA 6015

RESULT 7
AAD32845
ID   AAD32845 standard; cDNA; 5922 BP.
XX
AC   AAD32845;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #7.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5922
FT                   /*tag= a
FT                   /product= "Human ion channel protein #7"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20516.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 62-64; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
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CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;

Alignment Scores:
Pred. No.:                0          Length:          5922
Score:                    10197.00   Matches:         1972
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              98.08%     Indels:          0
DB:                       24         Gaps:            0

US-09-930-871-12 (1-2009) x AAD32845 (1-5922)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740

Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5916

RESULT 8
AAD32840
ID   AAD32840 standard; cDNA; 5889 BP.
XX
AC   AAD32840;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5889
FT                   /*tag= a
FT                   /product= "Human ion channel protein #2"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
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XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20511.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 35-36; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;

Alignment Scores:

Pred. No.:	0	Length:	5889
Score:	10124.50	Matches:	1961
Percent Similarity:	99.44%	Conservative:	0
Best Local Similarity:	99.44%	Mismatches:	0
Query Match:	97.38%	Indels:	11
DB:	24	Gaps:	1

US-09-930-871-12 (1-2009) x AAD32840 (1-5889)

```
Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
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Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
           ||||||||||||||||||||||||||||
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Db    2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db    2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy     721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Db    2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy     741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Db    2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy     761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy     781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db    2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy     801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy     821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy     841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy     861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy     881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Db    2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy     901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Db    2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy     921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db    2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy     941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Db    2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy     961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy     981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy    1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db    2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy    1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy    1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy    1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy    1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy    1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy    1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy    1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447
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Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy    1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy    1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy    1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
           ||||||||||||||||||||||||||||||||||
Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5883

RESULT 9
AAH55793
ID   AAH55793 standard; cDNA; 8349 BP.
XX
AC   AAH55793;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN2A nucleotide sequence SEQ ID NO:33.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99676.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 116-119; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8349 BP; 2496 A; 1591 C; 1775 G; 2487 T; 0 other;
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Alignment Scores:
Pred. No.:              0              Length:          8349
Score:                  9025.50        Matches:         1759
Percent Similarity:     92.63%         Conservative:    113
Best Local Similarity:  87.04%         Mismatches:      114
Query Match:            86.81%         Indels:          35
DB:                     22             Gaps:            13

US-09-930-871-12 (1-2009) x AAH55793 (1-8349)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||   |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||
Db    106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||:::|||||||||||||||||||||||||||||   ||||||   :::
Db    166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

Qy     41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
          :::||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy     60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
          :::||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy     80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy    100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119
          ||||||||||||||   ||||||||||||||||||||||||||||||:::||||||
Db    406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy    120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139
          :::||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db    466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525

Qy    140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 585

Qy    160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db    586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy    180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 705

Qy    200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765

Qy    220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825

Qy    240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885

Qy    260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db    886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945

Qy    280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr------ 297
          |||||||||   |||:::               |||   |||   |||||||||
Db    946 TGGCCTCCAGATAATTCT--------------TCCTTTGAAATAAATATCACTTCCTTC 990

Qy    298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
                       ::::::   |||||||||      |||   ||||||      |||:::
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Qy 1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050
Db 3169 CGTGAATTTATTCAGAAAGCCTTTGTTAGGAAGCAGAAAGCTTTAGATGAAATTAAACCG 3228
Qy 1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***---GluIle 1069
Db 3229 CTTGAAGATCTAAATAATAAAAAAGACAGCTGTATTTCCAACCATACCACCATAGAAATA 3288
Qy 1070 GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089
Db 3289 GGCAAAGACCTCAATTATCTCAAAGACGGAAATGGAACTACTAGTGGCATA------GGC 3342
Qy 1090 SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro 1109
Db 3343 AGCAGTGTAGAAAAATATGTCGTGGATGAAAGTGATTACATGTCATTTATAAACAACCCT 3402
Qy 1110 SerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr 1129
Db 3403 AGCCTCACTGTGACAGTACCAATTGCTGTTGGAGAATCTGACTTTGAAAATTTAAATACT 3462
Qy 1130 GluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSer 1149
Db 3463 GAAGAATTCAGCAGCGAGTCAGATATGGAGGAAAGCAAAGAGAAGCTAAAT---GCAACT 3519
Qy 1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168
Db 3520 AGTTCATCTGAAGGCAGCACGGTTGATATTGGAGCTCCCGCCGAGGGAGAACAGCCTGAG 3579
Qy 1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188
Db 3580 GTTGAACCTGAGGAATCCCTTGAACCTGAAGCCTGTTTTACAGAAGACTGTGTACGGAAG 3639
Qy 1189 PheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg 1208
Db 3640 TTCAAGTGTTGTCAGATAAGCATAGAAGAAGGCAAAGGGAAACTCTGGTGGAATTTGAGG 3699
Qy 1209 ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle 1228
Db 3700 AAAACATGCTATAAGATAGTGGAGCACAATTGGTTCGAAACCTTCATTGTCTTCATGATT 3759
Qy 1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248
Db 3760 CTGCTGAGCAGTGGGGCTCTGGCCTTTGAAGATATATACATTGAGCAGCGAAAAACCATT 3819
Qy 1249 LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeu 1268
Db 3820 AAGACCATGTTAGAATATGCTGACAAGGTTTTCACTTACATATTCATTCTGGAAATGCTG 3879
Qy 1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288
Db 3880 CTAAAGTGGGTTGCATATGGTTTTCAAGTGTATTTTACCAATGCCTGGTGCTGGCTAGAC 3939
Qy 1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308
Db 3940 TTCCTGATTGTTGATGTCTCACTGGTTAGCTTAACTGCAAATGCCTTGGGTTACTCAGAA 3999
Qy 1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328
Db 4000 CTTGGTGCCATCAAATCCCTCAGAACACTAAGAGCTCTGAGGCCACTGAGAGCTTTGTCC 4059
Qy 1329 ArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348
Db 4060 CGGTTTGAAGGAATGAGGGCTGTTGTAAATGCTCTTTTAGGAGCCATTCCATCTATCATG 4119
Qy 1349 AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu 1368
Db 4120 AATGTACTTCTGGTTTGTCTGATCTTTTGGCTAATATTCAGTATCATGGGAGTGAATCTC 4179
Qy 1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388
Db 4180 TTTGCTGGCAAGTTTTACCATTGTATTAATTACACCACTGGAGAGATGTTTGATGTAAGC 4239
Qy 1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408
Db 4240 GTGGTCAACAACTACAGTGAGTGCAAAGCTCTCATTGAGAGCAATCAAACTGCCAGGTGG 4299
Qy 1409 LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnVal 1428
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Qy 1429 AlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGlu 1448
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Qy 1449 LeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468
Db 4420 TTACAACCCAAGTATGAAGACAACCTGTACATGTATCTTTATTTTGTCATCTTTATTATT 4479
Qy 1469 PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln 1488
Db 4480 TTTGGTTCATTCTTTACCTTGAATCTTTTCATTGGTGTCATCATAGATAACTTCAACCAA 4539
Qy 1489 GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyr 1508
Db 4540 CAGAAAAAGAAGTTTGGAGGTCAAGACATTTTTATGACAGAAGAACAGAAGAAATACTAC 4599
Qy 1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528
Db 4600 AATGCAATGAAAAAACTGGGTTCAAAGAAACCACAAAAACCCATACCTCGACCTGCTAAC 4659
Qy 1529 LysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMet 1548
Db 4660 AAATTCCAAGGAATGGTCTTTGATTTTGTAACCAAACAAGTCTTTGATATCAGCATCATG 4719
Qy 1549 IleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyr 1568
Db 4720 ATCCTCATCTGCCTTAACATGGTCACCATGATGGTGGAAACCGATGACCAGAGTCAAGAA 4779
Qy 1569 ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCys 1588
Db 4780 ATGACAAACATTCTGTACTGGATTAATCTGGTGTTTATTGTTCTGTTCACTGGAGAATGT 4839
Qy 1589 ValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAsp 1608
Db 4840 GTGCTGAAACTGATCTCTCTTCGTTACTACTATTTCACTATTGGATGGAATATTTTTGAT 4899
Qy 1609 PheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyr 1628
Db 4900 TTTGTGGTGGTCATTCTCTCCATTGTAGGAATGTTTCTGGCTGAACTGATAGAAAAGTAT 4959
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Db 4960 TTTGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGT 5019
Qy 1649 LeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuPro 1668
Db 5020 CTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCT 5079
Qy 1669 AlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGly 1688
Db 5080 GCGTTGTTTAACATCGGCCTCCTTCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGG 5139
Qy 1689 MetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGlu 1708
Db 5140 ATGTCCAATTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAG 5199
Qy 1709 ThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGly 1728
Db 5200 ACCTTTGGCAACAGCATGATCTGCCTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGA 5259
Qy 1729 LeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnPro 1748
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Db    5320 GGAAGCTCAGTTAAAGGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGT 5379

Qy    1769 TyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsn 1788
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5380 TACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAAC 5439

Qy    1789 PheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPhe 1808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5440 TTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTC 5499

Qy    1809 TyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeu 1828
           ||||||||||||||||||||||||||||||||||||||||:::|||||||   ||||||
Db    5500 TATGAGGTTTGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTTGCCAAACTT 5559

Qy    1829 SerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGln 1848
           |||   ||||||   ||||||:::||||||||   :::   :::||||||||||:::|||
Db    5560 TCTGATTTTGCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAG 5619

Qy    1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5620 CTCATTGCCATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATCTTA 5679

Qy    1869 PheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGln 1888
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680 TTTGCTTTTACAAAGCGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAG 5739

Qy    1889 MetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrThr 1908
           ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    5740 ATGGAAGAGCGATTCATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCCATTACGACC 5799

Qy    1909 ThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArg 1928
           ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db    5800 ACGTTGAAACGCAAACAAGAGGAGGTGTCTGCTATTATTATCCAGAGGGCTTACAGACGC 5859

Qy    1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948
           :::||||||||:::   ||||||::   |||      |||   |||:::|||   |||
Db    5860 TACCTCTTGAAGCAAAAAGTTAAAAAGGTATCAAGTATATACAAGAAAGACAAAGGCAAA 5919

Qy    1949 GlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSer 1968
                       ||||||||||||   :::||||||::::::|||||||||||||
Db    5920 GAATGTGATGGAACACCCATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAATTCA 5979

Qy    1969 IleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988
              ||||||||||||:::|||   ||||||   :::   ||||||||||||||||
Db    5980 ACTCCAGAGAAAACCGATATGACGCCTTCCACCACGTCT---CCACCCTCGTATGATAGT 6036

Qy    1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
           ||||||||||||      ||||||   |||:::::      :::::::::   ||||||
Db    6037 GTGACCAAACCAGAAAAAGAAAAATTTGAAAAAGACAAATCAGAAAAGGAAGACAAAGGG 6096

Qy    2009 Lys 2009
           |||
Db    6097 AAA 6099

RESULT 10
AAH55794
ID   AAH55794 standard; cDNA; 8349 BP.
XX
AC   AAH55794;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human neonatal form of SCN2A nucleotide sequence SEQ ID NO:34.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99677.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 119-122; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8349 BP; 2496 A; 1591 C; 1775 G; 2487 T; 0 other;

Alignment Scores:
Pred. No.:                0                Length:          8349
Score:                    9025.50          Matches:         1759
Percent Similarity:       92.63%           Conservative:    113
Best Local Similarity:    87.04%           Mismatches:      114
Query Match:              86.81%           Indels:          35
DB:                       22               Gaps:            13

US-09-930-871-12 (1-2009) x AAH55794 (1-8349)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||   |||:::|||||||||||||||||||||||||||||||   ||||||||||||||
Db    106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||:::|||||||||||||||||||||||||   ||||||   :::
Db    166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

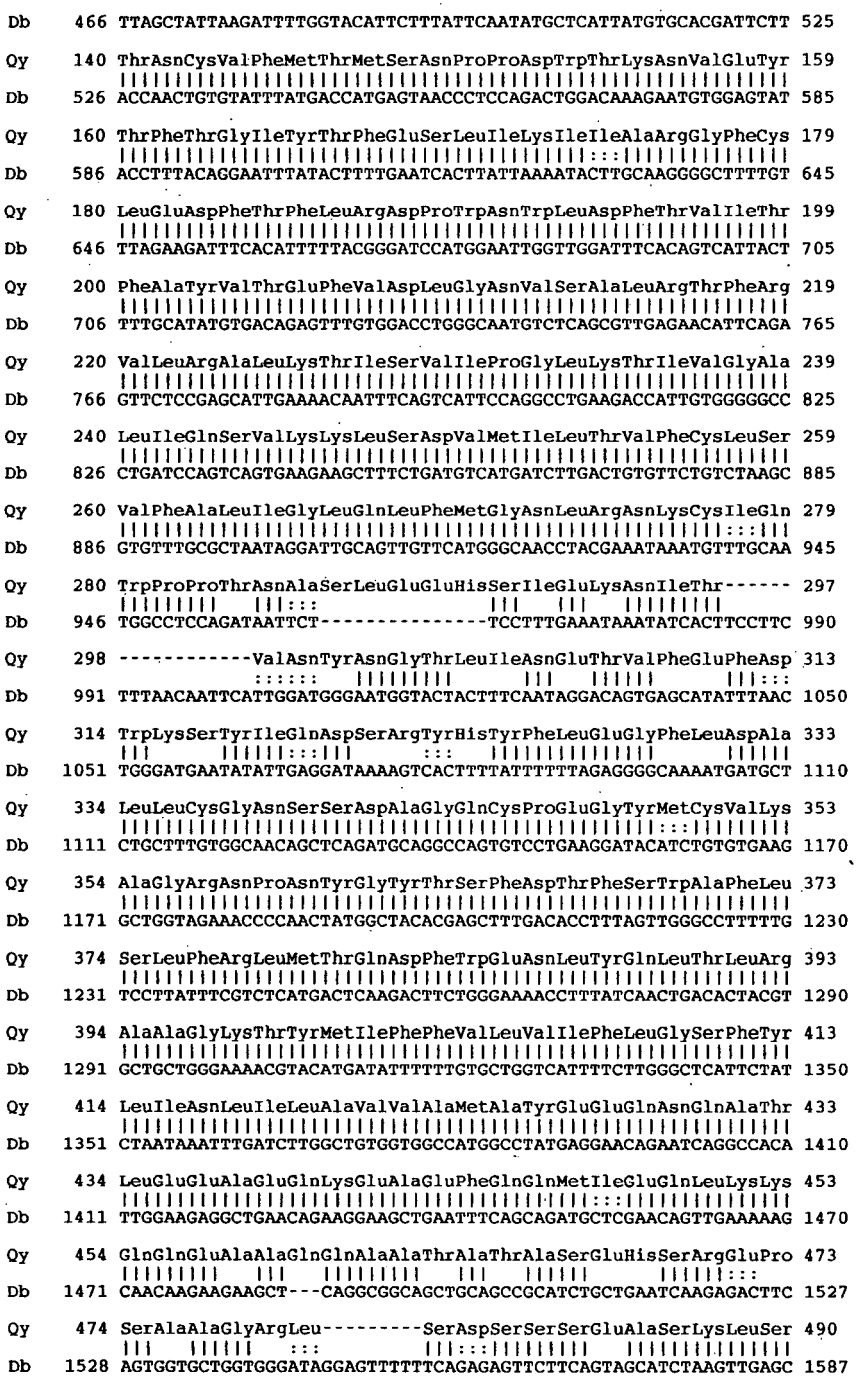
Qy     41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
          :::||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy     60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
          :::||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy     80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy    100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119
              ||||||||||||||   ||||||||||||||||||||||||||||:::|||||||
Db    406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy    120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139
          :::||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
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Db 466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525
Qy 140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159
Db 526 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 585
Qy 160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
Db 586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645
Qy 180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
Db 646 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 705
Qy 200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
Db 706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765
Qy 220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
Db 766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825
Qy 240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
Db 826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885
Qy 260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
Db 886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945
Qy 280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr------ 297
Db 946 TGGCCTCCAGATAATTCT--------------TCCTTTGAAATAAATATCACTTCCTTC 990
Qy 298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
Db 991 TTTAACAATTCATTGGATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAAC 1050
Qy 314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAla 333
Db 1051 TGGGATGAATATATTGAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCT 1110
Qy 334 LeuLeuCysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353
Db 1111 CTGCTTTGTGGCAACAGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAG 1170
Qy 354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373
Db 1171 GCTGGTAGAAACCCCAACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTG 1230
Qy 374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393
Db 1231 TCCTTATTTCGTCTCATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGT 1290
Qy 394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413
Db 1291 GCTGCTGGGAAAACGTACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTAT 1350
Qy 414 LeuIleAsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433
Db 1351 CTAATAAATTTGATCTTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACA 1410
Qy 434 LeuGluGluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLys 453
Db 1411 TTGGAAGAGGCTGAACAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAG 1470
Qy 454 GlnGlnGluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluPro 473
Db 1471 CAACAAGAAGAAGCT---CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTC 1527
Qy 474 SerAlaAlaGlyArgLeu---------SerAspSerSerSerGluAlaSerLysLeuSer 490
Db 1528 AGTGGTGCTGGTGGGATAGGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGC 1587
Qy 491 SerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSer 510
Db 1588 TCCAAAAGTGAAAAAGAGCTGAAAAACAGAAGAAAGAAAAAGAAACAGAAAGAACAGTCT 1647
Qy 511 GlyGlyGluGluLysAspGluAspGluPheGlnLysSerGluSerGluAspSerIleArg 530
Db 1648 GGAGAAGAAGAGAAAAAT---GACAGAGTCCTAAAATCGGAATCTGAAGACAGCATAAGA 1704
Qy 531 ArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSer 550
Db 1705 AGAAAAGGTTTCGTTTTTCCTTGGAAGGAAGTAGGCTGACATATGAAAAGAGATTTTCT 1764
Qy 551 SerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSer 570
Db 1765 TCTCCACACCAGTCCTTACTGAGCATCCGTGGCTCCCTTTTCTCTCCAAGACGCAACAGT 1824
Qy 571 ArgThrSerLeuPheSerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPhe 590
Db 1825 AGGGCGAGCCTTTTCAGCTTCAGAGGTCGAGCAAAGGACATTGGCTCTGAGAATGACTTT 1884
Qy 591 AlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheVal 610
Db 1885 GCTGATGATGAGCACAGCACCTTTGAGGACAATGACAGCCGAAGAGACTCTCTGTTCGTG 1944
Qy 611 ProArgArgHisGlyGluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArg 630
Db 1945 CCGCACAGACATGGAGAACGGCGCCACAGCAATGTCAGCCAGGCCAGCCGTGCCTCCAGG 2004
Qy 631 MetLeuAlaValProProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyVal 650
Db 2005 GTGCTCCCCATCCTGCCCATGAATGGGAAGATGCATAGCGCTGTGGACTGCAATGGTGTG 2064
Qy 651 ValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGlu 670
Db 2065 GTCTCCCTGGTCGGGGGCCCTTCTACCCTCACATCT---GCTGGGCAGCTCCTACCAGAG 2121
Qy 671 ValIleIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArg 690
Db 2122 --------------------------------GGCACAACTACTGAAACAGAAATAAGA 2148
Qy 691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710
Db 2149 AAGAGACGGTCCAGTTCTTATCATGTTTCCATGGATTTATTGGAAGATCCTACATCAAGG 2208
Qy 711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSer 730
Db 2209 CAAAGAGCAATGAGTATAGCCAGTATTTTGACCAACACCATGGAAGAACTTGAAGAATCC 2268
Qy 731 ArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCys 750
Db 2269 AGACAGAAATGCCCACCATGCTGGTATAAATTTGCTAATATGTGTTTGATTTGGGACTGT 2328
Qy 751 SerProTyrTrpLeuLysValLysHisValValAsnLeuValValMetAspProPheVal 770
Db 2329 TGTAAACCATGGTTAAAGGTGAAACACCTTGTCAACCTGGTTGTAATGGACCCATTTGTT 2388
Qy 771 AspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyr 790
Db 2389 GACCTGGCCATCACCATCTGCATTGTCTTAAATACACTCTTCATGGCTATGGAGCACTAT 2448
Qy 791 ProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIle 810
Db 2449 CCCATGACGGAGCAGTTCAGCAGTGTACTGTCTGTTGGAAACCTGGTCTTCACAGGGATC 2508
Qy 811 PheThrAlaGluMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGlu 830
Db 2509 TTCACAGCAGAAATGTTTCTCAAGATAATTGCCATGGATCCATATTATTACTTTCAAGAA 2568
Qy 831 GlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAla 850
Db 2569 GGCTGGAATATTTTTGATGGTTTTATTGTGAGCCTTAGTTTAATGGAACTTGGTTTGGCA 2628

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Qy    851 AsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAla 870
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 AATGTGGAAGGATTGTCAGTTCTCCGATCATTCCGGCTGCTCCGAGTTTTCAAGTTGGCA 2688

Qy    871 LysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeu 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 AAATCTTGGCCAACTCTAAATATGCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTA 2748

Qy    891 GlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGln 910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2749 GGAAACCTCACCTTGGTATTGGCCATCATCGTCTTCATTTTTGCTGTGGTCGGCATGCAG 2808

Qy    911 LeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuPro 930
          ||||||||||||||||||||||:::|||||||||||||||:::::|||||:::||||||
Db   2809 CTCTTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATTTCCAATGATTGTGAACTCCCA 2868

Qy    931 ArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGly 950
          ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db   2869 CGCTGGCACATGCATGACTTTTTCCACTCCTTCCTGATCGTGTTCCGCGTGCTGTGTGGA 2928

Qy    951 GluTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThr 970
          ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db   2929 GAGTGGATAGAGACCATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTACT 2988

Qy    971 ValPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeu 990
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2989 GTCTTCATGATGGTCATGGTGATTGGAAATCTAGTGGTTCTGAACCTCTTCTTGGCCTTG 3048

Qy    991 Leu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsn 1010
          |||   ||||||||||||:::|||||||||||||||||||||||||||||||||||||||.
Db   3049 CTTTTGAGTTCCTTCAGTTCTGACAATCTTGCTGCCACTGATGATGATAACGAAATGAAT 3108

Qy   1011 AsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrValLysArgLysIle 1030
          ||||||||||||||||||   ||||||   ||||||:::   :::||||||||||||||||
Db   3109 AATCTCCAGATTGCTGTGGGAAGGATGCAGAAAGGAATCGATTTTGTTAAAAGAAAAATA 3168

Qy   1031 TyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysPro 1050
             ||||||||||||:::::::|||:::|||||||||||||   ||||||||||||||||||
Db   3169 CGTGAATTTATTCAGAAAGCCTTTGTTAGGAAGCAGAAAGCTTTAGATGAAATTAAACCG 3228

Qy   1051 LeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr***---GluIle 1069
          |||:::|||||||||||||||||||||||||:::|||||||||||||      ||||||
Db   3229 CTTGAAGATCTAAATAATAAAAAAGACAGCTGTATTTCCAACCATACCACCATAGAAATA 3288

Qy   1070 GlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGly 1089
          ||||||||||||:::|||||||||||||   |||||||||||||||||||||      |||
Db   3289 GGCAAAGACCTCAATTATCTCAAAGACGGAAATGGAACTACTAGTGGCATA------GGC 3342

Qy   1090 SerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnPro 1109
          ||||||||||||||||||:::::|||||||||||||||||||||||||||||||||||||||
Db   3343 AGCAGTGTAGAAAAATATGTCGTGGATGAAAGTGATTACATGTCATTTATAAACAACCCT 3402

Qy   1110 SerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThr 1129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3403 AGCCTCACTGTGACAGTACCAATTGCTGTTGGAGAATCTGACTTTGAAAATTTAAATACT 3462

Qy   1130 GluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSer 1149
          |||:::|||||||||||||||||:::|||||||||||||||||||||||   ::::::
Db   3463 GAAGAATTCAGCAGCGAGTCAGATATGGAGGAAAGCAAAGAGAAGCTAAAT---GCAACT 3519

Qy   1150 SerSerSerGluGlySerThrValAspIleGlyAlaProValGlu---GluGlnProVal 1168
          ||||||||||||||||||||||||||||||||||||||||||   |||   |||||||||
Db   3520 AGTTCATCTGAAGGCAGCACGGTTGATATTGGAGCTCCCGCCGAGGGAGAACAGCCTGAG 3579

Qy   1169 ValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArg 1188
          ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db   3580 GTTGAACCTGAGGAATCCCTTGAACCTGAAGCCTGTTTTACAGAAGACTGTGTACGGAAG 3639

Qy   1189 PheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArg 1208
          ||||||||||||||||||:::::|||||||||:::||||||   ||||||||||||||||
Db   3640 TTCAAGTGTTGTCAGATAAGCATAGAAGAAGGCAAAGGGAAACTCTGGTGGAATTTGAGG 3699

Qy   1209 ArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIle 1228
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          :::||||||:::::|||||||||||||||||||||||||||||||||||||||||||||||
Db   3700 AAAACATGCTATAAGATAGTGGAGCACAATTGGTTCGAAACCTTCATTGTCTTCATGATT 3759

Qy   1229 LeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIle 1248
          ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db   3760 CTGCTGAGCAGTGGGGCTCTGGCCTTTGAAGATATATACATTGAGCAGCGAAAAACCATT 3819

Qy   1249 LysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeu 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3820 AAGACCATGTTAGAATATGCTGACAAGGTTTTCACTTACATATTCATTCTGGAAATGCTG 3879

Qy   1269 LeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAsp 1288
          ||||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db   3880 CTAAAGTGGGTTGCATATGGTTTTCAAGTGTATTTTACCAATGCCTGGTGCTGGCTAGAC 3939

Qy   1289 PheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGlu 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3940 TTCCTGATTGTTGATGTCTCACTGGTTAGCTTAACTGCAAATGCCTTGGGTTACTCAGAA 3999

Qy   1309 LeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSer 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4000 CTTGGTGCCATCAAATCCCTCAGAACACTAAGAGCTCTGAGGCCACTGAGAGCTTTGTCC 4059

Qy   1329 ArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMet 1348
          ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db   4060 CGGTTTGAAGGAATGAGGGCTGTTGTAAATGCTCTTTTAGGAGCCATTCCATCTATCATG 4119

Qy   1349 AsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeu 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4120 AATGTACTTCTGGTTTGTCTGATCTTTTGGCTAATATTCAGTATCATGGGAGTGAATCTC 4179

Qy   1369 PheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGlu 1388
          ||||||||||||||||||||||||||||||||   |||||||||:::   ||||||:::
Db   4180 TTTGCTGGCAAGTTTTACCATTGTATTAATTACACCACTGGAGAGATGTTTGATGTAAGC 4239

Qy   1389 AspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrp 1408
             |||||||||:::::::::|||      |||||||||   |||:::||||||||||||
Db   4240 GTGGTCAACAACTACAGTGAGTGCAAAGCTCTCATTGAGAGCAATCAAACTGCCAGGTGG 4299

Qy   1409 LysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnVal 1428
          ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db   4300 AAAAATGTGAAAGTAAACTTTGATAACGTAGGACTTGGATATCTGTCTCTACTTCAAGTA 4359

Qy   1429 AlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGlu 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4360 GCCACGTTTAAGGGATGGATGGATATTATGTATGCAGCTGTTGATTCACGAAATGTAGAA 4419

Qy   1449 LeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIle 1468
          ||||||||||||||||||:::::|||||||||||||||||||||||||||||||||||||||
Db   4420 TTACAACCCAAGTATGAAGACAACCTGTACATGTATCTTTATTTTGTCATCTTTATTATT 4479

Qy   1469 PheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGln 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4480 TTTGGTTCATTCTTTACCTTGAATCTTTTCATTGGTGTCATCATAGATAACTTCAACCAA 4539

Qy   1489 GlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyr 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4540 CAGAAAAAGAAGTTTGGAGGTCAAGACATTTTTATGACAGAAGAACAGAAGAAATACTAC 4599

Qy   1509 AsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsn 1528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db   4600 AATGCAATGAAAAAACTGGGTTCAAAGAAACCACAAAAACCCATACCTCGACCTGCTAAC 4659

Qy   1529 LysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMet 1548
          ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db   4660 AAATTCCAAGGAATGGTCTTTGATTTTGTAACCAAACAAGTCTTTGATATCAGCATCATG 4719

Qy   1549 IleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyr 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   4720 ATCCTCATCTGCCTTAACATGGTCACCATGATGGTGGAAACCGATGACCAGAGTCAAGAA 4779

Qy   1569 ValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCys 1588
          :::|||   ||||||      ||||||||||||||||||||||||||||||||||||||
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Db   4780 ATGACAAACATTCTGTACTGGATTAATCTGGTGTTTATTGTTCTGTTCACTGGAGAATGT 4839

Qy   1589 ValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAsp 1608
          ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db   4840 GTGCTGAAACTGATCTCTCTTCGTTACTACTATTTCACTATTGGATGGAATATTTTTGAT 4899

Qy   1609 PheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyr 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4900 TTTGTGGTGGTCATTCTCTCCATTGTAGGAATGTTTCTGGCTGAACTGATAGAAAAGTAT 4959

Qy   1629 PheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArg 1648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4960 TTTGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGT 5019

Qy   1649 LeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuPro 1668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5020 CTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCT 5079

Qy   1669 AlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGly 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5080 GCGTTGTTTAACATCGGCCTCCTTCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGG 5139

Qy   1689 MetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGlu 1708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5140 ATGTCCAATTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAG 5199

Qy   1709 ThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGly 1728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5200 ACCTTTGGCAACAGCATGATCTGCCTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGA 5259

Qy   1729 LeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnPro 1748
          |||||||||||||||||||||||   ||||||||||||||||:::|||   :::|||
Db   5260 TTGCTAGCACCTATTCTTAATAGTGGACCTCCAGACTGTGACCCTGACAAAGATCACCCT 5319

Qy   1749 GlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSer 1768
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5320 GGAAGCTCAGTTAAAGGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGT 5379

Qy   1769 TyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsn 1788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5380 TACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAAC 5439

Qy   1789 PheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPhe 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5440 TTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTC 5499

Qy   1809 TyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeu 1828
          ||||||||||||||||||||||||||||||||||||||||||:::||||||   ||||||
Db   5500 TATGAGGTTTGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTTGCCAAACTT 5559

Qy   1829 SerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGln 1848
          |||   ||||||   ||||||:::|||||||||   :::   :::|||||||||:::|||
Db   5560 TCTGATTTTGCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAG 5619

Qy   1849 LeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeu 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5620 CTCATTGCCATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATCTTA 5679

Qy   1869 PheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGln 1888
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5680 TTTGCTTTTACAAAGCGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAG 5739

Qy   1889 MetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrThr 1908
          ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db   5740 ATGGAAGAGCGATTCATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCCATTACGACC 5799

Qy   1909 ThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArg 1928
          ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db   5800 ACGTTGAAACGCAAACAAGAGGAGGTGTCTGCTATTATTATCCAGAGGGCTTACAGACGC 5859

Qy   1929 HisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLys 1948
          :::||||||||:::   ||||||:::   |||      |||   |||:::|||   |||
Db   5860 TACCTCTTGAAGCAAAAAGTTAAAAAGGTATCAAGTATATACAAGAAAGACAAAGGCAAA 5919
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Qy   1949 GlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSer 1968
                              ||||||||||||   :::||||||::::::||||||||||||
Db   5920 GAATGTGATGGAACACCCATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAATTCA 5979

Qy   1969 IleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArg 1988
               ||||||||||||:::|||   ||||||   :::   ||||||||||||||||
Db   5980 ACTCCAGAGAAAACCGATATGACGCCTTCCACCACGTCT---CCACCCTCGTATGATAGT 6036

Qy   1989 ValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGly 2008
          ||||||||||||      ||||||   |||::::::      :::::::::   ||||||
Db   6037 GTGACCAAACCAGAAAAAGAAAAATTTGAAAAAGACAAATCAGAAAAGGAAGACAAAGGG 6096

Qy   2009 Lys 2009
          |||
Db   6097 AAA 6099
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RESULT 11
ABL39690
ID ABL39690 standard; cDNA; 9123 BP.
XX
AC ABL39690;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN3A encoding cDNA SEQ ID NO:3.
XX
KW Human; sodium channel; SCN3A; chromosome 2q24-31; gene; ss;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   472..6474
FT   /*tag= a
FT   /product= "sodium channel SCN3A"
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP04956.
XX
PR 13-JUN-2000; 2000JP-0177540.
PR 13-JUN-2000; 2000JP-0177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX
DR WPI; 2002-098066/13.
DR P-PSDB; ABB06027.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate
PT and causes of diseases and developing drugs for motor endplate disease
PT -
XX
PS Claim 6; Page 50-71; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence encodes the human sodium channel SCN3A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful
CC in studying the physiological mechanism in which excitant cells
CC participate and cause human diseases, and in developing remedies for
CC e.g. familial hypercalcaemic periodic paralysis of extremities and
CC motor endplate disease.
XX
SQ Sequence 9123 BP; 2770 A; 1700 C; 1870 G; 2783 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 9123

Score:	8664.00	Matches:	1686
Percent Similarity:	90.28%	Conservative:	134
Best Local Similarity:	83.63%	Mismatches:	166
Query Match:	83.33%	Indels:	30
DB:	24	Gaps:	12

US-09-930-871-12 (1-2009) x ABL39690 (1-9123)

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Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
Db     472 ATGGCACAGGCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTTACTAGAGAA 531

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db     532 TCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAGAAGCCCAAAAAGGAA 591

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db     592 CAAGATAATGATGATGAGAACAAACCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 651

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db     652 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 711

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db     712 GATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTTC 771

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db     772 CGATTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAACCCTGTTAGGAAAATT 831

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db     832 GCTATCAAGATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCACTATTTTGACC 891

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db     892 AACTGTGTATTTATGACCTTGAGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACA 951

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db     952 TTCACTGGAATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGCTTA 1011

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db    1012 GAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTCAGTGTCATTGTGATG 1071

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db    1072 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTT 1131

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db    1132 CTCCGAGCACTGAAAACAATTTCAGTCATTCCAGGTTTAAAGACCATTGTGGGGGCCCTG 1191

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db    1192 ATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGCGTG 1251

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    1252 TTTGCTCTCATTGGGCTGCAGCTGTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGG 1311

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn 299
Db    1312 CCCCCAAGCGATTCTGCTTTTGAAACCAACACCACTTCCTACTTTAATGGCACAATGGAT 1371

Qy     300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
Db    1372 TCAAATGGGACATTTGTTAATGTAACAATGAGCACATTTAACTGGAAGGATTACATTGGA 1431

Qy     320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
Db    1432 GATGACAGTCACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAATGGC 1491

Qy     340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
Db    1492 TCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTCGAAACCCCAAC 1551

Qy     360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
Db    1552 TATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTTCCTGTCTCTATTTCGACTCATG 1611

Qy     380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
Db    1612 ACTCAAGACTATTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATAC 1671

Qy     400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
Db    1672 ATGATATTTTTTGTCCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTG 1731

Qy     420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
Db    1732 GCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTGGAAGAAGCAGAACAA 1791

Qy     440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
Db    1792 AAAGAGGCCGAATTTCAGCAGATGCTCGAACAGCTTAAAAAGCAACAGGAAGAAGCTCAG 1851

Qy     460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAla--------- 476
Db    1852 ------GCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTCAGTGGAGTAGGTGGGTTA 1905

Qy     477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496
Db    1906 GGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAGGTGCTAAAGAA 1965

Qy     497 ArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAsp 516
Db    1966 TGGAGGAACCGGAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAACAACAAAGGA 2025

Qy     517 Glu---AspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db    2026 GAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAAGAAGCAGCTTCCTT 2085

Qy     536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db    2086 TTCTCCATGGATGGAAACAGACTGACCAGTGACAAAAAATTCTGCTCCCCTCATCAGTCT 2145

Qy     556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db    2146 CTCTTGAGTATCCGTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACAAGCATTTTC 2205

Qy     576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db    2206 AGTTTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGATGATGAACAC 2265

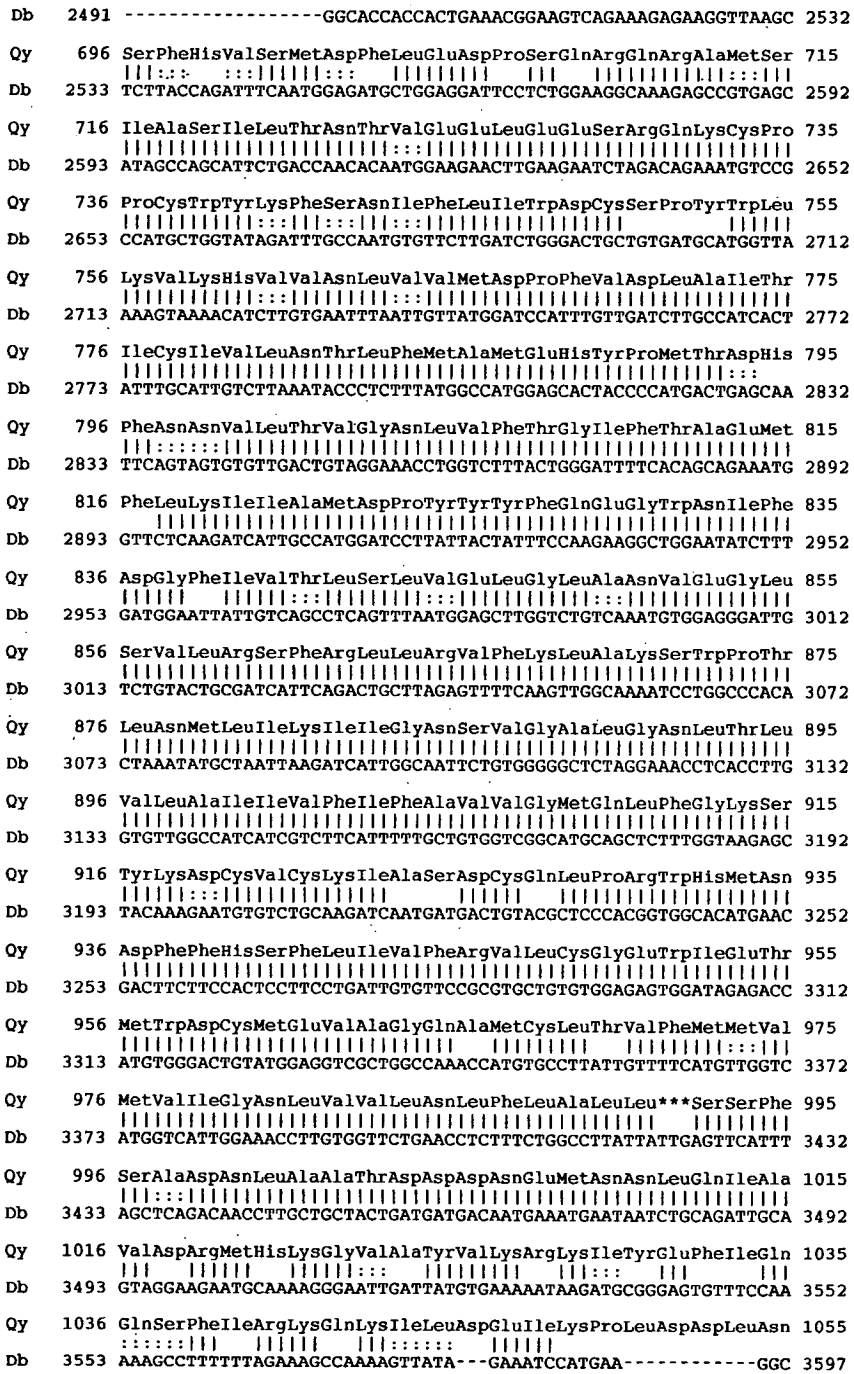
Qy     596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db    2266 AGCACATTTGAAGACGGCGAAAGCAGGAGAGACTCACTGTTTGTGCCGCACAGACATGGA 2325

Qy     616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635
Db    2326 GAGCGACGCAACAGTAACGTTAGTCAGGCCAGTATGTCATCCAGGATGGTGCCAGGGCTT 2385

Qy     636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655
Db    2386 CCAGCAAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGT 2445

Qy     656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675
Db    2446 GGACCTTCAGCTCTAACGTCACCTACTGGACAACTTCCCCCAGAG---------------- 2490

Qy     676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695
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Db 2491 ----------GGCACCACCACTGAAACGGAAGTCAGAAAGAGAAGGTTAAGC 2532
Qy 696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715
Db 2533 TCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAAGAGCCGTGAGC 2592
Qy 716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysPro 735
Db 2593 ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGACAGAAATGTCCG 2652
Qy 736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755
Db 2653 CCATGCTGGTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTA 2712
Qy 756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775
Db 2713 AAAGTAAAACATCTTGTGAATTTAATTGTTATGGATCCATTTGTTGATCTTGCCATCACT 2772
Qy 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795
Db 2773 ATTTGCATTGTCTTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA 2832
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Db 2833 TTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTCACAGCAGAAATG 2892
Qy 816 PheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePhe 835
Db 2893 GTTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGCTGGAATATCTTT 2952
Qy 836 AspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeu 855
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Qy 856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875
Db 3013 TCTGTACTGCGATCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA 3072
Qy 876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895
Db 3073 CTAAATATGCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTG 3132
Qy 896 ValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSer 915
Db 3133 GTGTTGGCCATCATCGTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGC 3192
Qy 916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935
Db 3193 TACAAAGAATGTGTCTGCAAGATCAATGATGACTGTACGCTCCCACGGTGGCACATGAAC 3252
Qy 936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955
Db 3253 GACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC 3312
Qy 956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetVal 975
Db 3313 ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTTTTCATGTTGGTC 3372
Qy 976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPhe 995
Db 3373 ATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTATTGAGTTCATTT 3432
Qy 996 SerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAla 1015
Db 3433 AGCTCAGACAACCTTGCTGCTACTGATGATGACAATGAAATGAATAATCTGCAGATTGCA 3492
Qy 1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035
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Db 3553 AAAGCCTTTTTTAGAAAGCCAAAAGTTATA---GAAATCCATGAA----------GGC 3597
Qy 1056 AsnLysLysAspSerCysMetSerAsnHisThr---***GluIleGlyLysAspLeuAsp 1074
Db 3598 AATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAAGAGCTTAAT 3657
Qy 1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLys 1094
Db 3658 TATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGTACTGGAAGCAGTGTTGAAAAA 3717
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Qy 1115 ValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSer 1134
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Qy 1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGly 1154
Db 3838 GAGTCAGAACTAGAAGAAAGCAAAGAGAAATTAAAT---GCAACCAGCTCATCTGAAGGA 3894
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Qy 1174 ThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGln 1193
Db 3955 GACTTTAAACCGGAAGCTTGTTTTACTGAAGGGTGTATTAAAAAGTTTCCATTCTGTCAA 4014
Qy 1194 IleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArg 1213
Db 4015 GTAAGTACAGAAGAAGGCAAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGT 4074
Qy 1214 IleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGly 1233
Db 4075 ATTGTTGAGCACAACTGGTTTGAGACTTTCATTGTGTTCATGATCCTTCTCAGTAGTGGT 4134
Qy 1234 AlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGlu 1253
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Db 4195 TATGCTGACAAAGTCTTTACCTATATATTCATTCTGGAAATGCTTCTCAAATGGGTTGCT 4254
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Db 4255 TATGGATTTCAAACATATTTCACTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGAT 4314
Qy 1294 ValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLys 1313
Db 4315 GTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCCATCAAA 4374
Qy 1314 SerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMet 1333
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Db 4435 AGGGTGGTTGTGAATGCTCTTGTTGGAGCAATTCCCTCTATCATGAATGTGCTGTTGGTC 4494
Qy 1354 CysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPhe 1373
Db 4495 TGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTC 4554
Qy 1374 TyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHis 1393
Db 4555 TACCACTGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAACAATTTG 4614
Qy 1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysVal 1413
Db 4615 AGTGACTGTCAGGCTCTT---------GGCAAGCAAGCTCGGTGGAAAAACGTGAAAGTA 4665

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Qy   1454 GluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePhe 1473
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Qy   1494 GlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLys 1513
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Qy   1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533
Db   4966 CTTGGATCCAAGAAACCTCAGAAACCCATACCTCGCCCAGCAAACAAATTCCAAGGAATG 5025

Qy   1534 ValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeu 1553
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Qy   1574 SerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIle 1593
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Qy   1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
Db   5326 TTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCA 5385

Qy   1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
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Qy   1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
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Qy   1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813
Db   5806 GAAGAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAA 5865

Qy   1814 LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAla 1833
Db   5866 AAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCT 5925

Qy   1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAsp 1853
Db   5926 GCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAGCTTATTGCCATGGAT 5985

Qy   1854 LeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLys 1873
Db   5986 CTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATTTTATTTGCCTTTACAAAG 6045

Qy   1874 ArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPhe 1893
Db   6046 CGTGTTTTGTGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAAGACAGGTTT 6105

Qy   1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913
Db   6106 ATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAACGTAAA 6165

Qy   1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArg 1933
Db   6166 CAAGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTCAGATGTTATCTTTTAAAGCAA 6225

Qy   1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeu 1953
Db   6226 AGGTTAAAAAATATATCAAGTAACTATAACAAAGAGGCAATTAAAGGGAGGATTGACTTA 6285

Qy   1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973
Db   6286 CCTATAAAACAAGACATGATTATTGACAAACTAAATGGGAACTCCACTCCAGAAAAAACA 6345

Qy   1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993
Db   6346 GATGGGAGTTCCTCTACCACCCCT---CCTCCTTCCTATGATAGTGTAACAAAACCAGAC 6402

Qy   1994 ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
Db   6403 AAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGAAAA 6450
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RESULT 12
AAH55823
ID AAH55823 standard; cDNA; 9112 BP.
XX
AC AAH55823;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN3A nucleotide sequence SEQ ID NO:65.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX

PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99678.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 150-154; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 9112 BP; 2769 A; 1695 C; 1861 G; 2785 T; 2 other;

Alignment Scores:

Pred. No.:	0	Length:	9112
Score:	8468.50	Matches:	1650
Percent Similarity:	88.44%	Conservative:	133
Best Local Similarity:	81.85%	Mismatches:	154
Query Match:	81.45%	Indels:	79
DB:	22	Gaps:	12

US-09-930-871-12 (1-2009) x AAH55823 (1-9112)

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Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||   |||   :::|||||||||||||||||||:::||||||     ||||||||||||
Db    633 ATGGCACAGGCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTTACTAGAGAA 692

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||:::|||   ||||||||||||||||||   ||||||   :::
Db    693 TCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAGAAGCCCAAAAAGGAA 752

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          :::   :::||||||||||||||   ||||||||||||||||||||||||||||||||||
Db    753 CAAGATAATGATGATGAGAACAAACCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 812

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 872

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db    873 GATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTCC 932

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    933 CGATTCAGTGCCACCTCTGCCTTGTATATTTTAACTCCACTAAACCCTGTTAGGAAAATT 992

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 GCTABSAAGATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCACTATTTTGACC 1052

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db   1053 AACTGTGTATTTATGACCTTGAGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACA 1112

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          |||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db   1113 TTCACTGGAATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGCTTA 1172

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   1173 GAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTCAGTGTCATTGTGATG 1232

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTT 1292

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 CTCCGAGCACTGAAAACAATTTCAGTCATTCCAGGTTTAAAGACCATTGTGGGGGCCCTG 1352

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 ATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGCGTG 1412

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   1413 TTTGCTCTCATTGGGCTGCAGCTGTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGG 1472

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn 299
          |||||:::::::::::::   |||   ::::::           |||   |||::::::
Db   1473 CCCCCAAGCGATTCTGCTTTTGAAACCAACACCACTTCCTACTTTAATGGCACAATGGAT 1532

Qy    300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
             |||||||||   :::|||   |||:::      |||:::||||||   ||||||
Db   1533 TCAAATGGGACATTTGTTAATGTAACAATGAGCACATTTAACTGGAAGGATTACATTGGA 1592

Qy    320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
          |||      :::   |||   |||:::|||      |||   ||||||||||||||||
Db   1593 GATGACAGTCACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAATGGC 1652

Qy    340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
          ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db   1653 TCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTCGAAACCCCAAC 1712

Qy    360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1713 TATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTTCCTGTCTCTATTTCGACTCATG 1772

Qy    380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db   1773 ACTCAAGACTACTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATAC 1832

Qy    400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
          ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db   1833 ATGATATTTTTTGTCCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTG 1892

Qy    420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
          ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db   1893 GCTGTGGTGGCCATGGCCTATGAGGGGCAGAATCAGGCCACCTTGGAAGAAGCAGAACAA 1952

Qy    440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
          |||||||||||||||||||||||:::|||||||||||||||||||||||||   ||||||
Db   1953 AAAGAGGCCGAATTTCAGCAGATGCTCGAACAGCTTAAAAAGCAACAGGAAGAAGCTCAG 2012

Qy    460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSer---------AlaAla 476
             |||   |||   ||||||      ||||||:::   |||
Db   2013 ------GCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTCAGTGGAATAGGTGGGTTA 2066

Qy    477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496
          |||   |||   :::||||||||||||||||||||||||||||||||||||||||||||
Db   2067 GGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAAGTGCTAAAGAA 2126

Qy    497 ArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAsp 516
             ||||||||||||||||||:::|||:::|||      |||      |||
Db   2127 TGGAGGAACCGAAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAACAACAAAGGA 2186

Qy    517 Glu---AspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
          |||   |||   |||   ||||||||||||||||||||||:::::|||      |||
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Db   2187 GAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAAGAAGCAGCTTCCTT 2246

Qy    536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
          ||||||::::::||||||||||||||||   :::|||::::::   ||||||||||||||||
Db   2247 TTCTCCATGGATGGAAACAGACTGACCAGTGACAAAAAATTCTGCTCCCCTCATCAGTCT 2306

Qy    556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
          ||||||||||||||||||||||||||||||||||||||||||||||:::|||||:::|||
Db   2307 CTCTTGAGTATCCGTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACAAGCATTTTC 2366

Qy    576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367 AGTTTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGATGATGAACAC 2426

Qy    596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
          ||||||||||||||:::|||||||||||||||||||||||||||||   |||||||||
Db   2427 AGCACATTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTTGTGCCGCACAGACATGGA 2486

Qy    616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635
          ||||||||||||||||
Db   2487 GAGCGACGCAACAGT---------------------------------------------- 2501

Qy    636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655

Db   2501 ---------------------------------------------------------- 2501

Qy    656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675

Db   2501 ---------------------------------------------------------- 2501

Qy    676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695
                          |||||||||||||||||||||||:::|||||||||||||   |||
Db   2502 ---------------AACGGCACCACCACTGAAACGGAAGTCAGAAAGAGAAGGTTAAGC 2546

Qy    696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715
          |||:::   :::|||||||:::   |||||||||   |||   ||||||||||||:::|||
Db   2547 TCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAAGAGCCGTGAGC 2606

Qy    716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysPro 735
          |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db   2607 ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGACAGAAATGTCCG 2666

Qy    736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755
          ||||||||||||:::|||:::|||:::|||||||||||||||||||   ||||||
Db   2667 CCATGCTGGTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTA 2726

Qy    756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775
          ||||||||||||:::|||||||||:::|||||||||||||||||||||||||||||||||||
Db   2727 AAAGTAAAACATCTTGTGAATTTAATTGTTATGGATCCATTTGTTGATCTTGCCATCACT 2786

Qy    776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   2787 ATTTGCATTGTCTTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA 2846

Qy    796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815
          |||:::::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2847 TTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTTACAGCAGAAATG 2906

Qy    816 PheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePhe 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2907 GTTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGCTGGAATATCTTT 2966

Qy    836 AspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeu 855
          ||||||   ||||||:::||||||||||:::||||||||||||:::|||||||||||||||
Db   2967 GATGGAATTATTGTCAGCCTCAGTTTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTG 3026

Qy    856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3027 TCTGTACTGCGATCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA 3086

Qy    876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3087 CTAAATATGCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTG 3146
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Qy    896 ValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSer 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3147 GTGTTGGCCATCATCGTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGC 3206

Qy    916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935
          ||||||:::|||||||||||||||||      ||||||   ||||||||||||||||||||
Db   3207 TACAAAGAATGTGTCTGCAAGATCAATGATGACTGTACGCTCCCACGGTGGCACATGAAC 3266

Qy    936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3267 GACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC 3326

Qy    956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetVal 975
          ||||||||||||||||||||||||||||||||   |||||||||   ||||||||:::|||
Db   3327 ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTTTTCATGTTGGTC 3386

Qy    976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPhe 995
          ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db   3387 ATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTGTTGAGTTCATTT 3446

Qy    996 SerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAla 1015
          |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3447 AGCTCAGACAACCTTGCTGCTACTGATGATGACAATGAAATGAATAATCTGCAGATTGCA 3506

Qy   1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035
          |||   ||||||   |||||:::   |||||||||   |||:::   |||      |||
Db   3507 GTAGGAAGAATGCAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA 3566

Qy   1036 GlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsn 1055
          ::::::|||   ||||||   |||::::::   ||||||
Db   3567 AAAGCCTTTTTTAGAAAGCCAAAAGTTATA---GAAATCCATGAA-----------GGC 3611

Qy   1056 AsnLysLysAspSerCysMetSerAsnHisThr---***GluIleGlyLysAspLeuAsp 1074
          ||||||   ||||||||||||||||||:::|||      ||||||   |||:::|||:::
Db   3612 AATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAAGAGCTTAAT 3671

Qy   1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLys 1094
          ||||||:::|||   ||||||||||||||||:::||||||||||||||||||||||||||
Db   3672 TATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGTACTGGAAGCAGTGTTGAAAAA 3731

Qy   1095 TyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThr 1114
          |||:::|||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db   3732 TACGTAATCGATGAAAATGATTATATGTCATTCATAAACAACCCCAGCCTCACCGTCACA 3791

Qy   1115 ValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSer 1134
          ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db   3792 GTGCCAATTGCTGTTGGAGAGTCTGACTTTGAAAACTTAAATACTGAAGAGTTCAGCAGT 3851

Qy   1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGly 1154
          ||||||:::|||||||||||||||||||||||||||||   ::::::|||||||||||||
Db   3852 GAGTCAGAACTAGAAGAAAGCAAGGAGAAATTAAAT---GCAACCAGCTCATCTGAAGGA 3908

Qy   1155 SerThrValAspIleGlyAlaProValGlu---GluGlnProValValGluProGluGlu 1173
          ||||||||||||:::      |||   |||   ||||||         ||||||||||||
Db   3909 AGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCTGAAACTGAACCCGAAGAA 3968

Qy   1174 ThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGln 1193
             ||:::|||||||||||||||||||||||||||||||||:::::::::|||      ||||||
Db   3969 GACCTTAAACCGGAAGCTTGTTTTACTGAAGGATGTATTAAAAAGTTTCCATTCTGTCAA 4028

Qy   1194 IleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArg 1213
          ::::::   |||||||||:::||||||   |||||||||||||:::||||||:::
Db   4029 GTAAGTACAGAAGAAGGCAAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGT 4088

Qy   1214 IleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGly 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4089 ATTGTTGAGCACAACTGGTTTGAGACTTTCATTGTGTTCATGATCCTTCTCAGTAGTGGT 4148

Qy   1234 AlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGlu 1253
          ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db   4149 GCATTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAACCATGCTAGAA 4208
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Qy 1254 TyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAla 1273
Db 4209 TATGCTGACAAAGTCTTTACCTATATATTCATTCTGGAAATGCTTCTCAAATGGGTTGCT 4268
Qy 1274 TyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAsp 1293
Db 4269 TATGGATTTCAAACATATTTCACTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGAT 4328
Qy 1294 ValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLys 1313
Db 4329 GTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCCATCAAA 4388
Qy 1314 SerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMet 1333
Db 4389 TCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTATCCCGGTTTGAAGGCATG 4448
Qy 1334 ArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuVal 1353
Db 4449 AGGGTGGTTGTGAATGCTCTTGTTGGAGCAATTCCCTCTATCATGAATGTGCTGTTGGTC 4508
Qy 1354 CysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPhe 1373
Db 4509 TGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTC 4568
Qy 1374 TyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHis 1393
Db 4569 TACCACTGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAACAATTTG 4628
Qy 1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysVal 1413
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Qy 1414 AsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGly 1433
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Qy 1434 TrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyr 1453
Db 4740 TGGATGGATATTATGTATGCAGCTGTTGATTCACGAGATGTTAAACTTCAGCCTGTATAT 4799
Qy 1454 GluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePhe 1473
Db 4800 GAAGAAAATCTGTACATGTATTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTC 4859
Qy 1474 ThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPhe 1493
Db 4860 ACTCTGAATCTATTCATTGGTGTCATCATAGATAACTTCAACCAGCAGAAAAAGAAGTTT 4919
Qy 1494 GlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLys 1513
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Qy 1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533
Db 4980 CTTGGATCCAAGAAACCTCAGAAACCCATACCTCGCCCAGCAAACAAATTCCAAGGAATG 5039
Qy 1534 ValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeu 1553
Db 5040 GTCTTTGATTTTGTAACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTC 5099
Qy 1554 AsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrValThrThrIleLeu 1573
Db 5100 AACATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACCCTAGTTTTG 5159
Qy 1574 SerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIle 1593
Db 5160 TCCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGAGAATTTGTGCTGAAGCTCGTC 5219
Qy 1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIle 1613
Db 5220 TCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGACTTTGTGGTGGTGATT 5279
Qy 1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633
Db 5280 CTCTCCATTGTAGGTATGTTTCTGGCTGAGATGATAGAAAAGTATTTTGTGTCCCCTACC 5339
Qy 1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
Db 5340 TTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCA 5399
Qy 1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
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Qy 1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
Db 5460 GGCCTCCTGCTCTTCCTGGTCATGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGCC 5519
Qy 1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713
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Qy 1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIle 1733
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Qy 1734 LeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLys 1753
Db 5640 CTTAATAGTGCACCACCCGACTGTGACCCTGACACAATTCACCCTGGCAGCTCAGTTAAG 5699
Qy 1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773
Db 5700 GGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGTTACATCATCATATCC 5759
Qy 1774 PheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793
Db 5760 TTCCTGGTGGTGGTGAACAGTTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACT 5819
Qy 1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813
Db 5820 GAAGAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAA 5879
Qy 1814 LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAla 1833
Db 5880 AAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCT 5939
Qy 1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAsp 1853
Db 5940 GCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAGCTTATTGCCATGGAT 5999
Qy 1854 LeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLys 1873
Db 6000 CTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATTTTATTTGCCTTTACAAAG 6059
Qy 1874 ArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPhe 1893
Db 6060 CGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAAGACAGGTTT 6119
Qy 1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913
Db 6120 ATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAACGTAAA 6179
Qy 1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArg 1933
Db 6180 CAAGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTCAGATGTTATCTTTTAAAGCAA 6239
Qy 1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeu 1953
Db 6240 AGGTTAAAAAATATATCAAGTAACTATAACAAAGAGGCAATAAAGGGGAGGATTGACTTA 6299
Qy 1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973
Db 6300 CCTATAAAACAAGACATGATTATTGACAAACTGAATGGGAACTCCACTCCAGAAAAAACA 6359
Qy 1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993

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Db    6360 GATGGGAGTTCCTCTACCACCTCT---CCTCCTTCCTATGATAGTGTAACAAAACCAGAC 6416

Qy    1994 ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
Db    6417 AAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGAAAA 6464

RESULT 13
AAH55824
ID   AAH55824 standard; cDNA; 9112 BP.
XX
AC   AAH55824;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human neonatal form of SCN3A nucleotide sequence SEQ ID NO:66.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99679.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 154-157; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 9112 BP; 2769 A; 1695 C; 1857 G; 2789 T; 2 other;

Alignment Scores:
Pred. No.:              0          Length:          9112
Score:                  8462.50    Matches:         1649
Percent Similarity:     88.39%     Conservative:    133
Best Local Similarity:  81.80%     Mismatches:      155
Query Match:            81.39%     Indels:          79
DB:                     22         Gaps:            12

US-09-930-871-12 (1-2009) x AAH55824 (1-9112)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20

Db    633 ATGGCACAGGCACTGTTGGTACCCCCAGGACCTGAAAGCTTCCGCCTTTTTACTAGAGAA 692

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db    693 TCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAGAAGCCCAAAAAGGAA 752

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db    753 CAAGATAATGATGATGAGAACAAACCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 812

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db    813 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 872

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
Db    873 GATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTCC 932

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db    933 CGATTCAGTGCCACCTCTGCCTTGTATATTTAACTCCACTAAACCCTGTTAGGAAAATT 992

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db    993 GCTABSAAGATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGCACTATTTTGACC 1052

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db   1053 AACTGTGTATTTATGACCTTGAGCAACCCTCCTGACTGGACAAAGAATGTAGAGTACACA 1112

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db   1113 TTCACTGGAATCTATACCTTTGAGTCACTTATAAAAATCTTGGCAAGAGGGTTTTGCTTA 1172

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db   1173 GAAGATTTTACGTTTCTTCGTGATCCATGGAACTGGCTGGATTTCAGTGTCATTGTGATG 1232

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db   1233 GCGTATGTAACAGAATTTGTAAGCCTAGGCAATGTTTCAGCCCTTCGAACTTTCAGAGTC 1292

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db   1293 TTGAGAGCTCTGAAAACTATTTCTGTAATCCCAGGTTTAAAGACCATTGTGGGGGCCCTG 1352

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db   1353 ATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGCGTG 1412

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db   1413 TTTGCTCTCATTGGGCTGCAGCTGTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGG 1472

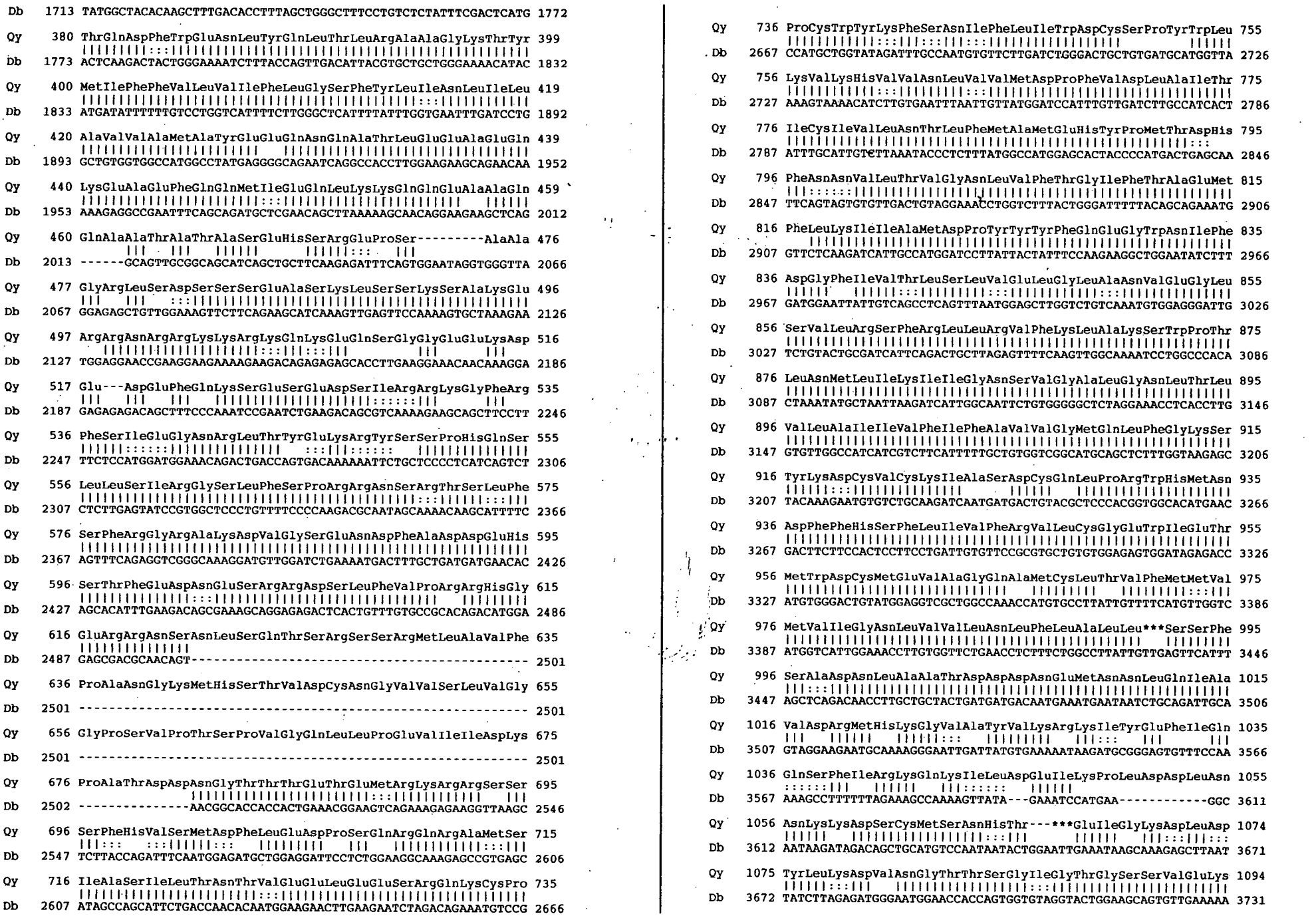
Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn 299
Db   1473 CCCCCAAGCGATTCTGCTTTTGAAACCAACACCACTTCCTACTTTAATGGCACAATGGAT 1532

Qy    300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
Db   1533 TCAAATGGGACATTTGTTAATGTAACAATGAGCACATTTAACTGGAAGGATTACATTGGA 1592

Qy    320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
Db   1593 GATGACAGTCACTTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAATGGC 1652

Qy    340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
Db   1653 TCAGATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTCGAAACCCCAAC 1712

Qy    360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
```


Db 1713 TATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTTCCTGTCTCTATTTCGACTCATG 1772
Qy 380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
Db 1773 ACTCAAGACTACTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATAC 1832
Qy 400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
Db 1833 ATGATATTTTTTGTCCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTG 1892
Qy 420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
Db 1893 GCTGTGGTGGCCATGGCCTATGAGGGGCAGAATCAGGCCACCTTGGAAGAAGCAGAACAA 1952
Qy 440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
Db 1953 AAAGAGGCCGAATTTCAGCAGATGCTCGAACAGCTTAAAAAGCAACAGGAAGAAGCTCAG 2012
Qy 460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSer---------AlaAla 476
Db 2013 ------GCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTCAGTGGAATAGGTGGGTTA 2066
Qy 477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496
Db 2067 GGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAAGTGCTAAAGAA 2126
Qy 497 ArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAsp 516
Db 2127 TGGAGGAACCGAAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAACAACAAAGGA 2186
Qy 517 Glu---AspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db 2187 GAGAGAGACAGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAAGAAGCAGCTTCCTT 2246
Qy 536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db 2247 TTCTCCATGGATGGAAACAGACTGACCAGTGACAAAAAATTCTGCTCCCCTCATCAGTCT 2306
Qy 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db 2307 CTCTTGAGTATCCGTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACAAGCATTTTC 2366
Qy 576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db 2367 AGTTTCAGAGGTCGGGCAAAGGATGTTGGATCTGAAAATGACTTTGCTGATGATGAACAC 2426
Qy 596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db 2427 AGCACATTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTTGTGCCGCACAGACATGGA 2486
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635
Db 2487 GAGCGACGCAACAGT---------- 2501
Qy 636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655
Db 2501 ---------- 2501
Qy 656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675
Db 2501 ---------- 2501
Qy 676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695
Db 2502 ----------AACGGCACCACCACTGAAACGGAAGTCAGAAAGAGAAGGTTAAGC 2546
Qy 696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715
Db 2547 TCTTACCAGATTTCAATGGAGATGCTGGAGGATTCCTCTGGAAGGCAAAGAGCCGTGAGC 2606
Qy 716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysPro 735
Db 2607 ATAGCCAGCATTCTGACCAACACAATGGAAGAACTTGAAGAATCTAGACAGAAATGTCCG 2666
Qy 736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755
Db 2667 CCATGCTGGTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTA 2726
Qy 756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775
Db 2727 AAAGTAAAACATCTTGTGAATTTAATTGTTATGGATCCATTTGTTGATCTTGCCATCACT 2786
Qy 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795
Db 2787 ATTTGCATTGTCTTAAATACCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAA 2846
Qy 796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815
Db 2847 TTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTTACAGCAGAAATG 2906
Qy 816 PheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePhe 835
Db 2907 GTTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGCTGGAATATCTTT 2966
Qy 836 AspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeu 855
Db 2967 GATGGAATTATTGTCAGCCTCAGTTTAATGGAGCTTGGTCTGTCAAATGTGGAGGGATTG 3026
Qy 856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875
Db 3027 TCTGTACTGCGATCATTCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCCACA 3086
Qy 876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895
Db 3087 CTAAATATGCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTG 3146
Qy 896 ValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSer 915
Db 3147 GTGTTGGCCATCATCGTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGC 3206
Qy 916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935
Db 3207 TACAAAGAATGTGTCTGCAAGATCAATGATGACTGTACGCTCCCACGGTGGCACATGAAC 3266
Qy 936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955
Db 3267 GACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACC 3326
Qy 956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetVal 975
Db 3327 ATGTGGGACTGTATGGAGGTCGCTGGCCAAACCATGTGCCTTATTGTTTTCATGTTGGTC 3386
Qy 976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPhe 995
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Qy 996 SerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAla 1015
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Qy 1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035
Db 3507 GTAGGAAGAATGCAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAA 3566
Qy 1036 GlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsn 1055
Db 3567 AAAGCCTTTTTTAGAAAGCCAAAAGTTATA---GAAATCCATGAA-----------GGC 3611
Qy 1056 AsnLysLysAspSerCysMetSerAsnHisThr---***GluIleGlyLysAspLeuAsp 1074
Db 3612 AATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAGCAAAGAGCTTAAT 3671
Qy 1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLys 1094
Db 3672 TATCTTAGAGATGGGAATGGAACCACCAGTGGTGTAGGTACTGGAAGCAGTGTTGAAAAA 3731

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Qy   1095 TyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThr 1114
          |||:::|||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db   3732 TACGTAATCGATGAAAATGATTATATGTCATTCATAAACAACCCCAGCCTCACCGTCACA 3791

Qy   1115 ValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSer 1134
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Db   3792 GTGCCAATTGCTGTTGGAGAGTCTGACTTTGAAAACTTAAATACTGAAGAGTTCAGCAGT 3851

Qy   1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGly 1154
          ||||||:::|||||||||||||||||||||||||   ::::::|||||||||||||||||
Db   3852 GAGTCAGAACTAGAAGAAAGCAAGGAGAAATTAAAT---GCAACCAGCTCATCTGAAGGA 3908

Qy   1155 SerThrValAspIleGlyAlaProValGlu---GluGlnProValValGluProGluGlu 1173
          |||||||||||:::       |||   |||   ||||||          ||||||||||||
Db   3909 AGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCTGAAACTGAACCCGAAGAA 3968

Qy   1174 ThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGln 1193
             |||:::|||||||||||||||||||||||||||||:::::::::|||      ||||||
Db   3969 GACCTTAAACCGGAAGCTTGTTTTACTGAAGGATGTATTAAAAAGTTTCCATTCTGTCAA 4028

Qy   1194 IleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArg 1213
          ::::::   |||||||||:::||||||   ||||||||||||||:::|||||:::
Db   4029 GTAAGTACAGAAGAAGGCAAAGGGAAGATCTGGTGGAATCTTCGAAAAACCTGCTACAGT 4088

Qy   1214 IleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGly 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4089 ATTGTTGAGCACAACTGGTTTGAGACTTTCATTGTGTTCATGATCCTTCTCAGTAGTGGT 4148

Qy   1234 AlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGlu 1253
          ||||||||||||||||||||||||||::||||||||||||||||||||||||||||||||
Db   4149 GCATTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAACCATGCTAGAA 4208

Qy   1254 TyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAla 1273
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Db   4209 TATGCTGACAAAGTCTTTACCTATATATTCATTCTGGAAATGCTTCTCAAATGGGTTGCT 4268

Qy   1274 TyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAsp 1293
          ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4269 TATGGATTTCAAACATATTTCACTAATGCCTGGTGCTGGCTAGATTTCTTGATCGTTGAT 4328

Qy   1294 ValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLys 1313
          ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db   4329 GTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCCATCAAA 4388

Qy   1314 SerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMet 1333
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Db   4389 TCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCTTATCCCGGTTTGAAGGCATG 4448

Qy   1334 ArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuVal 1353
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Db   4449 AGGGTGGTTGTGAATGCTCTTGTTGGAGCAATTCCCTCTATCATGAATGTGCTGTTGGTC 4508

Qy   1354 CysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPhe 1373
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Db   4509 TGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGCTGGCAAGTTC 4568

Qy   1374 TyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHis 1393
          |||||||||:::|||   |||||||||::   |||||||||   ||||||||||||
Db   4569 TACCACTGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAACAATTTG 4628

Qy   1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysVal 1413
          :::|||||||      |||           :::   ||||||||||||||||||||||||
Db   4629 AGTGACTGTCAGGCTCTT---------GGCAAGCAAGCTCGGTGGAAAAACGTGAAAGTA 4679

Qy   1414 AsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGly 1433
          ||||||||||||||||   ||||||||||:::||||||||||||||||||||||||||||
Db   4680 AACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTTCAAGTGGCCACATTTAAAGGC 4739

Qy   1434 TrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyr 1453
          ||||||||||||||||||||||||||||||||||:::|||:::|||||||||   |||
Db   4740 TGGATGGATATTATGTATGCAGCTGTTGATTCACGAGATGTTAAACTTCAGCCTGTATAT 4799

Qy   1454 GluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePhe 1473
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          ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4800 GAAGAAAATCTGTACATGTATTTATACTTTGTCATCTTTATCATCTTTGGGTCATTCTTC 4859

Qy   1474 ThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPhe 1493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4860 ACTCTGAATCTATTCATTGGTGTCATCATAGATAACTTCAACCAGCAGAAAAAGAAGTTT 4919

Qy   1494 GlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLys 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4920 GGAGGTCAAGACATCTTTATGACAGAGGAACAGAAAAAATATTACAATGCAATGAAGAAA 4979

Qy   1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533
          ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db   4980 CTTGGATCCAAGAAACCTCAGAAACCCATACCTCGCCCAGCAAACAAATTCCAAGGAATG 5039

Qy   1534 ValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeu 1553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5040 GTCTTTGATTTTGTAACCAGACAAGTCTTTGATATCAGCATCATGATCCTCATCTGCCTC 5099

Qy   1554 AsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrValThrThrIleLeu 1573
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Db   5100 AACATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACCCTAGTTTTG 5159

Qy   1574 SerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIle 1593
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Db   5160 TCCCGGATCAACCTAGTGTTCATTGTTCTGTTCACTGGAGAATTTGTGCTGAAGCTCGTC 5219

Qy   1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIle 1613
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Db   5220 TCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGACTTTGTGGTGGTGATT 5279

Qy   1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633
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Db   5280 CTCTCCATTGTAGGTATGTTTCTGGCTGAGATGATAGAAAAGTATTTTGTGTCCCCTACC 5339

Qy   1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5340 TTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCA 5399

Qy   1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
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Db   5400 AAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATC 5459

Qy   1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
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Db   5460 GGCCTCCTGCTCTTCCTGGTCATGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGCC 5519

Qy   1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713
          |||||||||:::|||   ||||||||||||||||||||||||||||||||||||||||||
Db   5520 TATGTTAAAAAGGAAGCTGGAATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGC 5579

Qy   1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIle 1733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5580 ATGATCTGCTTGTTCCAAATTACAACCTCTGCTGGATGGGATGGATTGCTAGCACCTATT 5639

Qy   1734 LeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLys 1753
          |||||||||   ||||||||||||||||:::   ::::::||||||||||||||||||||
Db   5640 CTTAATAGTGCACCACCCGACTGTGACCCTGACACAATTCACCCTGGCAGCTCAGTTAAG 5699

Qy   1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773
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Qy   1774 PheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793
          ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db   5760 TTCCTGGTGGTGGTGAACAGTTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACT 5819

Qy   1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5820 GAAGAAAGTGCAGAGCCCCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAA 5879

Qy   1814 LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAla 1833
          ||||||||||||||||||||||||||||:::|||||   |||||||||   |||||||||
```

```
Db    5880 AAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCT 5939

Qy    1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAsp 1853
           ||||||:::|||||||||   :::   :::|||||||||:::||||||||||||||||||
Db    5940 GCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAGCTTATTGCCATGGAT 5999

Qy    1854 LeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLys 1873
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6000 CTGCCCATGGTCAGTGGTGACCGGATCCACTGTCTTGATATTTTATTTGCCTTTACAAAG 6059

Qy    1874 ArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPhe 1893
           ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    6060 CGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATACAGATGGAAGACAGGTTT 6119

Qy    1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913
           ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    6120 ATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACTTTGAAACGTAAA 6179

Qy    1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArg 1933
           ||||||||||||||||||   ||||||||||||   :::|||   :::||||||||:::
Db    6180 CAAGAGGAGGTGTCTGCCGCTATCATTCAGCGTAATTTCAGATGTTATCTTTTAAAGCAA 6239

Qy    1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeu 1953
              :::|||      |||      |||||||||      |||||||||      :::|||
Db    6240 AGGTTAAAAAATATATCAAGTAACTATAACAAAGAGGCAATAAAGGGGAGGATTGACTTA 6299

Qy    1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973
           ||||||:::|||||||||||||||:::::|||   ||||||      |||||||||
Db    6300 CCTATAAAACAAGACATGATTATTGACAAACTGAATGGGAACTCCACTCCAGAAAAAACA 6359

Qy    1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993
           |||   :::   ||||||   :::   ||||||||||||||   ||||||||||||
Db    6360 GATGGGAGTTCCTCTACCACCTCT---CCTCCTTCCTATGATAGTGTAACAAAACCAGAC 6416

Qy    1994 ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
              ||||||   |||:::::      ::::::::::::|||||||||
Db    6417 AAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGAAAA 6464

RESULT 14
ABK63697
ID   ABK63697 standard; cDNA; 6822 BP.
XX
AC   ABK63697;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Rat sequence differentially expressed in response to a hepatotoxin #1604.
XX
KW   Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
KW   differential expression; centrilobular necrosis; steatosis.
XX
OS   Rattus norvegicus.
XX
PN   WO200210453-A2.
XX
PD   07-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US23872.
XX
PR   31-JUL-2000; 2000US-222040P.
PR   02-NOV-2000; 2000US-244880P.
PR   11-MAY-2001; 2001US-290029P.
PR   15-MAY-2001; 2001US-290645P.
PR   22-MAY-2001; 2001US-292336P.
PR   06-JUN-2001; 2001US-295798P.
PR   13-JUN-2001; 2001US-297457P.
PR   19-JUN-2001; 2001US-298884P.
PR   09-JUL-2001; 2001US-303459P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Mendrick D,  Porter MW,  Johnson KR,  Castle AL,  Elashoff MR;
XX
DR   WPI; 2002-241625/29.
XX
PT   Predicting toxic effects of compounds or the progression of these toxic
PT   effects by determining the changes in gene expression in tissues or
PT   cells exposed to the toxin and comparing these to gene expression in
PT   unexposed tissues or cells -
XX
PS   Claim 1; Seq ID No 1604; 239pp; English.
XX
CC   The invention relates to methods for predicting toxic effects of
CC   compounds or the progression of these toxic effects by determining the
CC   global changes in gene expression in tissues or cells exposed to the
CC   toxin and comparing these to gene expression in unexposed tissues or
CC   cells. Also included are methods of predicting at least one toxic
CC   effect of a compound or progression of a toxic effect, preferably the
CC   hepatotoxicity of a compound, comprising detecting the level of
CC   expression in a tissue or cell sample exposed to the compound of two or
CC   more genes listed in the specification, where  differential expression of
CC   the genes is indicative of at least one toxic effect or progression.
CC   The method can also be used to identify an agent which modulates the
CC   toxic response and predict cellular pathways that a compound modulates
CC   in a cell. The methods utilise a set of at least two probes (on a solid
CC   support in kit form), where each of the probes comprises a sequence that
CC   specifically hybridises to a gene listed in the specification, a computer
CC   system comprising a database containing information identifying the
CC   expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC   set of genes comprising at least two genes listed in the specification,
CC   and a user interface to view the information used to present information
CC   identifying the expression level in a tissue or cell of at least one gene
CC   listed in the specification. The method is useful for elucidating global
CC   changes in gene expression and for identifying toxicity markers in
CC   tissues or cell exposed to a known toxin. The genes may be used as
CC   toxicity markers in drug screening and toxicity assays. The genes and
CC   gene expression information may be used as diagnostic markers for the
CC   prediction or identification of the physiological state of tissue or cell
CC   sample that has been exposed to a compound or agent. Hepatotoxicity
CC   is characterised by centrilobular necrosis and steatosis. The present
CC   sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC   which is differentially expressed in response to a hepatotoxic agent.
XX
SQ   Sequence 6822 BP; 1861 A; 1525 C; 1650 G; 1786 T; 0 other;

Alignment Scores:
Pred. No.:                0                 Length:          6822
Score:                    8448.50           Matches:         1648
Percent Similarity:       88.49%            Conservative:    136
Best Local Similarity:    81.75%            Mismatches:      153
Query Match:              81.26%            Indels:          79
DB:                       24                Gaps:            12

US-09-930-871-12 (1-2009) x ABK63697 (1-6822)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           |||   |||   :::||||||||||||||||||:::||||||      ||||||||||||
Db     414 ATGGCCCAGGCACTGCTGGTACCCCCGGGACCTGAGAGCTTCCGCCTTTTCACTCGAGAA 473

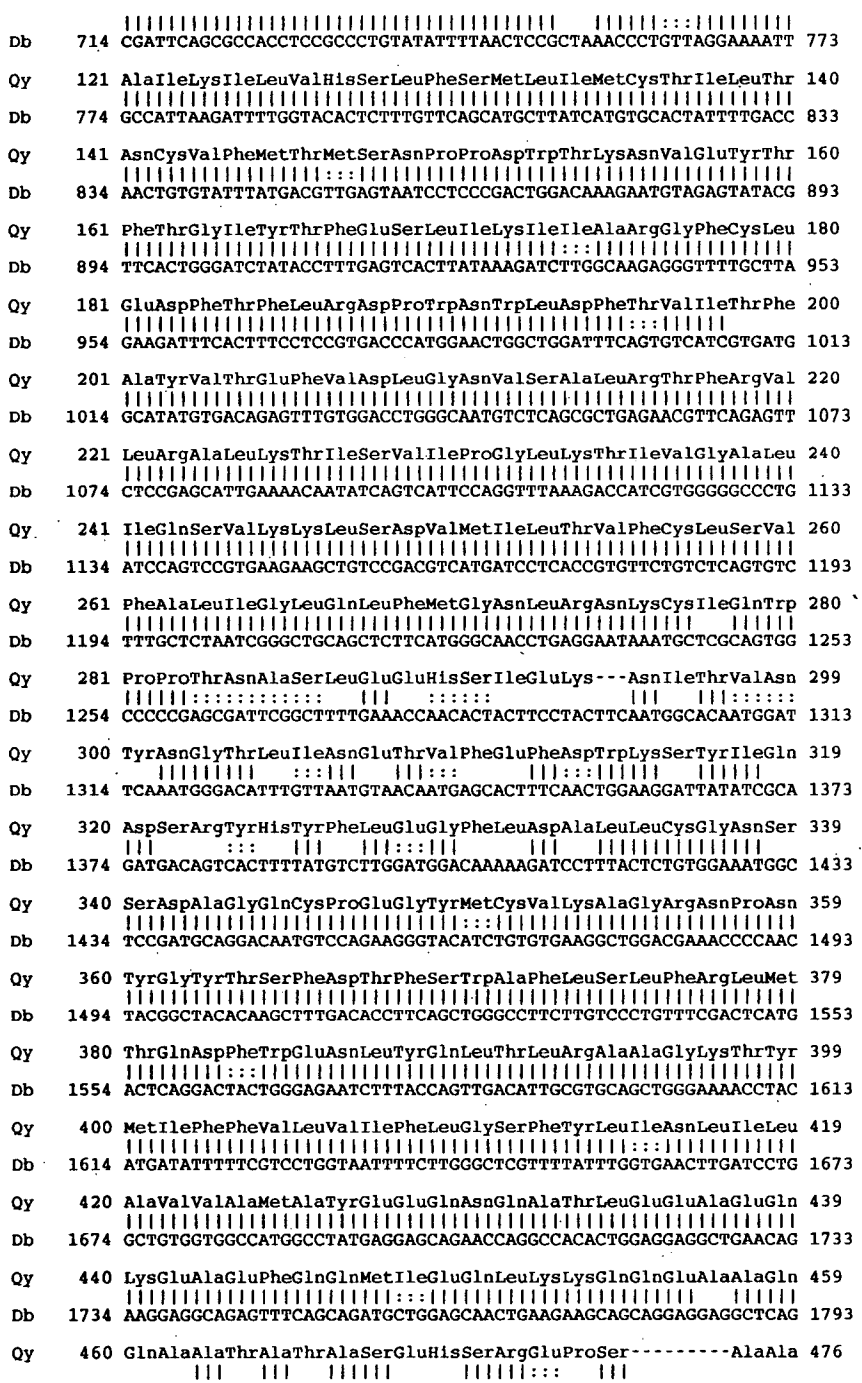
Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||:::|||   ||||||||||||||||   ||||||   :::
Db     474 TCTCTTGCTGCTATCGAAAAGCGTGCTGCAGAAGAGAAAGCCAAGAAACCCAAGAAAGAG 533

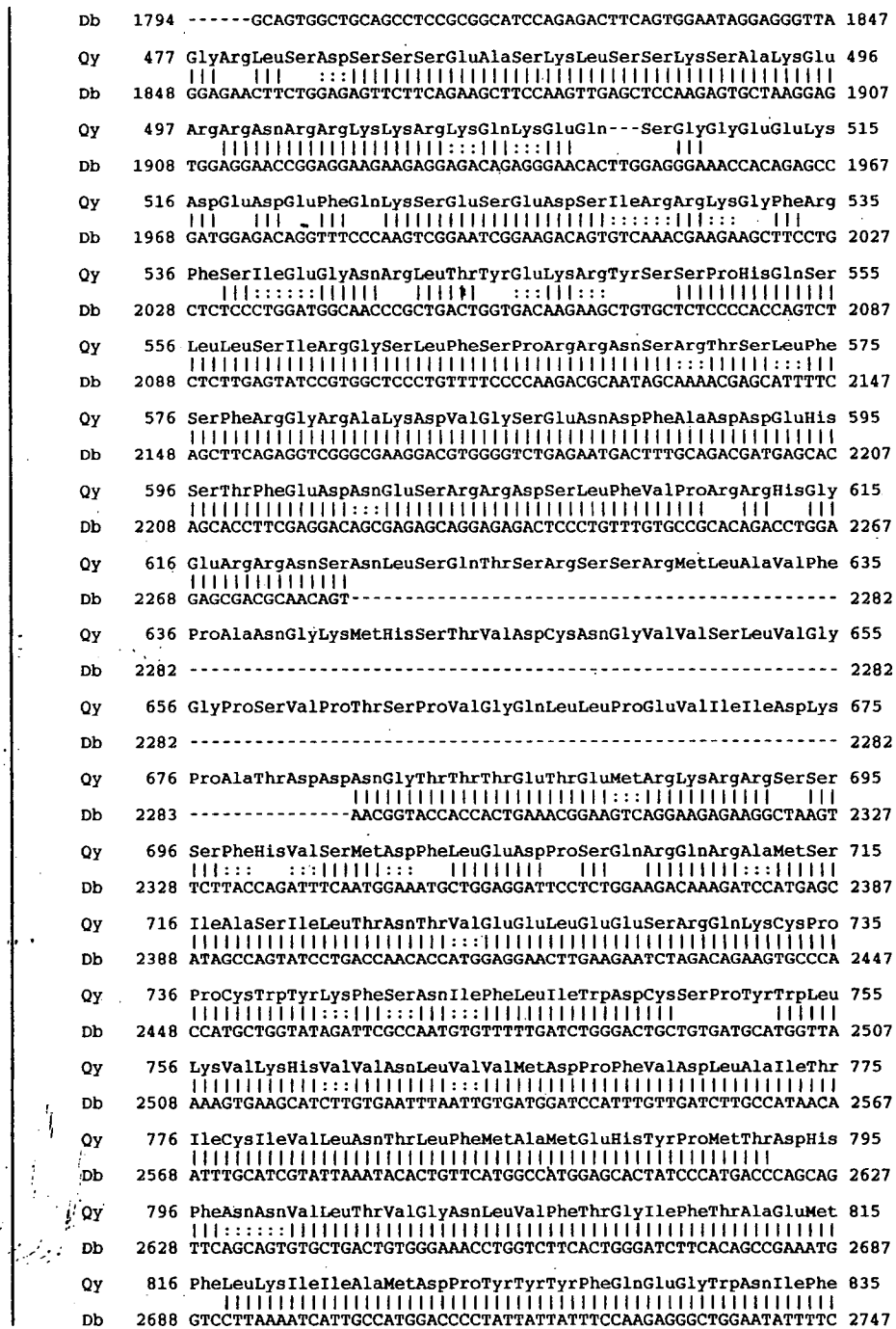
Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           :::      ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     534 CAAGACATTGACGATGAGAACAAACCAAAGCCAAACAGCGACTTGGAAGCTGGGAAGAAC 593

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     594 CTTCCATTTATCTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 653

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||:::::|||||||||||:::||||||||||||||||||||||||||||||
Db     654 GACCCCTACTATGTCAGTAAGAAAACTTTTGTAGTGTTGAATAAAGGGAAGGCGATTTTT 713

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
```


Db 714 CGATTCAGCGCCACCTCCGCCCTGTATATTTTAACTCCGCTAAACCCTGTTAGGAAAATT 773
Qy 121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
Db 774 GCCATTAAGATTTTGGTACACTCTTTGTTCAGCATGCTTATCATGTGCACTATTTTGACC 833
Qy 141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db 834 AACTGTGTATTTATGACGTTGAGTAATCCTCCCGACTGGACAAAGAATGTAGAGTATACG 893
Qy 161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db 894 TTCACTGGGATCTATACCTTTGAGTCACTTATAAAGATCTTGGCAAGAGGGTTTTGCTTA 953
Qy 181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db 954 GAAGATTTCACTTTCCTCCGTGACCCATGGAACTGGCTGGATTTCAGTGTCATCGTGATG 1013
Qy 201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db 1014 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACGTTCAGAGTT 1073
Qy 221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db 1074 CTCCGAGCATTGAAAACAATATCAGTCATTCCAGGTTTAAAGACCATCGTGGGGGCCCTG 1133
Qy 241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db 1134 ATCCAGTCCGTGAAGAAGCTGTCCGACGTCATGATCCTCACCGTGTTCTGTCTCAGTGTC 1193
Qy 261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db 1194 TTTGCTCTAATCGGGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTCGCAGTGG 1253
Qy 281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn 299
Db 1254 CCCCCGAGCGATTCGGCTTTTGAAACCAACACTACTTCCTACTTCAATGGCACAATGGAT 1313
Qy 300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
Db 1314 TCAAATGGGACATTTGTTAATGTAACAATGAGCACTTTCAACTGGAAGGATTATATCGCA 1373
Qy 320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
Db 1374 GATGACAGTCACTTTTATGTCTTGGATGGACAAAAAGATCCTTTACTCTGTGGAAATGGC 1433
Qy 340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
Db 1434 TCCGATGCAGGACAATGTCCAGAAGGGTACATCTGTGTGAAGGCTGGACGAAACCCCAAC 1493
Qy 360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
Db 1494 TACGGCTACACAAGCTTTGACACCTTCAGCTGGGCCTTCTTGTCCCTGTTTCGACTCATG 1553
Qy 380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
Db 1554 ACTCAGGACTACTGGGAGAATCTTTACCAGTTGACATTGCGTGCAGCTGGGAAAACCTAC 1613
Qy 400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
Db 1614 ATGATATTTTTCGTCCTGGTAATTTTCTTGGGCTCGTTTTATTTGGTGAACTTGATCCTG 1673
Qy 420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
Db 1674 GCTGTGGTGGCCATGGCCTATGAGGAGCAGAACCAGGCCACACTGGAGGAGGCTGAACAG 1733
Qy 440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
Db 1734 AAGGAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAGCAGCAGGAGGAGGCTCAG 1793
Qy 460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSer---------AlaAla 476


Db 1794 ------GCAGTGGCTGCAGCCTCCGCGGCATCCAGAGACTTCAGTGGAATAGGAGGGTTA 1847
Qy 477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496
Db 1848 GGAGAACTTCTGGAGAGTTCTTCAGAAGCTTCCAAGTTGAGCTCCAAGAGTGCTAAGGAG 1907
Qy 497 ArgArgAsnArgArgLysLysArgLysGlnLysGluGln---SerGlyGlyGluGluLys 515
Db 1908 TGGAGGAACCGGAGGAAGAAGAGGAGACAGAGGGAACACTTGGAGGGAAACCACAGAGCC 1967
Qy 516 AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db 1968 GATGGAGACAGGTTTCCCAAGTCGGAATCGGAAGACAGTGTCAAACGAAGAAGCTTCCTG 2027
Qy 536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db 2028 CTCTCCCTGGATGGCAACCCGCTGACTGGTGACAAGAAGCTGTGCTCTCCCCACCAGTCT 2087
Qy 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db 2088 CTCTTGAGTATCCGTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACGAGCATTTTC 2147
Qy 576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db 2148 AGCTTCAGAGGTCGGGCGAAGGACGTGGGGTCTGAGAATGACTTTGCAGACGATGAGCAC 2207
Qy 596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db 2208 AGCACCTTCGAGGACAGCGAGAGCAGGAGAGACTCCCTGTTTGTGCCGCACAGACCTGGA 2267
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635
Db 2268 GAGCGACGCAACAGT---------- 2282
Qy 636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655
Db 2282 ---------- 2282
Qy 656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675
Db 2282 ---------- 2282
Qy 676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695
Db 2283 ----------AACGGTACCACCACTGAAACGGAAGTCAGGAAGAGAAGGCTAAGT 2327
Qy 696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715
Db 2328 TCTTACCAGATTTCAATGGAAATGCTGGAGGATTCCTCTGGAAGACAAAGATCCATGAGC 2387
Qy 716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysPro 735
Db 2388 ATAGCCAGTATCCTGACCAACACCATGGAGGAACTTGAAGAATCTAGACAGAAGTGCCCA 2447
Qy 736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755
Db 2448 CCATGCTGGTATAGATTCGCCAATGTGTTTTTGATCTGGGACTGCTGTGATGCATGGTTA 2507
Qy 756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775
Db 2508 AAAGTGAAGCATCTTGTGAATTTAATTGTGATGGATCCATTTGTTGATCTTGCCATAACA 2567
Qy 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795
Db 2568 ATTTGCATCGTATTAAATACACTGTTCATGGCCATGGAGCACTATCCCATGACCCAGCAG 2627
Qy 796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815
Db 2628 TTCAGCAGTGTGCTGACTGTGGGAAACCTGGTCTTCACTGGGATCTTCACAGCCGAAATG 2687
Qy 816 PheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePhe 835
Db 2688 GTCCTTAAAATCATTGCCATGGACCCCTATTATTATTTCCAAGAGGGCTGGAATATTTTC 2747

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Qy    836 AspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeu 855
Db   2748 GATGGAATTATTGTTAGCCTGAGTTTAATGGAGCTAGGCCTGGCAAATGTGGAGGGGCTG 2807

Qy    856 SerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThr 875
Db   2808 TCTGTGCTTCGGTCCTTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAGTCCTGGCCCACA 2867

Qy    876 LeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeu 895
Db   2868 CTGAACATGCTCATTAAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTG 2927

Qy    896 ValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSer 915
Db   2928 GTGCTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTTGGAAAGAGC 2987

Qy    916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935
Db   2988 TACAAGGAGTGTGTCTGCAAGATCAATGTGGACTGCAAGCTGCCGCGCTGGCACATGAAC 3047

Qy    936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955
Db   3048 GACTTCTTCCACTCCTTCCTGATCGTGTTCCGAGTGCTGTGTGGGGAGTGGATAGAGACC 3107

Qy    956 MetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetVal 975
Db   3108 ATGTGGGACTGCATGGAGGTCGCGGGCCAGACCATGTGCCTTATTGTGTTCATGTTGGTC 3167

Qy    976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPhe 995
Db   3168 ATGGTGATTGGGAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTGTTGAGTTCCTTT 3227

Qy    996 SerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAla 1015
Db   3228 AGTTCAGATAACCTTGCTGCTACTGACGATGATAACGAAATGAACAACCTCCAGATCGCG 3287

Qy   1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035
Db   3288 GTGGGAAGGATGCAAAAGGGAATTGATTTTGTGAAAAATAAGATACGGGAGTGCTTCCGA 3347

Qy   1036 GlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsn 1055
Db   3348 AAAGCGTTTTTCAGAAAGCCGAAAGTGATA---GAAATCCAAGAA------------GGC 3392

Qy   1056 AsnLysLysAspSerCysMetSerAsnHisThr---***GluIleGlyLysAspLeuAsp 1074
Db   3393 AACAAAATAGACAGCTGCATGTCCAATAACACGGGCATCGAAATAAGCAAAGAGCTTAAC 3452

Qy   1075 TyrLeuLysAspValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLys 1094
Db   3453 TACCTTAAAGACGGTAATGGAACCACCAGCGGCGTGGGAACCGGAAGCAGTGTGGAAAAA 3512

Qy   1095 TyrIleIleAspGluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThr 1114
Db   3513 TACGTAATCGATGAAAATGACTACATGTCATTCATAAACAATCCCAGCCTCACCGTGACT 3572

Qy   1115 ValProIleAlaValGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSer 1134
Db   3573 GTGCCAATTGCTGTGGGAGAGTCTGACTTTGAAAATTTAAATACGGAAGAGTTCAGCAGT 3632

Qy   1135 GluSerAspLeuGluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGly 1154
Db   3633 GAGTCAGAATTGGAAGAAAGTAAGGAGAAATTAAAT---GCAACCAGCTCTTCTGAAGGA 3689

Qy   1155 SerThrValAspIleGlyAlaProValGlu---GluGlnProValValGluProGluGlu 1173
Db   3690 AGCACAGTTGATGTTGCTCCACCCCGAGAAGGTGAACAAGCAGAAATTGAACCTGAGGAG 3749

Qy   1174 ThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGln 1193
Db   3750 GACCTTAAGCCAGAAGCTTGTTTTACTGAAGGGTGCATTAAAAAATTCCCCTTCTGTCAA 3809
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Qy   1194 IleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArg 1213
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Qy   1214 IleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGly 1233
Db   3870 ATTGTGGAGCACAACTGGTTTGAGACATTCATTGTGTTCATGATTCTCCTCAGTAGTGGC 3929

Qy   1234 AlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGlu 1253
Db   3930 GCTTTGGCCTTTGAGGATATATACATTGAGCAACGAAAGACGATCAAGACCATGCTGGAG 3989

Qy   1254 TyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAla 1273
Db   3990 TATGCAGACAAGGTCTTCACGTACATCTTCATCCTGGAGATGCTCCTCAAATGGGTGGCC 4049

Qy   1274 TyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAsp 1293
Db   4050 TATGGATTTCAAACCTATTTCACCAATGCCTGGTGCTGGTTGGACTTCCTGATCGTTGAT 4109

Qy   1294 ValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLys 1313
Db   4110 GTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTTGGTTACTCAGAACTTGGTGCCATCAAA 4169

Qy   1314 SerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMet 1333
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Qy   1334 ArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuVal 1353
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Qy   1354 CysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPhe 1373
Db   4290 TGTCTCATCTTCTGGCTGATTTTTAGCATCATGGGTGTGAATCTGTTTGCTGGAAAGTTC 4349

Qy   1374 TyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHis 1393
Db   4350 TATCACTGTGTTAACACGACAACAGGCAACATGTTTGAAATAAAAGAAGTGAACAATTTC 4409

Qy   1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysVal 1413
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Qy   1414 AsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGly 1433
Db   4461 AACTTTGACAACGTTGGGGCTGGCTACCTGGCATTGCTGCAAGTGGCCACATTCAAAGGC 4520

Qy   1434 TrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyr 1453
Db   4521 TGGATGGACATCATGTATGCAGCTGTTGATTCGCGGGACGTCAAACTGCAGCCCATATAT 4580

Qy   1454 GluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePhe 1473
Db   4581 GAAGAAAACCTGTACATGTACCTGTACTTTGTCATCTTCATCATCTTCGGCTCGTTCTTC 4640

Qy   1474 ThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPhe 1493
Db   4641 ACTCTAAATCTATTCATCGGTGTCATCATAGACAACTTCAACCAGCAGAAGAAGAAGTTT 4700

Qy   1494 GlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLys 1513
Db   4701 GGAGGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTACAATGCAATGAAGAAG 4760

Qy   1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533
Db   4761 CTCGGCTCAAAGAAACCTCAGAAGCCCATCCCTCGGCCTGCAAACAAATTTCAAGGGATG 4820

Qy   1534 ValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeu 1553
Db   4821 GTCTTTGATTTTGTAACCAGACAAGTGTTTGACATCAGCATCATGATCCTCATCTGCCTC 4880

Qy   1554 AsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrValThrThrIleLeu 1573
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Db   4881 AACATGGTGACCATGATGGTGGAAACGGATGACCAGAGCAAATACATGACCCTGGTTTTG 4940

Qy   1574 SerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIle 1593

Db   4941 TCCCGAATCAACCTAGTGTTCATTGTCCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATC 5000

Qy   1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIle 1613

Db   5001 TCCCTCAGATACTACTACTTCACGATAGGGTGGAACATCTTTGACTTTGTGGTGGTGATT 5060

Qy   1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633

Db   5061 CTCTCGATTGTAGGAATGTTTCTCGCAGAGCTGATAGAGAAGTATTTCGTGTCCCCTACC 5120

Qy   1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653

Db   5121 CTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC 5180

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Db   5241 GGCCTCCTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 5300

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Db   5301 TATGTTAAAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGC 5360

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Db   5541 TTCCTGGTGGTGGTGAACATGTACATCGCTGTCATCCTGGAGAACTTCAGCGTCGCCACC 5600

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Db   5661 AAGTTCGACCCTGACGCCACTCAGTTCATAGAGTTCTGCAAGCTTTCTGACTTTGCAGCT 5720

Qy   1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAsp 1853

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Db   5781 CTGCCCATGGTGAGTGGAGACCGCATCCACTGCCTGGACATCTTGTTTGCTTTTACAAAG 5840

Qy   1874 ArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPhe 1893

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Qy   1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913

Db   5901 ATGGCTTCCAACCCCTCCAAGGTCTCTTATGAGCCCATTACCACCACCCTGAAACGGAAA 5960

Qy   1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArg 1933

Db   5961 CAAGAGGAGGTGTCTGCTGCTATCATTCAGCGTAATTATAGATGTTATCTTTTAAAGCAA 6020

Qy   1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeu 1953

Db   6021 CGGTTAAAAAACATATCGAGTAAATACGACAAAGAGACAATCAAGGGAAGGATTGACTTG 6080

Qy   1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973

Db   6081 CCTATAAAAGGAGATATGGTTATTGACAAATTGAATGGGAATTCCACCCCAGAAAAGACG 6140

Qy   1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993

Db   6141 GATGGGAGTTCCTCCACAACCTCT---CCTCCTTCCTATGACAGTGTAACAAAACCAGAT 6197

Qy   1994 ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009

Db   6198 AAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAATCAAAGGGAAA 6245
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RESULT 15
AAT30195
ID AAT30195 standard; cDNA; 6404 BP.
XX
AC AAT30195;
XX
DT 25-OCT-1996 (first entry)
XX
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit gene.
XX
KW Human; peripheral nervous system; sodium channel; PN1B;
KW dorsal root ganglion; sodium-agonist; sodium-antagonist;
KW drug screening; analgesic; hypotensive; antiinflammatory; trauma;
KW pain; neurological disorder; antisense; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   49..6015
FT   /*tag= a
FT   /product= PN1B protein
FT misc_difference 334..336
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FT   /codon= seq:ACA, aa:Ala
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FT   /codon= seq:ATA, aa:Leu
XX
PN WO9614077-A1.
XX
PD 17-MAY-1996.
XX
PF 02-NOV-1995; 95WO-US14251.
XX
PR 07-JUN-1995; 95US-0482401.
PR 02-NOV-1994; 94US-0334029.
XX
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
XX
PI Borden LA, Halegoua S, Mandel G;
XX
DR WPI; 1996-251547/25.
DR P-PSDB; AAR99641.
XX
PT Nucleic acid encoding peripheral nervous system specific sodium
PT channel peptide - useful for sodium channel-associated disease or
PT trauma.
XX
PS Example 4; Fig 14; 80pp; English.
XX
CC The sequence encodes a human peripheral nervous system sodium channel
CC peptide-1 alpha-subunit (PN1B), with sodium channel activity. A
CC probe has been isolated by PCR from a human peripheral nervous
CC system cDNA library, using probes derived from the rat PN1 protein

CC sequence (AAR99638-39), and has been used to screen a human dorsal
CC root ganglion cDNA library, to give the full-length sequence, using
CC PCR primers AAT30198-99 and AAT18167. A related sequence (AAT30194) has
CC also been isolated. The sodium channel peptide may be used to
CC isolate sodium-agonists and sodium-antagonists for use as
CC analgesics, hypotensives, antiinflammatories, and in therapy of
CC sodium channel-associated pathology or trauma, e.g. neurological
CC disorders. The DNA (in sense or antisense orientation) may be used
CC in gene therapy.
XX
SQ Sequence 6404 BP; 1961 A; 1236 C; 1381 G; 1826 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	6404
Score:	7903.00	Matches:	1538
Percent Similarity:	86.00%	Conservative:	194
Best Local Similarity:	76.37%	Mismatches:	244
Query Match:	76.01%	Indels:	38
DB:	17	Gaps:	13

US-09-930-871-12 (1-2009) x AAT30195 (1-6404)

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Qy     22 LeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLys 41
Db    106 CTTGCCCTCATTGAACAACGCATTGCTGAAAGAAAATCAAAGGAACCCAAAGAAGAAAAG 165

Qy     42 LysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
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Qy     62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
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Qy    162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
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Qy    182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
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Qy    202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
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Qy    302 GlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAspSer 321
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Qy    342 AlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGly 361
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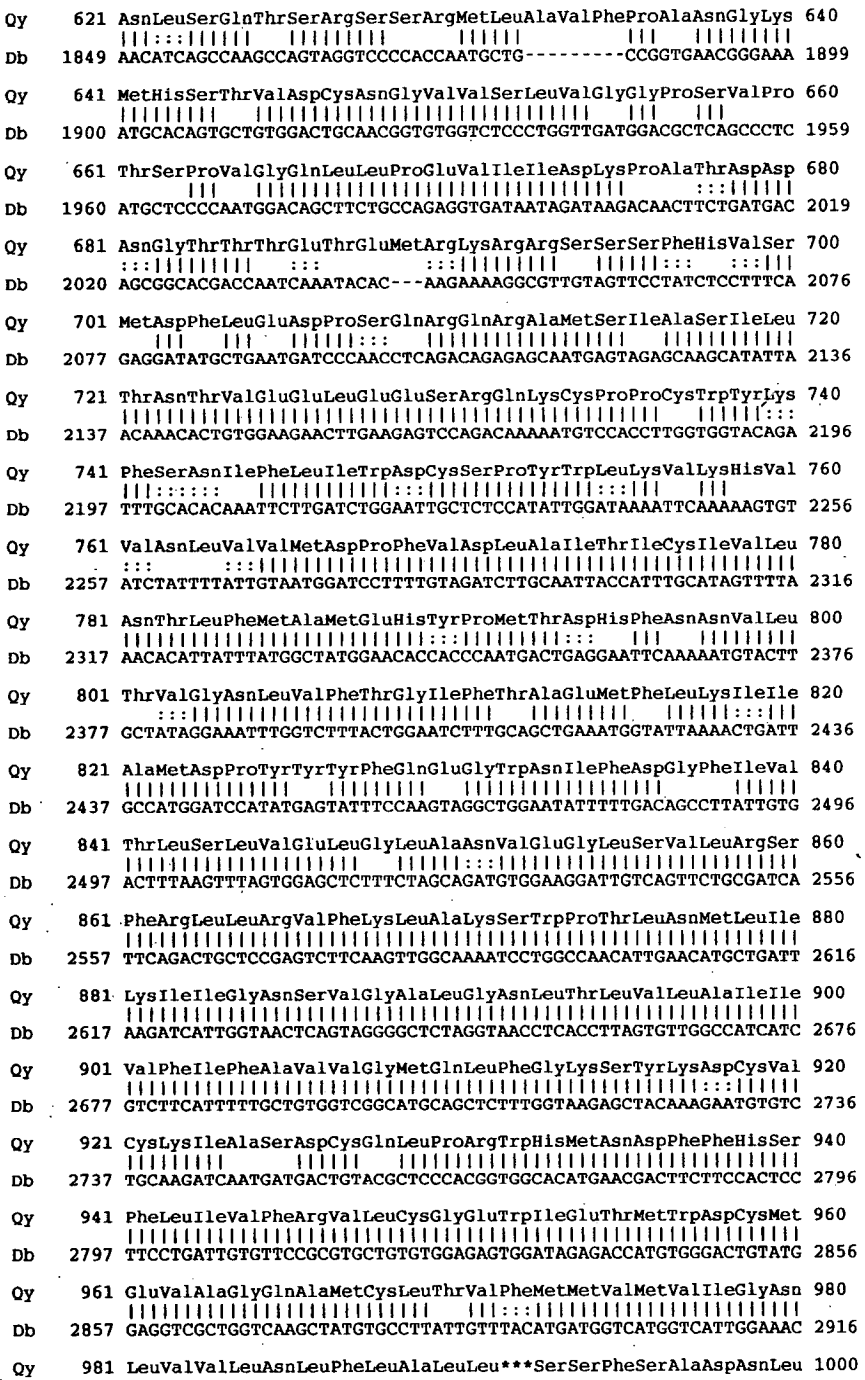
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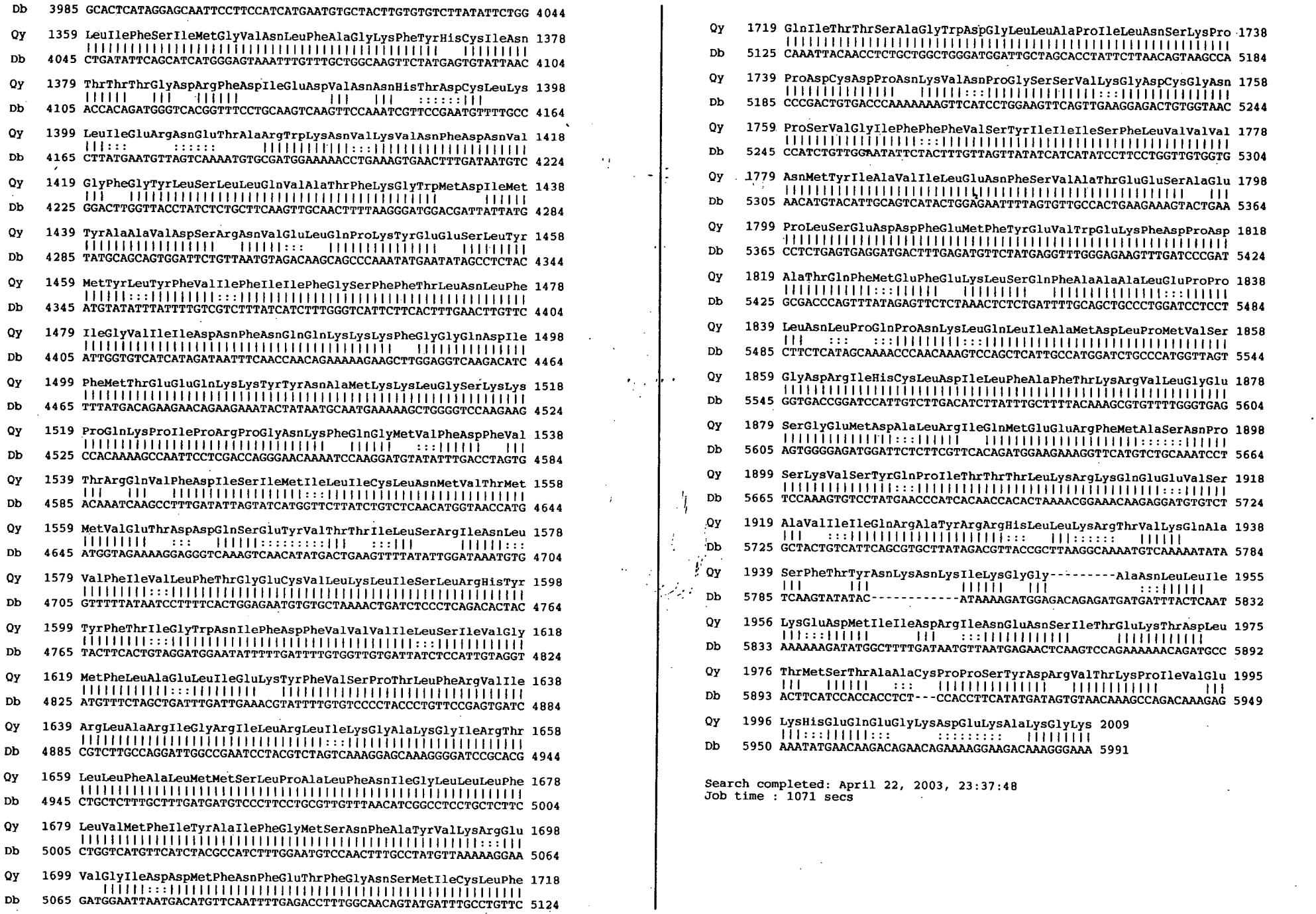
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Db   1669 GGCTCCTTGTTTTCTGCAAGGCGAAGCAGCAGAACAAGTCTTTTTAGTTTCAAAGGCAGA 1728

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09930871/runat_16042003_114838_8471/app_query.fasta_1.2183
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09930871_@CGN_1_1_2946_@runat_16042003_114838_8471 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2231	21.5	1777	11	BC029489	BC029489 Homo sapi
	2	1368	13.2	928	14	BQ715936	BQ715936 AGENCOURT
	3	1167.5	11.2	816	14	BQ444145	BQ444145 UI-M-EX0-
	4	1148	11.0	735	13	BI488967	BI488967 603021693
	5	1107	10.6	908	14	BQ946179	BQ946179 AGENCOURT
	6	1100	10.6	674	12	BG342331	BG342331 602374246
	7	1093	10.5	951	9	AL533359	AL533359 AL533359
	8	1076	10.3	902	12	BG761119	BG761119 602717452
	9	1062	10.2	778	9	AU035605	AU035605 AU035605
	10	1046	10.1	665	10	BB653350	BB653350 BB653350
	11	1019	9.8	618	10	BB622500	BB622500 BB622500
	12	1007.5	9.7	809	12	BG541438	BG541438 602570863
c	13	987.5	9.5	706	9	AA984063	AA984063 am76b09.s
	14	976.5	9.4	689	12	BF347024	BF347024 602021819
	15	974	9.4	602	9	AL706368	AL706368 DKFZp686H
	16	965	9.3	774	13	BI488799	BI488799 603021394
	17	952	9.2	579	14	BM718214	BM718214 UI-E-EJ1-
c	18	940	9.0	731	9	AI796228	AI796228 wh44d06.x
c	19	927	8.9	562	14	BM682680	BM682680 UI-E-EJ1-
	20	903.5	8.7	1043	17	CNS02Y6B	AL219260 Tetraodon
	21	894	8.6	671	13	BM488035	BM488035 pgm2n.pk0
	22	888	8.5	831	12	BG403969	BG403969 602419830
	23	880	8.5	547	12	BF470392	BF470392 UI-M-BH3-
	24	876	8.4	934	9	AL517958	AL517958 AL517958
	25	853.5	8.2	952	13	BI458325	BI458325 603199282
	26	851	8.2	662	12	BG253038	BG253038 602365660
	27	846.5	8.1	608	10	AW140953	AW140953 EST290960
	28	845.5	8.1	700	10	BB631922	BB631922 BB631922
	29	844	8.1	561	12	BF076296	BF076296 225823 MA
	30	843.5	8.1	939	13	BI600029	BI600029 603251413
	31	830	8.0	610	9	AL588672	AL588672 AL588672
	32	823	7.9	873	12	BF527027	BF527027 602039918
	33	819.5	7.9	694	9	AL705279	AL705279 DKFZp686E
	34	817	7.9	598	14	BM726341	BM726341 UI-E-EJ0-
c	35	806.5	7.8	656	10	AV721039	AV721039 AV721039
	36	801.5	7.7	944	14	BQ731018	BQ731018 AGENCOURT
	37	800.5	7.7	615	10	AW133907	AW133907 fi13c05.y
	38	800	7.7	665	10	AV956239	AV956239 AV956239
	39	794.5	7.6	544	12	BF323267	BF323267 maa38e08.
	40	791	7.6	509	11	BC034643	BC034643 Mus muscu
	41	791	7.6	510	11	BC023034	BC023034 Mus muscu
	42	789	7.6	547	12	BE724185	BE724185 198931 MA
	43	758	7.3	877	12	BF682878	BF682878 602117665
c	44	754	7.3	1066	17	CNS05GAK	AL336053 Tetraodon
	45	751.5	7.2	812	12	BG666779	BG666779 DRABWE08

ALIGNMENTS

RESULT 1
BC029489
LOCUS BC029489 1777 bp mRNA linear HTC 16-MAY-2002
DEFINITION Homo sapiens, clone IMAGE:5278436, mRNA.
ACCESSION BC029489
VERSION BC029489.1 GI:20809571
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1777)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian

```
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 48 Row: h Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 10337596
            This clone has the following problem: frame shifted.
FEATURES              Location/Qualifiers
     source           1. .1777
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5278436"
                      /tissue_type="Brain, hypothalamus"
                      /clone_lib="NIH_MGC_96"
                      /lab_host="DH10B"
                      /note="Vector: pBluescript"
BASE COUNT      526 a    333 c    395 g    523 t
ORIGIN

Alignment Scores:
Pred. No.:              3.48e-208       Length:         1777
Score:                  2231.00         Matches:        441
Percent Similarity:     90.31%          Conservative:   25
Best Local Similarity:  85.47%          Mismatches:     34
Query Match:            21.46%          Indels:         16
DB:                     11              Gaps:           5

US-09-930-871-12 (1-2009) x BC029489 (1-1777)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           |||   |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||
Db     248 ATGGCACAGTCGGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 307

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||:::|||||||||||||||||||||||||||   ||||||   :::
Db     308 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 367

Qy      41 LysLysAsp---AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLys 59
           :::||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 427

Qy      60 AsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAsp 79
           :::|||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db     428 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 487

Qy      80 LeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIle 99
           ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db     488 CTGGACCCCTACTATGTCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 547

Qy     100 PheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLys 119
           ||||||||||||||   |||||||||||||||||||||||||||||:::||||||
Db     548 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 607

Qy     120 IleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeu 139
           :::|||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db     608 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 667

Qy     140 ThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyr 159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 727

Qy     160 ThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCys 179
           ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db     728 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 787

Qy     180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 847

Qy     200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     848 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 907

Qy     220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     908 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 967

Qy     240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     968 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 1027

Qy     260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db    1028 GTGTTCGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 1087

Qy     280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr------ 297
           ||||||||   |||:::                |||   |||   |||||||||
Db    1088 TGGCCTCCAGATAATTCT--------------TCCTTTGAAATAAATATCACTTCCTTC 1132

Qy     298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAsp 313
                        ::::::   |||||||||      |||   ||||||      |||:::
Db    1133 TTTAACAATTCATTGGATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAAC 1192

Qy     314 TrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAla 333
           |||       ||||||:::|||      :::   ||||||||||||||      ||||||
Db    1193 TGGGATGAATATATTGAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCT 1252

Qy     334 LeuLeuCysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLys 353
           ||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db    1253 CTGCTTTGTGGCAACAGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAG 1312

Qy     354 AlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeu 373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 GCTGGTAGAAACCCCAACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTG 1372

Qy     374 SerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArg 393
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1373 TCCTTATTTCGTCTCATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGT 1432

Qy     394 AlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyr 413
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1433 GCTGCTGGGAAAACGTACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTAT 1492

Qy     414 LeuIleAsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThr 433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1493 CTAATAAATTTGATCTTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACA 1552

Qy     434 LeuGluGluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLys 453
           ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db    1553 TTGGAAGAGGCTGAACAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAG 1612

Qy     454 GlnGlnGluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluPro 473
           |||||||||   |||   |||||||||   |||   ||||||      ||||||:::
Db    1613 CAACAAGAAGAAGCT---CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTC 1669

Qy     474 SerAlaAlaGlyArgLeu---------SerAspSerSerSerGluAlaSerLysLeuSer 490
           |||   ||||||   :::          |||:::||||||||   ||||||||||||||
Db    1670 AGTGGTGCTGGTGGGATAGGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGC 1729

Qy     491 SerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGln 506
```

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          ||||||||||   ||||||   :::||||||||||||||||:::|||:::
Db   1730 TCCAAAAGTGAAAAAGAGCTGAAAAACAGAAGAAAAAAAAAAAAAAAA 1777

RESULT 2
BQ715936
LOCUS       BQ715936                928 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8294886 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6309535
            5', mRNA sequence.
ACCESSION   BQ715936
VERSION     BQ715936.1  GI:21854835
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13730  row: g  column: 08
            High quality sequence stop: 715.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6309535"
                     /clone_lib="NIH_MGC_129"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: olfactory epithelium; Vector:
                     pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
                     unidirectionally. Primer: Oligo dT. Average insert size
                     2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                     is a NIH_MGC Library."
BASE COUNT      204 a    247 c    227 g    249 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                1.11e-123       Length:          928
Score:                    1368.00         Matches:         279
Percent Similarity:       94.52%          Conservative:    14
Best Local Similarity:    90.00%          Mismatches:      13
Query Match:              13.16%          Indels:          4
DB:                       14              Gaps:            0

US-09-930-871-12 (1-2009) x BQ715936 (1-928)

Qy   1610 ValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPhe 1629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGGTGGTGATTCTCTCAATTGTAGGAATGTTCCTTGCTGAGCTGATAGAGAAGTATTTT 60

Qy   1630 ValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeu 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGTCTCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTG 120

Qy   1650 IleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAla 1669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATCAAAGGCGCCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCG 180

Qy   1670 LeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMet 1689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTGTTCAACATCGGCCTCCTGCTTTTCCTCGTCATGTTCATCTACGCCATCTTTGGGATG 240

Qy   1690 SerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThr 1709
          ||||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||||
Db    241 TCCAACTTTGCCTATGTTAAAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACT 300

Qy   1710 PheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeu 1729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTTGGCAACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTG 360

Qy   1730 LeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnProGly 1749
          ||||||||||||||||||||   ||||||||||||||||:::   ::::::||||||
Db    361 TTGGCCCCCATCCTCAACAGTGCACCTCCTGACTGTGACCCTGATGCAATTCACCCTGGA 420

Qy   1750 SerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyr 1769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGCTCAGTGAAGGGAGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGCTAC 480

Qy   1770 IleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPhe 1789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATTGCTGTCATCCTGGAGAACTTC 540

Qy   1790 SerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyr 1809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AGCGTTGCCACAGAAGAAAGTGCAGAGCCCCTGAGTGAGGACGACTTTGAGATGTTCTAC 600

Qy   1810 GluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSer 1829
          ||||||||||||||||||||||||||||||||||||||||||:::||||||   |||||||||
Db    601 GAGGTCTGGGAGAAGTTCGACCCTGACGCCACCCAGTTCATAGAGTTCTGCAAGCTCTCT 660

Qy   1830 GlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeu 1849
               ||||||||||||||:::|||||||||   :::   :::|||||||||:::||||||
Db    661 GACTTTGCAGCTGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACAAAGTCCAGCTC 720

Qy   1850 IleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPhe 1869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATCCACTGCCTGGACATCTTATTT 780

Qy   1870 AlaPheThrLysArgVal-LeuGly-GluSerGlyGluMetAspAlaLeu-ArgIleGln 1888
          ||||||||||||||||||  ||||||    ||||||||||||||||||||| :::|||:::
Db    781 GCTTTTACAAAGCGGGTCCCTGGGTGANAAGTGGAGAAATGGATGCCCTTTCAAATCAGA 840

Qy   1889 MetGluGluArg-PheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrTh 1908
          ||||||:::||| ||||||||||||||||||||:::   ||||||      |||   ||
Db    841 ATGGAAGATCGGGTTCATGGCTTCCAATCCCTCCAGGGGCTCTTATTGAGCCATTAACAC 900

Qy   1908 rThrLeuLysArgLysGlnGlu 1915
          |||||||||||||:::   |||
Db    901 CACTCTGAAGCGCCAACCAGAA 922

RESULT 3
BQ444145
LOCUS       BQ444145                816 bp    mRNA    linear   EST 29-MAY-2002
DEFINITION  UI-M-EX0-bxj-d-14-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone
            IMAGE:5708893 5', mRNA sequence.
ACCESSION   BQ444145
VERSION     BQ444145.1  GI:21247257
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, Univeristy of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
```

```
          Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Mus musculus"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5708893"
                     /clone_lib="NIH_BMAP_EX0"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 15.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured mRNa was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site.  Double stranded
                     cDNA was size selected according to mRNA size fraction,
                     ligated with EcoR I adaptor, digested with Not I, and then
                     cloned directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     , is GTGCGTGGAA. This library was created for the
                     University of Iowa Mouse Brain Molecular Anatomy Project
                     (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                     System', supported by National Instututes of Mental Health
                     (NIMH), Hemin Chin, Ph.D., program coordinator."
BASE COUNT      192 a    209 c    208 g    205 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:                4.92e-104      Length:          816
Score:                    1167.50        Matches:         219
Percent Similarity:       89.67%         Conservative:    24
Best Local Similarity:    80.81%         Mismatches:      27
Query Match:              11.23%         Indels:          1
DB:                       14             Gaps:            1

US-09-930-871-12 (1-2009) x BQ444145 (1-816)

Qy    691 LysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArg 710
          |||::          |||      ||||||||::   |||             ::::::
Db      3 AAGAAAGGCCCTGGATCGCTCTTAGTCTCCATGGAACAACTCGCCTCCTACGGACGGAAG 62

Qy    711 GlnArgAlaMetSerIleAlaSerIleLeuThrAsnThr---ValGluGluLeuGluGlu 729
            |||      ||||||   |||::::::||||||||   ||||||||||||||||||
Db     63 GACAGAATCAACAGTATAATGAGCGTTGTCACAAACACACTAGTGGAAGAGCTGGAAGAG 122

Qy    730 SerArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAsp 749
          |||::::::||||||||||||||||||||||||||:::|||   ||||||||||||:::
Db    123 TCTCAGAGAAAGTGCCCACCATGCTGGTATAAGTTTGCCAATACTTTCCTCATCTGGGAG 182

Qy    750 CysSerProTyrTrpLeuLysValLysHisValValAsnLeuValValMetAspProPhe 769
          |||   |||||||||:::|||:::|||   :::||||||||:::||||||||||||||||
Db    183 TGTCACCCCTACTGGATAAAACTGAAGGAGATTGTGAACCTGATCGTCATGGACCCTTTC 242

Qy    770 ValAspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHis 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GTAGACTTAGCCATAACCATCTGCATTGTCCTGAACACACTATTTATGGCAATGGAGCAC 302

Qy    790 TyrProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGly 809
          :::|||||||||      |||   :::||||||   ||||||||||||||||||||||||
Db    303 CATCCCATGACGCCACAATTCGAACATGTCCTGGCCGTAGGGAACCTGGTGTTCACTGGG 362

Qy    810 IlePheThrAlaGluMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGln 829
          ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    363 ATCTTCACGGCGGAAATGTTCCTGAAGCTCATAGCCATGGATCCCTACTATTACTTCCAA 422

Qy    830 GluGlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeu 849
          ||||||||||||||||||||||||||||:::|||||||||::||||||||||||||||||
Db    423 GAAGGCTGGAACATTTTTGACGGATTTATCGTCTCCCTCAGTTTAATGGAGCTGGGCCTT 482

Qy    850 AlaAsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeu 869
          |||:::|||||||||||||||||||||||||||||||||||||||||||||||||   |||
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Db    483 GCAGACGTGGAGGGGCTCTCAGTGCTGCGATCTTTCCGATTGCTCCGAGTCTTCANATTG 542

Qy    870 AlaLysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAla 889
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 GCCAAGTCCTGGCCCACCCTGAACATGCTGATCAAGATCATTGGGAACTCCGTTGGCGCC 602

Qy    890 LeuGlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMet 909
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 CTGNGCAACCTGACCCTGGTGCTGGCCATCATTGTCTTCATCTTTGCCGTGGTGGGGATG 662

Qy    910 GlnLeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeu 929
          ||||||||||||||||||||||||:::|||||||||||||||||:::   :::|||:::|||
Db    663 CAGCTCTTTGGAAAGAGCTACAAGGAGTGCGTCTGTAAGATCAGCCAGGAGTGCAAGCTC 722

Qy    930 ProArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCys 949
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    723 CCGCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTCATCGTCTTCCGAGTGCTGTGT 782

Qy    950 GlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||        ||||||
Db    783 GGGGAGTGGATCGAGACATGTGGGATTTGCATG 815

RESULT 4
BI488967
LOCUS       BI488967                735 bp    mRNA    linear   EST 28-AUG-2001
DEFINITION  603021693F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192182 5',
            mRNA sequence.
ACCESSION   BI488967
VERSION     BI488967.1  GI:15328195
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11480  row: j  column: 23
            High quality sequence stop: 728.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5192182"
                     /clone_lib="NIH_MGC_114"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is  destroyed
                     upon cloning).  Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      164 a    173 c    175 g    223 t
ORIGIN

Alignment Scores:
Pred. No.:                3.53e-102      Length:          735
Score:                    1148.00        Matches:         228
Percent Similarity:       96.31%         Conservative:    7
Best Local Similarity:    93.44%         Mismatches:      9
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Query Match:            11.04%      Indels:        1
DB:                     13          Gaps:          0

US-09-930-871-12 (1-2009) x BI488967 (1-735)

Qy   1632 ProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLys 1651
          ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db      1 CCTACCCTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCGA-ATCCTACGACTGATCAAA 59

Qy   1652 GlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPhe 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 GGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTT 119

Qy   1672 AsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsn 1691
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db    120 AACATCGGCCTCCTTCTTTTCCTGGTCATGTTCATCTACGCCATCTTAGGGATGTCCAAT 179

Qy   1692 PheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGly 1711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 TTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGC 239

Qy   1712 AsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAla 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240 AACAGCATGATCTGCCTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCA 299

Qy   1732 ProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSer 1751
          ||||||||||||||   ||||||||||||||||:::|||   :::||||||||||||
Db    300 CCTATTCTTAATAGTGGACCTCCAGACTGTGACCCTGACAAAGATCACCCTGGAAGCTCA 359

Qy   1752 ValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIle 1771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360 GTTAAAGGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGTTACATCATC 419

Qy   1772 IleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerVal 1791
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 ATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTT 479

Qy   1792 AlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluVal 1811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTG 539

Qy   1812 TrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPhe 1831
          ||||||||||||||||||||||||||||||||:::||||||   |||||||||   |||
Db    540 TGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCGCCAAACTTTCTGATTTT 599

Qy   1832 AlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAla 1851
          |||   ||||||:::|||||||||   :::   :::|||||||||:::||||||||||||
Db    600 GCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAGCTCATTGCC 659

Qy   1852 MetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPhe 1871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 ATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATCTTATTTGCTTTT 719

Qy   1872 ThrLysArgVal 1875
          ||||||||||||
Db    720 ACAAAGCGTGTA 731

RESULT 5
BQ946179
LOCUS       BQ946179                908 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8926526 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6469275
            5', mRNA sequence.
ACCESSION   BQ946179
VERSION     BQ946179.1  GI:22361657
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13998  row: c  column: 04
            High quality sequence stop: 596.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6469275"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      225 a    246 c    202 g    234 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              5.08e-98        Length:         908
Score:                  1107.00         Matches:        234
Percent Similarity:     84.95%          Conservative:   20
Best Local Similarity:  78.26%          Mismatches:     37
Query Match:            10.65%          Indels:         8
DB:                     14              Gaps:           4

US-09-930-871-12 (1-2009) x BQ946179 (1-908)

Qy   1394 ThrAspCysLeuLysLeuIleGluArgAsnGluThr---AlaArgTrpLysAsnValLys 1412
          |||||||||   |||||||:::|||   |||   |||      ||||||||||||||||||
Db      6 ACCGACTGTGAGAAGCTCATGGAGGGCAACAACACAGAGATCCGATGGAAGAACGTCAAG 65

Qy   1413 ValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLys 1432
          :::|||||||||||||||||   |||||||||:::||||||||||||||||||||||||
Db     66 ATCAACTTCGACAACGTCGGGGCAGGCTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAA 125

Qy   1433 GlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLeuGlnProLys 1452
          ||||||||||||||||||||||||||||||||||||||||||||      :::   ||||||
Db    126 GGCTGGATGGACATCATGTATGCAGCTGTAGATTCCCGAAAGCCGGACGAGCAGCCTGAT 185

Qy   1453 TyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePheGlySerPhe 1472
          ||||||   ::::::||||||||:::||||||||||||||||||||||||||||||||||
Db    186 TATGAGGGCAACATCTACATGTACATCTACTTCGTCATCTTCATCATCTTCGGCTCCTTC 245

Qy   1473 PheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLys 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 TTCACCCTCAACCTGTTCATCGGTGTCATCATCGACAATTTCAATCAACAGAAGAAAAAG 305

Qy   1493 PheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLys 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 TTTGGAGGTCAGGACATCTTCATGACAGAGGAACAGAAGAAGTACTACAACGCCATGAAG 365

Qy   1513 LysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGly 1532
          ||||||||||||||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db    366 AAGCTAGGCTCCAAGAAGCCACAGAAGCCCATCCCCCGACCTTTGAACAAAATCCAAGGG 425

Qy   1533 MetValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIleCys 1552
          :::|||||||||||||||||:::|||   |||||||||   ||||||:::||||||||
Db    426 ATTGTCTTTGATTTCGTCACGCAACAAGCCTTCGACATCGTGATCATGATGCTTATCTGC 485

Qy   1553 LeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrValThrThrIle 1572
          ||||||||||||||||||||||||||||||||   ||||||:::   :::      |||
Db    486 CTTAACATGGTGACCATGATGGTGGAGACAGACACACAGAGCAAGCAGATGGAGAACATT 545
```

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Qy   1573 LeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeu 1592
          |||      |||||||||||||||::::::   ||||||   |||||||||||||||::: 
Db    546 CTCTACTGGATTAATCTGGTCTTCGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAAATG 605

Qy   1593 IleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValVal 1612
            :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 TTTGCCTTGAGACACTACTATTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTC 665

Qy   1613 IleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGlu-LysTyrPheValSerPr 1632
          |||||||||||||||||||||||||||||::::::|||||| ||||||||||||||||  
Db    666 ATTCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGGAAGTACTTCGTCTCCCC 725

Qy   1632 oThrLeuPheArgValIleArgLeu-AlaArgIle-GlyArgIleLeuArg-LeuIleLy 1651
          ||||||||||||||||||||||||| ||||||||| |||||||||||||| ||||||||  
Db    726 GACCCTATTCCGCGTCATCCGATTGGGCCCGCATCGGGGCGCATCTTGCGTCTTGATCAA 785

Qy   1651 sGlyAlaLysGlyIleArg---ThrLeuLeuPheAlaLeuMetMetSerLeuPro---Al 1669
          |||||||:::   ||||||                |||||||||||||||           
Db    786 AGGCGCCCAAAGGATCCGCCACCCCTGCTCTTTGGCCTTAATGATGTCCGCTGCCCGCCC 845

Qy   1669 aLeuPheAsnIleGlyLeuLeuLeu---PheLeuValMetPheIleTyr 1684
            |||   ||||||||||||             ||||||||:::
Db    846 CTGTTTCACAATCGGCCTCCTGGCTCCTTCCTGGGNCATGTTCATCTTT 894

RESULT 6
BG342331
LOCUS       BG342331                674 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602374246F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5',
            mRNA sequence.
ACCESSION   BG342331
VERSION     BG342331.1  GI:13148769
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 674)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10317  row: l  column: 12
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
     source          1. .674
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4481819"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      146 a    167 c    161 g    200 t
ORIGIN

Alignment Scores:
Pred. No.:              1.65e-97        Length:         674
Score:                  1100.00         Matches:        220
Percent Similarity:     98.67%          Conservative:   2
Best Local Similarity:  97.78%          Mismatches:     3
Query Match:            10.58%          Indels:         1
DB:                     12              Gaps:           0

US-09-930-871-12 (1-2009) x BG342331 (1-674)

Qy   1532 GlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMetIleLeuIle 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGAATGGTTTTTGACTTTGTAACCAGACAAGTGTTTGATATCAGCATCATGATCCTCATC 60

Qy   1552 CysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrValThrThr 1571
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||:::
Db     61 TGTCTGAACATGGTGACCATGATGGTGGAAACGGATGACCAGAGCGATTATGTGACAAGC 120

Qy   1572 IleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLys 1591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATTTTGTCACGCATCAACCTGGTGTTCATCGTCCTGTTCACCGGCGAGTGTGTGCTCAAG 180

Qy   1592 LeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValVal 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCATCTCGCTCCGCCATTATTATTTCACCATTGGATGGAACATTTTCGATTTTGTGGTG 240

Qy   1612 ValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSer 1631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTCATCCTCTCCATTGTAGGGATGTTTCTTGCGGAGCTAATAGAAAAGTATTTTGTGTCT 300

Qy   1632 ProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLys 1651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAA 360

Qy   1652 GlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPhe 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGTGCCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTT 420

Qy   1672 AsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsn 1691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATCGGCCTCCTGCTTTTTCTCGTCATGTTCATCTACGCCATCTTTGGGATGTCCAAC 480

Qy   1692 PheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGly 1711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTGCCTATGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTCGGC 540

Qy   1712 AsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAla 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTGCTGGCC 600

Qy   1732 ProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSer 1751
          |||||||||      |||   ||||||||||||||||||||||||||||||||||||||||
Db    601 CCCATCCTCAAAAGGAAACC-CCTGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCG 659

Qy   1752 ValLysGlyAspCys 1756
          |||||||||||||||
Db    660 GTGAAGGGAGACTGT 674

RESULT 7
AL533359
LOCUS       AL533359                951 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL533359 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN004YF22 5
            prime, mRNA sequence.
ACCESSION   AL533359
VERSION     AL533359.1  GI:12796852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
```

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     source          1. .951
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DN004YF22"
                     /clone_lib="LTI_FL015_Brn1"
                     /sex="male"
                     /tissue_type="Adult brain"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was constructed by Life Technologies.
                     Contact : Feng Liang Life Technologies, a division of
                     Invitrogen 9800 Medical Center Drive Rockville, Maryland
                     20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      303 a    189 c    203 g    247 t      9 others
ORIGIN

Alignment Scores:
Pred. No.:              1.29e-96        Length:         951
Score:                  1093.00         Matches:        215
Percent Similarity:     96.43%          Conservative:   1
Best Local Similarity:  95.98%          Mismatches:     8
Query Match:            10.51%          Indels:         0
DB:                     9               Gaps:           0

US-09-930-871-12 (1-2009) x AL533359 (1-951)

Qy   1786 LeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPhe 1805
           ||||||||||||   ||||||||||||||||||||||||||||||   ||||||||||||
Db      3 CTGGAGAACTTCWKTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAKTGAGGATGACTTT 62

Qy   1806 GluMetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPhe 1825
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 TAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTT 122

Qy   1826 GluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsn 1845
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAAC 182

Qy   1846 LysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeu 1865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTT 242

Qy   1866 AspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeu 1885
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTA 302

Qy   1886 ArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnPro 1905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 CGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCA 362

Qy   1906 IleThrThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAla 1925
           ||||||||||||||   |||||||  ||||||||||||||||||||||||||||||||||
Db    363 ATCACTACTACTTTAAWACGAAAACWAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCT 422

Qy   1926 TyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsn 1945
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    423 TACAGACGCCACCTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAAAC 482

Qy   1946 LysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsn 1965
           ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db    483 AAAATCAAAGGTGGGGCTAATCTTCTTATAAWAKAAGACATGATAATTGACAGAATAAAT 542

Qy   1966 GluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSer 1985
           :::||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db    543 GATAACTCTATTACAGNAAAAACTGATCTGACCATGTCCACTGCAGCTTGTCCACCTTCC 602

Qy   1986 TyrAspArgValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLys 2005
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    603 TATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAAGATGAAAAA 662

Qy   2006 AlaLysGlyLys 2009
           ||||||||||||
Db    663 GCCAAAGGGAAA 674

RESULT 8
BG761119
LOCUS       BG761119                 902 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602717452F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4841124 5',
            mRNA sequence.
ACCESSION   BG761119
VERSION     BG761119.1  GI:14071772
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 902)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1673  row: g  column: 13
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
     source          1. .902
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4841124"
                     /clone_lib="NIH_MGC_49"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
BASE COUNT      251 a    174 c    215 g    262 t
ORIGIN

Alignment Scores:
Pred. No.:              5.64e-95        Length:         902
Score:                  1076.00         Matches:        229
Percent Similarity:     81.33%          Conservative:   28
Best Local Similarity:  72.47%          Mismatches:     43
Query Match:            10.35%          Indels:         23
DB:                     12              Gaps:           1

US-09-930-871-12 (1-2009) x BG761119 (1-902)

Qy    125 LeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsnCysValPhe 144
          |||:::||||||:::|||||||||:::|||||||||||||||||||||||||||||||||
Db     10 TTGATACATTCAGTATTTAGCATGATCATTATGTGCACTATTTTGACCAACTGTGTATTC 69

Qy    145 MetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPheThrGlyIle 164
          ||||||   ||||||||||||||||:::|||||||||||||||||||||||||||||||
Db     70 ATGACTTTTAGTAACCCTCCTGACTGGTCGAAGAATGTGGAGTACACGTTCACAGGGATT 129

Qy    165 TyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGluAspPheThr 184
          ||||||||||||||||||:::|||||||||||||||||||||::::::   ||||||
Db    130 TATACATTTGAATCACTAGTGAAAATCATTGCAAGAGGTTTCTGCATAGATGGCTTTACC 189
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Qy    185 PheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAlaTyrValThr 204
          ||||||||||||||||||||||||||||||||||:::||||||      ||||||:::|||
Db    190 TTTTTACGGGATCCATGGAACTGGTTAGATTTCAGTGTCATCATGATGGCGTATATAACA 249

Qy    205 GluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeuArgAlaLeu 224
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GAGTTTGTAAACCTAGGCAATGTTTCAGCTCTACGCACTTTCAGGGTACTGAGGGCTTTG 309

Qy    225 LysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIleGlnSerVal 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 AAAACTATTTCGGTAATCCCAGGCCTGAAGACAATTGTGGGTGCCCTGATTCAGTCTGTG 369

Qy    245 LysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPheAlaLeuIle 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 AAGAAACTGTCAGATGTGATGATCCTGACAGTGTTCTGCCTGAGTGTTTTTGCCTTGATC 429

Qy    265 GlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpProProThrAsn 284
          ||||||||||||||||||||||||||||||||||:::   ||||||
Db    430 GGACTGCAGCTGTTCATGGGGAACCTTCGAAACAAGTGTGTAGTGTGGCCC--------- 480

Qy    285 AlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsnGlyThrLeu 304
                                          :::|||:::|||   :::
Db    481 -----------------------------------ATAAACTTCAACGAGAGCTAT 501

Qy    305 IleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAspSerArgTyrHis 324
          :::                  ||||||||:::   ||||||   :::
Db    502 CTTGAACATGGCACCAAAGGCTTTGATTGGGAAGAGTATATCAACAATAAAACAAATTTC 561

Qy    325 TyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSerAspAlaGlyGln 344
          |||   :::   |||   |||:::   ||||||||||||||||||||||||||||||||
Db    562 TACACAGTTCCTGGCATGCTGGAACCTTTACTCTGTGGGAACAGTTCTGATGCTGGGCAA 621

Qy    345 CysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGlyTyrThrSer 364
          ||||||||||||||   |||:::||||||||||||   |||   ||||||||||||
Db    622 TGCCCAGAGGGATACCAGTGTATGAAAGCCGGAAGGAAACCGCAATATGGTTACACAAG- 680

Qy    365 PheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGlnAspPheTrp 384
          |||||||||   ||||||||||||      :::   ||||||||||||||||||:::
Db    681 TTTGACACTTTAAGCTGGGCCTTCT--GGCATTATTCGCCTTATGACCCAGGACTATAG- 737

Qy    385 GluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIlePhePheVal 404
          ||||||||||||   ||||||||||||||||||   |||   ||||||||||||||||
Db    738 GAAAACTTGTATCACTTGACTTTACGAGCAGCCTGGAAACCATACATGATCTTCTTCGC- 796

Qy    405 LeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaValValAlaMet 424
          |||   |||:::   |||   :::||||||:::||||||||||||   ||||||||||:::
Db    797 TTGGCCATCTATGA-GGGTACTACTATCTGGTGAACTTGATCTTGGGTGTGGTGGCACTG 855

Qy    425 AlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
             |||||||||:::||||||   ||||||   ||||||||||||:::
Db    856 GT-TATGAAGAACGGAATCAGGA-ACACTGGCAGAGGCAGAACAAAGA 901
```

RESULT 9
AU035605

LOCUS	AU035605	778 bp mRNA linear EST 12-JUL-2000
DEFINITION	AU035605 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-0634, mRNA sequence.	
ACCESSION	AU035605	
VERSION	AU035605.1 GI:3718608	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 778)	
AUTHORS	Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K., Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.	
TITLE	Construction of mouse full length-enriched cDNA libraries	
JOURNAL	Unpublished (1998)	
COMMENT	Contact: Katsuyuki Hashimoto	
	Division of Genetic Resources	
	National Institute of Infectious Diseases	
	23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan	
	Email: khashi@nih.go.jp	
	POLYA=No.	

FEATURES	Location/Qualifiers
source	1. .778
	/organism="Mus musculus"
	/strain="C57BL"
	/db_xref="taxon:10090"
	/clone="MNCb-0634"
	/clone_lib="Sugano mouse brain mncb"
	/sex="female"
	/dev_stage="adult"
	/lab_host="TOP10"
	/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al.(University of Tokyo, Institute of Medical Science). Custom primer used for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGCG], 3' end primer [CGACCTGCAGCTCGAGCACA]"

BASE COUNT 196 a 192 c 165 g 223 t 2 others
ORIGIN

Alignment Scores:

Pred. No.:	1.1e-93	Length:	778
Score:	1062.00	Matches:	228
Percent Similarity:	90.04%	Conservative:	7
Best Local Similarity:	87.36%	Mismatches:	21
Query Match:	10.21%	Indels:	6
DB:	9	Gaps:	2

US-09-930-871-12 (1-2009) x AU035605 (1-778)

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Qy   1459 MetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ATGTATCTGTACTTTGTCATCTTCATCATCTTTGGGTCGTTCTTCACTCTAAATCTATTC 61

Qy   1479 IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIle 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 ATCGGCGTCATCATAGACAACTTCAACCAGCAGAAGAAGAAGTTTGGAGGTCAAGACATC 121

Qy   1499 PheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLys 1518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 TTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAGAAACTTGGCTCCAAAAAA 181

Qy   1519 ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal 1538
          |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db    182 CCTCAGAAGCCCATCCCTCGACCTGCAAACAAATTTCAAGGAATGGTCTTTGACTTTGTA 241

Qy   1539 ThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1558
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 ACCAGACAAGTGTTTGACATCAGCATCATGATCCTCATCTGCCTCAACATGGTGACCATG 301

Qy   1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578
          ||||||||||||||||||||||:::|||:::|||   :::||||||||||||||||||||
Db    302 ATGGTGGAAACGGACGACCAGAGCAAATACATGACCCTGGTTTTGTCCCGAATCAACCTG 361

Qy   1579 ValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyr 1598
          ||||||||||||||||||||||||||   :::|||||||||||||||||||||:::|||
Db    362 GTATTCATCGTCCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCAGATACTAC 421

Qy   1599 TyrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGly 1618
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 TACTTCACGATTGGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCAATTGTAGGA 481

Qy   1619 MetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIle 1638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 ATGTTCCTTGCTGAGCTGATAGAGAAGTATTTTGTGTCTCCTACCCTGTTCCGAGTCATC 541
```

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Qy   1639 ArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThr 1658
          ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    542 CGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCCAG-GGGATCCGCACG 600

Qy   1659 LeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsn-IleGlyLeuLeuLeuPh 1678
          ||||||||||||||   |||||||||   ||||||   ||| ||||||          ||
Db    601 CTGCTCTTTGCTCTGACCATGTCCCTTTCTGCGCTGGTCAACAATCGGGCCTCCTGCTTT 660

Qy   1678 e---LeuValMetPheIleTyrAlaIlePheGly---MetSerAsnPheAlaTyr-ValL 1696
          |               ||||||   |||||||||           |||||||| ||||
Db    661 TTCCTCGGCATGGGTCATCTACCCCATCTTTGGGGANTGTCCAACTTTTGCCTATGGTAA 720

Qy   1696 ysArgGluValGlyIleAspAspMetPheAsnPheGlu-ThrPheGlyAsnSerMet 1714
          ||:::   :::|||||||   ||||||||||||||||| ||||||||||||   |||
Db    721 AAAAGAGGCTGGGAATTTATGACATGTTCAACTTTGAGAACNTTTGGCAACCGCATG 777
```

RESULT 10
BB653350
LOCUS BB653350 665 bp mRNA linear EST 26-OCT-2001
DEFINITION BB653350 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone C630029C19 5', mRNA sequence.
ACCESSION BB653350
VERSION BB653350.1 GI:16487207
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 665)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .665
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630029C19"
/clone_lib="RIKEN full-length enriched, adult male hippocampus"
/sex="male"
/tissue_type="hippocampus"
/dev_stage="adult"
/lab_host="SOLR"
/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']"
BASE COUNT 134 a 171 c 190 g 170 t
ORIGIN

Alignment Scores:

Pred. No.:	3.33e-92	Length:	665
Score:	1046.00	Matches:	200
Percent Similarity:	97.67%	Conservative:	10
Best Local Similarity:	93.02%	Mismatches:	5
Query Match:	10.06%	Indels:	0
DB:	10	Gaps:	0

US-09-930-871-12 (1-2009) x BB653350 (1-665)

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Qy    802 ValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIleAla 821
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db      1 GTAGGGAACCTGGTGTTCACTGGGATCTTCACGGCGGAAATGTTCCTGAAGCTCATAGCC 60

Qy    822 MetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleValThr 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db     61 ATGGATCCCTACTATTACTTCCAAGAAGGCTGGAACATTTTTGACGGATTTATCGTCTCC 120

Qy    842 LeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSerPhe 861
          |||||||||:::||||||||||||||:::|||||||||||||||||||||||||||||||
Db    121 CTCAGTTTAATGGAGCTGGGCCTTGCAGACGTGGAGGGGCTCTCAGTGCTGCGATCTTTC 180

Qy    862 ArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLys 881
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGATTGCTCCGAGTCTTCAAATTGGCCAAGTCCTGGCCCACCCTGAACATGCTGATCAAG 240

Qy    882 IleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleVal 901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCATTGGGAACTCCGTTGGCGCCCTGGGCAACCTGACCCTGGTGCTGGCCATCATTGTC 300

Qy    902 PheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCys 921
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Db    301 TTCATCTTTGCCGTGGTGGGGATGCAGCTCTTTGGAAAGAGCTACAAGGAGTGCGTCTGT 360

Qy    922 LysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSerPhe 941
          ||||||:::   :::|||:::||||||||||||||||||||||||||||||||||||||
Db    361 AAGATCAGCCAGGAGTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTTC 420

Qy    942 LeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetGlu 961
          ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db    421 CTCATCGTCTTCCGAGTGCTGTGTGGGGAGTGGATCCAGACCATGTGGGATTGCATGGAA 480

Qy    962 ValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsnLeu 981
          ||||||||||||||||||||||   ||||||||||||||||||   ||||||||||||
Db    481 GTGGCCGGCCAGGCCATGTGCCTTATCGTGTTCATGATGGTCATGGGCATCGGCAACCTG 540
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Qy     982 ValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAla 1001
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Db     541 GTGGTGCTGAACTTATTTCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAATCTGGCG 600

Qy    1002 AlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaVal 1016
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Db     601 GCCACGGACGACGACGGGGAAATGAACAACCTGCAGATATCGGTG 645

RESULT 11
BB622500
LOCUS       BB622500                618 bp    mRNA    linear   EST 31-AUG-2001
DEFINITION  BB622500 RIKEN full-length enriched, adult male olfactory brain Mus
            musculus cDNA clone 6430408L10 5', mRNA sequence.
ACCESSION   BB622500
VERSION     BB622500.1  GI:15397780
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
            Ishii,Y. and Hayashizaki,Y.
             Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
            Func. Genomics 2 pre, L72-L86 (2001
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .618
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="6430408L10"
                     /clone_lib="RIKEN full-length enriched, adult male
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                     /sex="male"
                     /tissue_type="olfactory brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with BamHI and XhoI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT      133 a    155 c    157 g    173 t
ORIGIN

Alignment Scores:
Pred. No.:              1.36e-89        Length:         618
Score:                  1019.00         Matches:        200
Percent Similarity:     98.06%          Conservative:   2
Best Local Similarity:  97.09%          Mismatches:     4
Query Match:            9.80%           Indels:         0
DB:                     10              Gaps:           0

US-09-930-871-12 (1-2009) x BB622500 (1-618)

Qy    1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTCTCCATTGTAGGGATGTTTCTCGCGGAGCTGATAGAGAAGTATTTCGTGTCCCCTACC 60

Qy    1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC 120

Qy    1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTTAACATC 180

Qy    1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GGCCTCCTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 240

Qy    1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TACGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGC 300

Qy    1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIle 1733
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Db     301 ATGATCTGCCTGTTCCAAATCACCACTTCTGCGGGCTGGGATGGACTGCTGGCCCCTATA 360

Qy    1734 LeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLys 1753
           |||||||||   ||||||||||||||||||   |||   :::||||||||||||||||||
Db     361 CTAAATAGTGGACCTCCCGATTGTGACCCTGAAAAAGATCATCCTGGAAGCTCGGTGAAG 420

Qy    1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773
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Db     421 GGAGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGCTACATCATCATATCC 480

Qy    1774 PheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793
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Db     481 TTCCTGGTTGTGGTGAACATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACA 540

Qy    1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813
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Db     541 GAAGAAAATGCAGAGCCTCTGAGTGAGGACGACTTTGAGATGTTCTACGAAGTCTGGGAG 600
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Qy   1814 LysPheAspProAspAla 1819
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Db    601 AAAGTCGACCCTGACGCA 618

RESULT 12
BG541438
LOCUS       BG541438                809 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602570863F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695375 5',
            mRNA sequence.
ACCESSION   BG541438
VERSION     BG541438.1  GI:13533671
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1520  row: n  column: 16
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      214 a    202 c    198 g    195 t
ORIGIN

Alignment Scores:
Pred. No.:                2.66e-88        Length:          809
Score:                    1007.50         Matches:         213
Percent Similarity:       84.34%          Conservative:    24
Best Local Similarity:    75.80%          Mismatches:      28
Query Match:              9.69%           Indels:          20
DB:                       12              Gaps:            2

US-09-930-871-12 (1-2009) x BG541438 (1-809)

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db      3 GGCTCCCTTTTCTCTCCAAGACGCAACAGTAGGGCGAGCCTTTTCAGCTTCAGAGGTCGA 62

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 GCAAAGGACATTGGCTCTGAGAATGACTTTGCTGATGATGAGCACAGCACCTTTGAGGAC 122

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          |||:::|||||||||||||||||||||||||||   ||||||||||||||||||:::|||
Db    123 AATGACAGCCGAAGAGACTCTCTGTTCGTGCCGCACAGACATGGAGAACGGCGCCACAGC 182

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
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Db    183 AATGTCAGCCAGGCCAGCCGTGCCTCCAGGGTGCTCCCCATCCTGCCCATGAATGGGAAG 242

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 ATGCATAGCGCTGTGGACTGCAATGGTGTGGTCTCCCTGGTCGGGGGCCCTTCTACCCTC 302

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||      ||||||||||||||||||
Db    303 ACATCT---GCTGGGCAGCTCCTACCAGAG---------------------------- 329

Qy    681 AsnGlyThrThrThrGluThrGluMet-ArgLysArgArgSerSerSerPheHisValSe 700
          ||||||||||||||||||||||:::|||||||||||||||||||||:::||||||||
Db    330 ---GGCACAACTACTGAAACAGAAATAACGAAAGAGACGGTCCAGTTCTTATCATGTTTC 386

Qy    700 rMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLe 720
          |||||||   ||||||||||||:::   ||||||||||||||||||||||||||   ||
Db    387 CATGGATTTATTGGAAGATCCTACATCAAGGCAAAGAGCAATGAGTATAGCCAGTAT-TT 445

Qy    720 uThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLy 740
          ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db    446 GACCAACACCATGGAAGAACTTGAAGAATCCAGACAGAAATGCCCACCATGCTGGTATAC 505

Qy    740 sPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVa 760
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Db    506 -ATTGCTAATATGTG-TTGATTTGGGACTGTCGTAAACCATGGTTACAGGTGACACACCT 563

Qy    760 lValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLe 780
          :||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    564 TGTCAACCTGGTTGTAATGGACCCATTTGTTGACCTTGGCATCACCATCTGCATTGTCTT 623

Qy    780 uAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPhe-AsnAsnValL 800
          ||||||||||||||||||||||||||||||||||||||||||::   ||| ::::::||||
Db    624 AAATACACTCTTCATGGCTATGGAGCACTATCCCATGACGGAGCAGTTCAAGCAGTGTAC 683

Qy    800 euThrValGlyAsnLeuValPheThrGlyIlePhe-ThrAlaGluMetPheLeuLysIle 819
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Db    684 TGTCTGTCGGAAACCTGGTCTTCACAGGGATCTTCCACAGCAGAAATGTTCTCAAGGATA 743

Qy    820 IleAlaMetAspProTyr-TyrTyrPheGlnGluGlyTrpAsnIlePheAspGly 837
          :::   ||||||||||| ::::::|||||||:::||||||          |||
Db    744 ATGGC-ATGGATCCATATTCATCACTTTCAGCAAGGCTGGAAATATTCCGGAGGT 797

RESULT 13
AA984063/c
LOCUS       AA984063                706 bp    mRNA    linear   EST 27-MAY-1998
DEFINITION  am76b09.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
            IMAGE:1616345 3' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN
            II ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AA984063
VERSION     AA984063.1  GI:3162588
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
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          High quality sequence stop: 425.
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                     /clone_lib="Stratagene schizo brain S11"
                     /sex="male"
                     /tissue_type="schizophrenic brain S-11 frontal lobe"
                     /dev_stage="34 years old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI;  Library
                     constructed from S-11 frontal lobe, male, 34 years old,
                     50% caucasian, 50% Aleutian.  Schizophrenic suicide.
                     Random primed into EcoRI site of ZAP II Vector.  Mass
                     excised. Custom library. Avg insert length 1.4kb.
                     Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                     and the Stanley Neuropathology Consortium - Analysis of
                     RNAs from the Brains of Individuals with Psychiatric
                     Diseases (Unpublished) Stanley Neurovirology Laboratory,
                     Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT      232 a    155 c    135 g    184 t
ORIGIN

Alignment Scores:
Pred. No.:                2.05e-86       Length:          706
Score:                    987.50         Matches:         201
Percent Similarity:       86.72%         Conservative:    8
Best Local Similarity:    83.40%         Mismatches:      20
Query Match:              9.50%          Indels:          13
DB:                       9              Gaps:            2

US-09-930-871-12 (1-2009) x AA984063 (1-706)

Qy    180 LeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThr 199
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db    706 TTAGAGGATTTCACATTTTTACGGGATCCATGAAATTGGTTGGATTTCACAGTCATTACT 647

Qy    200 PheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArg 219
            ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    646 CTTGCATATGTGACAGAGTTTGTGGACCTGGCAAATGTCTCAGCGTTGAGAACATTCAGA 587

Qy    220 ValLeuArgAlaLeu-LysThrIleSerValIleProGlyLeuLysThrIleValGlyAl 239
          |||||||||||||| |||||||||||||||||||||||||||||||||   |||||
Db    586 GTTCTCCGAGCATTGAAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGT-GGTGC 528

Qy    239 aLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSe 259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    527 CCTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAG 468

Qy    259 rValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGl 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||
Db    467 CGTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCA 408

Qy    279 nTrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThr----- 297
          ||||||||||   |||:::              |||   |||   |||||||||
Db    407 ATGGCCTCCAGATAATTCT--------------TCCTTTGAAATAAATATCACTTCCTT 363

Qy    298 ------------ValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAs 313
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Db    362 CTTTAACAATTCATTGGATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAA 303

Qy    313 pTrpLysSerTyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAl 333
          :|||      ||||||:::|||      :::   ||||||||||||||      |||||
Db    302 CTGGGATGAATATATTGAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGC 243

Qy    333 aLeuLeuCysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLy 353
          ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db    242 TCTGCTTTGTGGCAACAGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAA 183

Qy    353 sAlaGlyArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLe 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GGCTGGTAGAAACCCCAACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTT 123

Qy    373 uSerLeuPheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuAr 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GTCCTTATTTCGTCTCATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACG 63

Qy    393 gAlaAlaGlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTy 413
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Db     62 TGCTGCTGGGAAAACGTACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTA 3

Qy    413 r 413
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Db      2 T 2

RESULT 14
BF347024
LOCUS       BF347024                689 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  602021819F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157189
            5', mRNA sequence.
ACCESSION   BF347024
VERSION     BF347024.1  GI:11294619
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9431  row: f  column: 06
            High quality sequence start: 3
            High quality sequence stop: 654.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4157189"
                     /clone_lib="NCI_CGAP_Brn67"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      179 a    130 c    158 g    222 t
ORIGIN

Alignment Scores:
Pred. No.:                2.4e-85        Length:          689
Score:                    976.50         Matches:         198
Percent Similarity:       90.13%         Conservative:    12
Best Local Similarity:    84.98%         Mismatches:      18
Query Match:              9.39%          Indels:          6
DB:                       12             Gaps:            1

US-09-930-871-12 (1-2009) x BF347024 (1-689)

Qy   1284 TrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAla 1303
          ||||||||||||||||||||||   ||||||||||||||||||||   |||||||||
Db      3 TGGTGCTGGCTAGATTTCTTGATCGT-GATGTTTCTTTGGTTAGCCTGGTAGCCAATGCT 61

Qy   1304 LeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgPro 1323
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Db      62 CTTGGCTACTCAGAACTCGGTGCCATCAAATCATTACGGACATTAAGAGCTTTAAGACCT 121

Qy    1324 LeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAla 1343
           ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db     122 CTAAGAGCCTTATCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTATGTGGAGCA 181

Qy    1344 IleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIle 1363
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ATTCCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTGATCTTTAGCATC 241

Qy    1364 MetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAsp 1383
           |||||||||||||||||||||||||||||||||||:::|||   |||||||||:::
Db     242 ATGGGTGTGAATTTGTTTGCTGGCAAGTTCTACCACTGTGTTAACATGACAACGGGTAAC 301

Qy    1384 ArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsn 1403
             |||||||||   ||||||||||||   :::|||||||      |||
Db     302 ATGTTTGACATTAGTGATGTTAACAATTTGAGTGACTGTCAGGCTCTT---------GGC 352

Qy    1404 GluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeu 1423
           :::   ||||||||||||||||||||||||||||||||||||||||   |||||||||
Db     353 AAGCAAGCTCGGTGGAAAAACGTGAAAGTAAACTTTGATAATGTTGGCGCTGGCTATCTT 412

Qy    1424 SerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAsp 1443
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Db     413 GCACTGCTTCAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTTGAT 472

Qy    1444 SerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPhe 1463
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Qy    1464 ValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIle 1483
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Db     533 GTCATCTTTATCATCTTTGGGTCATTCTTCACTCTGAATCTATTCATGGGTGTCATCATA 592

Qy    1484 AspAsnPheAsnGlnGlnLys-LysLysPheGlyGlyGlnAspIlePheMetThrGluGl 1503
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Qy    1503 uGlnLys-LysTyrTyrAsnAlaMetLysLysLeu 1514
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Db     653 ACCGAAACACATATTACCACTGCACTGAAGAACTC 687

RESULT 15
AL706368
LOCUS       AL706368                602 bp    mRNA    linear   EST 22-MAR-2002
DEFINITION  DKFZp686H1140_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686H1140 5', mRNA sequence.
ACCESSION   AL706368
VERSION     AL706368.1  GI:19689723
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Ansorge W
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686H1140) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="DKFZp686H1140"
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                     /dev_stage="adult"
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                     cDNA-collection"
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Score:                    974.00        Matches:         188
Percent Similarity:       97.49%        Conservative:    6
Best Local Similarity:    94.47%        Mismatches:      5
Query Match:              9.37%         Indels:          0
DB:                       9             Gaps:            0

US-09-930-871-12 (1-2009) x AL706368 (1-602)

Qy    1584 PheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGly 1603
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Db       5 TTCACTGGAGAATTTGTGCTGAAGCTCGTCTCCCTCAGACACTACTACTTCACTATAGGC 64

Qy    1604 TrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGlu 1623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 TGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGTATGTTTCTGGCTGAG 124

Qy    1624 LeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIle 1643
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 ATGATAGAAAAGTATTTTGTGTCCCCTACCTTGTTCCGAGTGATCCGTCTTGCCAGGATT 184

Qy    1644 GlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeu 1663
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Db     185 GGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTG 244

Qy    1664 MetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIle 1683
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Db     245 ATGACGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTCCTGGTCATGTTTATC 304

Qy    1684 TyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAsp 1703
           ||||||||||||||||||||||||||||||||||||||:::|||   ||||||||||||
Db     305 TATGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAAAAGGAAGCTGGAATTGATGAC 364

Qy    1704 MetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSer 1723
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Qy    1724 AlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspPro 1743
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Qy    1744 AsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIle 1763
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Db     485 GACACAATTCACCCTGGCAGTTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGGATT 544

Qy    1764 PhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIle 1782
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Job time : 3720 secs
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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 22, 2003, 21:17:35 ; Search time 98 Seconds
(without alignments)
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Title: US-09-930-871-12
Perfect score: 10397
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7877	75.8	6452	3	US-08-836-325-9	Sequence 9, Appli
3	7861.5	75.6	6371	3	US-08-836-325-13	Sequence 13, Appl
4	7755.5	74.6	6007	3	US-09-024-020B-2	Sequence 2, Appli
5	7755.5	74.6	6007	4	US-09-425-043-2	Sequence 2, Appli
6	7720.5	74.3	5977	3	US-09-024-020B-1	Sequence 1, Appli
7	7720.5	74.3	5977	4	US-09-425-043-1	Sequence 1, Appli
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17	5426	52.2	6527	4	US-08-669-656A-7	Sequence 7, Appli
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25	4309.5	41.4	6519	2	US-08-808-793-24	Sequence 24, Appl
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42	1541	14.8	5904	1	US-08-455-543A-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1
US-08-836-325-14
; Sequence 14, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rationa
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6404 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
US-08-836-325-14

Alignment Scores:
Pred. No.:                0              Length:          6404
Score:                    7913.00        Matches:         1540
Percent Similarity:       86.05%         Conservative:    193
Best Local Similarity:    76.46%         Mismatches:      243
Query Match:              76.11%         Indels:          38
DB:                       3              Gaps:            13

US-09-930-871-12 (1-2009) x US-08-836-325-14 (1-6404)

Qy       2 GluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGluSer 21
Db      46 AAGATGGCAATGTTGCCTCCCCCAGGACCTCAGAGCTTTGTCCATTTCACAAAACAGTCT 105

Qy      22 LeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLys 41
Db     106 CTTGCCCTCATTGAACAACGCATTGCTGAAAGAAAATCAAAGGAACCCAAAGAAGAAAAG 165

Qy      42 LysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
Db     166 AAAGATGATGATGAAGAAGCCCCAAAGCCAAGCAGTGACTTGGAAGCTGGCAAACAACTG 225

Qy      62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
Db     226 CCCTTCATCTATGGGGACATTCCTCCCGGCATGGTGTCAGAGCCCCTGGAGGACTTGGAC 285

Qy      82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
Db     286 CCCTACTATGCAGACAAAAAGACTTTCATAGTATTGAACAAAGGGAAAACAATCTTCCGT 345

Qy     102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
Db     346 TTCAATGCCACACCTGCTTTATATATGCTTTCTCCTTTCAGTCCTCTAAGAAGAATATCT 405

Qy     122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
Db     406 ATTAAGATTTTAGTACACTCCTTATTCAGCATGCTCATCATGTGCACTATTCTGACAAAC 465

Qy     142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
Db     466 TGCATATTTATGACCATGAATAACCCGCCGGACTGGACCAAAAATGTCGAGTACACTTTT 525

Qy     162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
Db     526 ACTGGAATATATACTTTTGAATCACTTGTAAAAATCCTTGCAAGAGGCTTCTGTGTAGGA 585

Qy     182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
Db     586 GAATTCACTTTTCTTCGTGACCCGTGGAACTGGCTGGATTTTGTCGTCATTGTTTTTGCG 645

Qy     202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
Db     646 TATTTAACAGAATTTGTAAACCTAGGCAATGTTTCAGCTCTTCGAACTTTCAGAGTATTG 705

Qy     222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
Db     706 AGAGCTTTGAAAACTATTTCTGTAATCCCAGGCCTGAAGACAATTGTAGGGGCTTTGATC 765

Qy     242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
Db     766 CAGTCAGTGAAGAAGCTTTCTGATGTCATGATCCTGACTGTGTTCTGTCTGAGTGTGTTT 825

Qy     262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpPro 281
Db     826 GCACTAATTGGACTACAGCTGTTCATGGGAAACCTGAAGCATAAATGTTTTCGA------ 879

Qy     282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
Db     880 ----------------------AATTCACTTGAAAATAATGAAACATTAGAA------ 909

Qy     302 GlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAspSer 321
Db     910 ---AGCATAATGAATACCCTAGAGAGTGAAGAAGACTTTAGA---------------- 948

Qy     322 ArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSerAsp 341
Db     949 AAATATTTTTATTACTTGGAAGGATCCAAAGATGCTCTCCTTTGTGGTTTCAGCACAGAT 1008

Qy     342 AlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGly 361
Db    1009 TCAGGTCAGTGTCCAGAGGGGTACACCTGTGTGAAAATTGGCAGAAACCCTGATTATGGC 1068

Qy     362 TyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGln 381
Db    1069 TACACGAGCTTTGACACTTTCAGCTGGGCCTTCTTAGCCTTGTTTAGGCTAATGACCCAA 1128

Qy     382 AspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIle 401
Db    1129 GATTACTGGGAAAACCTTTACCAACAGACGCTGCGTGCTGCTGGCAAAACCTACATGATC 1188

Qy     402 PhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaVal 421
Db    1189 TTCTTTGTCGTAGTGATTTTCCTGGGCTCCTTTTATCTAATAAACTTGATCCTGGCTGTG 1248

Qy     422 ValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlu 441
Db    1249 GTTGCCATGGCATATGAAGAACAGAACCAGGCAAACATTGAAGAAGCTAAACAGAAAGAA 1308

Qy     442 AlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGlnAla 461
Db    1309 TTAGAATTTCAACAGATGTTAGACCGTCTTAAAAAAGAGCAAGAAGAAGCTGAGGCAATT 1368

Qy     462 AlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSerAsp 481
Db    1369 GCAGCGGCAGCGGCTGAATATACAAGTATTAGGAGAAGCAGAATTATGGGCCTCTCAGAG 1428

Qy     482 SerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArgArg 501
Db    1429 AGTTCTTCTGAAACATCCAAACTGAGCTCTAAAAGTGCTAAAGAAAGAAGAAACAGAAGA 1488

Qy     502 LysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLys---AspGluAspGluPhe 520
Db    1489 AAGAAAAAGAATCAAAAGAAGCTCTCCAGTGGAGAGGAAAAGGGAGATGCTGAGAAATTG 1548

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db    1549 TCGAAATCAGAATCAGAGGACAGCATCAGAAGAAAAAGTTTCCACCTTGGTGTCGAAGGG 1608

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db    1609 CATAGGCGAGCACATGAAAAGAGGTTGTCTACCCCCAATCAGTCACCACTCAGCATTCGT 1668

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db    1669 GGCTCCTTGTTTTCTGCAAGGCGAAGCAGCAGAACAAGTCTTTTTAGTTTCAAAGGCAGA 1728

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db  1729 GGAAGAGATATAGGATCTGAGACTGAATTTGCCGATGATGAGCACAGCATTTTTGGAGAC 1788

Qy   601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db  1789 AATGAGAGCAGAAGGGGCTCACTGTTTGTGCCCCACAGACCCCAGGAGCGACGCAGCAGT 1848

Qy   621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
Db  1849 AACATCAGCCAAGCCAGTAGGTCCCCACCAATGCTG---------CCGGTGAACGGGAAA 1899

Qy   641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db  1900 ATGCACAGTGCTGTGGACTGCAACGGTGTGGTCTCCCTGGTTGATGGACGCTCAGCCCTC 1959

Qy   661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db  1960 ATGCTCCCCAATGGACAGCTTCTGCCAGAGGTGATAATAGATAAGACAACTTCTGATGAC 2019

Qy   681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db  2020 AGCGGCACGACCAATCAAATACAC---AAGAAAAGGCGTTGTAGTTCCTATCTCCTTTCA 2076

Qy   701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db  2077 GAGGATATGCTGAATGATCCCAACCTCAGACAGAGAGCAATGAGTAGAGCAAGCATATTA 2136

Qy   721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db  2137 ACAAACACTGTGGAAGAACTTGAAGAGTCCAGACAAAAATGTCCACCTTGGTGGTACAGA 2196

Qy   741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db  2197 TTTGCACACAAATTCTTGATCTGGAATTGCTCTCCATATTGGATAAAATTCAAAAAGTGT 2256

Qy   761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db  2257 ATCTATTTTATTGTAATGGATCCTTTTGTAGATCTTGCAATTACCATTTGCATAGTTTTA 2316

Qy   781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db  2317 AACACATTATTTATGGCTATGGAACACCACCCAATGACTGAGGAATTCAAAAATGTACTT 2376

Qy   801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db  2377 GCTATAGGAAATTTGGTCTTTACTGGAATCTTTGCAGCTGAAATGGTATTAAAACTGATT 2436

Qy   821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db  2437 GCCATGGATCCATATGAGTATTTCCAAGTAGGCTGGAATATTTTTGACAGCCTTATTGTG 2496

Qy   841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db  2497 ACTTTAAGTTTAGTGGAGCTCTTTCTAGCAGATGTGGAAGGATTGTCAGTTCTGCGATCA 2556

Qy   861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db  2557 TTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAATCCTGGCCAACATTGAACATGCTGATT 2616

Qy   881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db  2617 AAGATCATTGGTAACTCAGTAGGGGCTCTAGGTAACCTCACCTTAGTGTTGGCCATCATC 2676

Qy   901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db  2677 GTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTC 2736

Qy   921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db  2737 TGCAAGATCAATGATGACTGTACGCTCCCACGGTGGCACATGAACGACTTCTTCCACTCC 2796

Qy   941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db  2797 TTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACCATGTGGGACTGTATG 2856

Qy   961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db  2857 GAGGTCGCTGGTCAAGCTATGTGCCTTATTGTTTACATGATGGTCATGGTCATTGGAAAC 2916

Qy   981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db  2917 CTGGTGGTCCTAAACCTATTTCTGGCCTTATTATTGAGCTCATTTAGTTCAGACAATCTT 2976

Qy  1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db  2977 ACAGCAATTGAAGAAGACCCTGATGCAAACAACCTCCAGATTGCAGTGACTAGAATTAAA 3036

Qy  1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db  3037 AAGGGAATAAATTATGTGAAACAAACCTTACGTGAATTTATTCTAAAAGCATTTTCCAAA 3096

Qy  1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db  3097 AAGCCAAAGATTTCCAGGGAGATAAGACAAGCAGAAGATCTGAATACTAAGAAGGAAAAC 3156

Qy  1061 CysMetSerAsnHisThr---***GluIleGlyLysAspLeuAspTyrLeuLysAspVal 1079
Db  3157 TATATTTCTAACCATACACTTGCTGAAATGAGCAAAGGTCACAATTTCCTCAAGGAAAAA 3216

Qy  1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGlu 1099
Db  3217 GATAAAATCAGT----------GGTTTTGGAAGCAGCGTGGACAAACACTTGATGGAAGAC 3267

Qy  1100 SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal 1119
Db  3268 AGTGATGGTCAATCATTTATTCACAATCCCAGCCTCACAGTGACAGTGCCAATTGCACCT 3327

Qy  1120 GlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139
Db  3328 GGGGAATCCGATTTGGAAAATATGAATGCTGAGGAACTTAGCAGTGATTCGGATAGTGAA 3387

Qy  1140 GluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIle 1159
Db  3388 TACAGCAAAGTGAGATTAAACCGG---TCAAGCTCCTCAGAGTGCAGCACAGTTGATAAC 3444

Qy  1160 GlyAlaProValGlu---GluGlnProValValGluProGluGluThrLeuGluProGlu 1178
Db  3445 CCTTTGCCTGGAGAAGGAGAAGAAGCAGAGGCTGAACCTATGAATTCCGATGAGCCAGAG 3504

Qy  1179 AlaCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGlu 1198
Db  3505 GCCTGTTTCACAGATGGTTGTGTACGGAGGTTCTCATGCTGCCAAGTTAACATAGAGTCA 3564

Qy  1199 GlyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsn 1218
Db  3565 GGGAAAGGAAAAATCTGGTGGAACATCAGGAAAACCTGCTACAAGATTGTTGAACACAGT 3624

Qy  1219 TrpPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGlu 1238
Db  3625 TGGTTTGAAAGCTTCATTGTCCTCATGATCCTGCTCAGCAGTGGTGCCCTGGCTTTTGAA 3684

Qy  1239 AspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysVal 1258
Db  3685 GATATTTATATTGAAAGGAAAAAGACCATTAAGATTATCCTGGAGTATGCAGACAAGATC 3744

Qy  1259 PheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThr 1278
Db  3745 TTCACTTACATCTTCATTCTGGAAATGCTTCTAAAATGGATAGCATATGGTTATAAAACA 3804

Qy  1279 TyrPheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSer 1298
Db  3805 TATTTCACCAATGCCTGGTGTTGGCTGGATTTCCTAATTGTTGATGTTTCTTTGGTTACT 3864

Qy  1299 LeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeu 1318
Db  3865 TTAGTGGCAAACACTCTTGGCTACTCAGATCTTGGCCCCATTAAATCCCTTCGGACACTG 3924
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Qy   1319 ArgAlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsn 1338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3925 AGAGCTTTAAGACCTCTAAGAGCCTTATCTAGATTTGAAGGAATGAGGGTCGTTGTGAAT 3984

Qy   1339 AlaLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrp 1358
          ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3985 GCACTCATAGGAGCAATTCCTTCCATCATGAATGTGCTACTTGTGTGTCTTATATTCTGG 4044

Qy   1359 LeuIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsn 1378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4045 CTGATATTCAGCATCATGGGAGTAAATTTGTTTGCTGGCAAGTTCTATGAGTGTATTAAC 4104

Qy   1379 ThrThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLys 1398
          ||||||   |||   ||||||           |||   |||   ::::::|||
Db   4105 ACCACAGATGGGTCACGGTTTCCTGCAAGTCAAGTTCCAAATCGTTCCGAATGTTTTGCC 4164

Qy   1399 LeuIleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnVal 1418
          |||:::      ::::::      ||||||||||||:::||||||||||||||||||||||
Db   4165 CTTATGAATGTTAGTCAAAATGTGCGATGGAAAAACCTGAAAGTGAACTTTGATAATGTC 4224

Qy   1419 GlyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMet 1438
          |||   ||||||||||||||||||||||||||||||||||||||||||      ||||||
Db   4225 GGACTTGGTTACCTATCTCTGCTTCAAGTTGCAACTTTTAAGGGATGGACGATTATTATG 4284

Qy   1439 TyrAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyr 1458
          ||||||||||||||||   ||||||:::   ||||||||||||   |||||||||
Db   4285 TATGCAGCAGTGGATTCTGTTAATGTAGACAAGCAGCCCAAATATGAATATAGCCTCTAC 4344

Qy   1459 MetTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe 1478
          ||||||:::|||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   4345 ATGTATATTTATTTTGTCGTCTTTATCATCTTTGGGTCATTCTTCACTTTGAACTTGTTC 4404

Qy   1479 IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIle 1498
          ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db   4405 ATTGGTGTCATCATAGATAATTTCAACCAACAGAAAAAGAAGCTTGGAGGTCAAGACATC 4464

Qy   1499 PheMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLys 1518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4465 TTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAGCTGGGGTCCAAGAAG 4524

Qy   1519 ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal 1538
          ||||||||||||||||||||||||||||||   ||||||   :::||||||   |||
Db   4525 CCACAAAAGCCAATTCCTCGACCAGGGAACAAAATCCAAGGATGTATATTTGACCTAGTG 4584

Qy   1539 ThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1558
          |||   |||   ||||||||||||||||||:::||||||||||||||||||||||||||||
Db   4585 ACAAATCAAGCCTTTGATATTAGTATCATGGTTCTTATCTGTCTCAACATGGTAACCATG 4644

Qy   1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578
          |||||||||   :::   ||||||:::::::::|||   :::|||      |||||||:::
Db   4645 ATGGTAGAAAAGGAGGGTCAAAGTCAACATATGACTGAAGTTTTATATTGGATAAATGTG 4704

Qy   1579 ValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyr 1598
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4705 GTTTTTATAATCCTTTTCACTGGAGAATGTGTGCTAAAACTGATCTCCCTCAGACACTAC 4764

Qy   1599 TyrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGly 1618
          |||||||||:::||||||||||||||||||||||||||||||||||:::||||||||||||
Db   4765 TACTTCACTGTAGGATGGAATATTTTTGATTTTGTGGTTGTGATTATCTCCATTGTAGGT 4824

Qy   1619 MetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIle 1638
          ||||||||||:::|||||||||   ||||||||||||||||||||||||||||||||||||
Db   4825 ATGTTTCTAGCTGATTTGATTGAAACGTATTTTGTGTCCCCTACCCTGTTCCGAGTGATC 4884

Qy   1639 ArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThr 1658
          ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db   4885 CGTCTTGCCAGGATTGGCCGAATCCTACGTCTAGTCAAAGGAGCAAAGGGGATCCGCACG 4944

Qy   1659 LeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPhe 1678
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4945 CTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTC 5004

Qy   1679 LeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGlu 1698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db   5005 CTGGTCATGTTCATCTACGCCATCTTTGGAATGTCCAACTTTGCCTATGTTAAAAAGGAA 5064

Qy   1699 ValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPhe 1718
          ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5065 GATGGAATTAATGACATGTTCAATTTTGAGACCTTTGGCAACAGTATGATTTGCCTGTTC 5124

Qy   1719 GlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysPro 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5125 CAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCTATTCTTAACAGTAAGCCA 5184

Qy   1739 ProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsn 1758
          ||||||||||||||   ||||||:::||||||||||||||:::||||||||||||||||||
Db   5185 CCCGACTGTGACCCAAAAAAAGTTCATCCTGGAAGTTCAGTTGAAGGAGACTGTGGTAAC 5244

Qy   1759 ProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValVal 1778
          ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   5245 CCATCTGTTGGAATATTCTACTTTGTTAGTTATATCATCATATCCTTCCTGGTTGTGGTG 5304

Qy   1779 AsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGlu 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db   5305 AACATGTACATTGCAGTCATACTGGAGAATTTTAGTGTTGCCACTGAAGAAAGTACTGAA 5364

Qy   1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAsp 1818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5365 CCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGAT 5424

Qy   1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProPro 1838
          ||||||||||:::||||||   |||||||||   ||||||||||||:::||||||
Db   5425 GCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCT 5484

Qy   1839 LeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSer 1858
          |||   :::   :::||||||||:::||||||||||||||||||||||||||||||||||
Db   5485 CTTCTCATAGCAAAACCCAACAAAGTCCAGCTCATTGCCATGGATCTGCCCATGGTTAGT 5544

Qy   1859 GlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlu 1878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5545 GGTGACCGGATCCATTGTCTTGACATCTTATTTGCTTTTACAAAGCGTGTTTTGGGTGAG 5604

Qy   1879 SerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnPro 1898
          ||||||||||||||:::||||||   ||||||||||||||||||:::::||||||
Db   5605 AGTGGGGAGATGGATTCTCTTCGTTCACAGATGGAAGAAAGGTTCATGTCTGCAAATCCT 5664

Qy   1899 SerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSer 1918
          ||||||||||||||:::||||||||||||||||||||||||||||||:::||||||
Db   5665 TCCAAAGTGTCCTATGAACCCATCACAACCACACTAAAACGGAAACAAGAGGATGTGTCT 5724

Qy   1919 AlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAla 1938
          |||   :::||||||||||||||||||||:::   |||::::::   ||||||
Db   5725 GCTACTGTCATTCAGCGTGCTTATAGACGTTACCGCTTAAGGCAAAATGTCAAAAATATA 5784

Qy   1939 SerPheThrTyrAsnLysAsnLysIleLysGlyGly---------AlaAsnLeuLeuIle 1955
          |||      |||            ||||||   |||            :::||||||
Db   5785 TCAAGTATATAC-----------ATAAAAGATGGAGACAGAGATGATGATTTACTCAAT 5832

Qy   1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975
          |||:::||||||      |||  :::||||||||||||      ||||||||||||
Db   5833 AAAAAAGATATGGCTTTTGATAATGTTAATGAGAACTCAAGTCCAGAAAAAACAGATGCC 5892

Qy   1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
          |||   ||||||   :::   ||||||||||||||   ||||||||||||      |||
Db   5893 ACTTCATCCACCACCTCT---CCACCTTCATATGATAGTGTAACAAAGCCAGACAAAGAG 5949

Qy   1996 LysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
          |||:::||||||:::      ::::::::   |||||||||
Db   5950 AAATATGAACAAGACAGAACAGAAAAGGAAGACAAAGGGAAA 5991
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RESULT 2
US-08-836-325-9
; Sequence 9, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:

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;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6452 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  326..6277
US-08-836-325-9

Alignment Scores:
Pred. No.:                0          Length:          6452
Score:                 7877.00       Matches:         1538
Percent Similarity:      85.74%      Conservative:     188
Best Local Similarity:   76.40%      Mismatches:       249
Query Match:             75.76%      Indels:            38
DB:                         3        Gaps:              12

US-09-930-871-12 (1-2009) x US-08-836-325-9 (1-6452)

Qy       2 GluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGluSer 21
Db     323 AAGATGGCGATGCTGCCTCCTCCAGGACCTCAGAGTTTCGTTCACTTCACAAAACAGTCC 382

Qy      22 LeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLys 41
Db     383 CTTGCCCTCATTGAACAGCGTATTTCTGAAGAAAAAGCCAAGGAACACAAAGACGAAAAG 442

Qy      42 LysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
Db     443 AAAGATGATGAGGAAGAAGGCCCCAAGCCCAGCAGTGACTTGGAAGCTGGGAAACAGCTC 502

Qy      62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
Db     503 CCCTTCATCTATGGAGACATTCCCCCTGGAATGGTGTCAGAGCCCCTGGAGGACCTGGAC 562

Qy      82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
Db     563 CCATACTATGCTGACAAAAAAACTTTTATAGTATTGAACAAAGGGAAAGCAATCTTCCGT 622

Qy     102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
Db     623 TTCAACGCCACCCCTGCTTTGTACATGCTGTCTCCCTTCAGTCCTCTAAGAAGAATATCT 682

Qy     122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
Db     683 ATTAAGATCTTAGTGCACTCCTTATTCAGCATGCTAATCATGTGCACAATTCTGACGAAC 742

Qy     142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
Db     743 TGCATATTCATGACCTTGAGCAACCCTCCAGAATGGACCAAAAATGTAGAGTACACTTTT 802

Qy     162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
Db     803 ACTGGGATATATACTTTTGAATCACTCATAAAAATCCTTGCAAGAGGCTTTTGCGTGGGA 862

Qy     182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
Db     863 GAATTCACCTTCCTCCGTGACCCTTGGAACTGGCTGGACTTTGTTGTCATTGTTTTTGCG 922

Qy     202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
Db     923 TATTTAACAGAATTTGTAAACCTAGGCAATGTTTCAGCTCTTCGAACTTTCAGAGTCTTG 982

Qy     222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
Db     983 AGAGCTTTGAAAACTATTTCTGTAATCCCAGGACTAAAGACCATCGTGGGGGCCCTGATC 1042

Qy     242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
Db    1043 CAGTCAGTGAAGAAGCTCTCTGACGTCATGATCCTCACTGTGTTCTGTCTCAGTGTGTTT 1102

Qy     262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpPro 281
Db    1103 GCACTAATTGGACTACAGCTGTTTATGGGCAACTTGAAGCATAAATGTTTCAGG------ 1156

Qy     282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
Db    1157 ----------------------AAGGAACTCGAAGAGAATGAAACATTAGAA------ 1186

Qy     302 GlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAspSer 321
Db    1187 ---AGTATCATGAATACTGCTGAGAGTGAAGAAGAATTGAAA---------------- 1225

Qy     322 ArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSerAsp 341
Db    1226 AAATATTTTTATTACTTGGAGGGATCCAAAGATGCTCTACTCTGCGGCTTCAGCACAGAT 1285

Qy     342 AlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGly 361
Db    1286 TCAGGGCAGTGTCCAGAAGGCTACATCTGTGTGAAGGCTGGCAGAAACCCGGATTATGGC 1345

Qy     362 TyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGln 381
Db    1346 TACACGAGCTTTGACACATTCAGCTGGGCCTTCTTGGCCTTGTTTCGGCTAATGACTCAG 1405

Qy     382 AspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIle 401
Db    1406 GACTACTGGGAGAACCTTTACCAACAGACTCTGCGTGCTGCTGGCAAAACCTACATGATT 1465

Qy     402 PhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaVal 421
Db    1466 TTCTTTGTCGTGGTTATTTTTCTGGGCTCCTTTTACCTGATAAACTTGATCCTGGCTGTG 1525
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Qy    422 ValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlu 441
Db   1526 GTAGCCATGGCGTATGAGGAACAGAACCAGGCCAACATCGAAGAAGCTAAACAGAAAGAG 1585

Qy    442 AlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGlnAla 461
Db   1586 TTAGAATTTCAGCAGATGTTAGACCGACTCAAAAAGGAGCAGGAAGAAGCTGAGGCGATC 1645

Qy    462 AlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSerAsp 481
Db   1646 GCTGCAGCTGCTGCTGAGTTCACGAGTATAGGGCGGAGCAGGATCATGGGACTCTCTGAG 1705

Qy    482 SerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArgArg 501
Db   1706 AGCTCTTCAGAAACCTCCAGGCTGAGCTCAAAGAGTGCCAAGGAGAGAAGAAACCGAAGA 1765

Qy    502 LysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPheGln 521
Db   1766 AAGAAAAAGAAACAGAAGATGTCCAGTGGCGAGGAAAAGGGTGACGATGAGAAGCTGTCC 1825

Qy    522 LysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGlyAsn 541
Db   1826 AAGTCAGGATCAGAGGAAAGCATCCGAAAGAAAAGCTTCCATCTCGGTGTGGAAGGGCAC 1885

Qy    542 ArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArgGly 561
Db   1886 CACCGGACCCGGGAAAAGAGGCTGTCCACCCCCAACCAGTCGCCACTCAGCATTCGCGGG 1945

Qy    562 SerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArgAla 581
Db   1946 TCCCTGTTTTCTGCCAGGCGCAGCAGCAGGACGAGTCTCTTCAGTTTTAAGGGGCGAGGA 2005

Qy    582 LysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAspAsn 601
Db   2006 AGAGATCTGGGATCTGAGACAGAATTCGCTGATGATGAGCATAGCATTTTTGGAGACAAC 2065

Qy    602 GluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSerAsn 621
Db   2066 GAGAGCAGAAGGGGTTCACTATTCGTACCCCATAGACCCCGGGAGCGGCGCAGCAGTAAC 2125

Qy    622 LeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLysMet 641
Db   2126 ATCAGTCAGGCCAGTAGGTCCCCG---------CCAGTGCTACCGGTGAACGGGAAGATG 2176

Qy    642 HisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValProThr 661
Db   2177 CACAGTGCAGTGGACTGCAATGGAGTCGTGTCGCTTGTTGATGGACCCTCAGCCCTCATG 2236

Qy    662 SerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAspAsn 681
Db   2237 CTCCCCAATGGACAGCTTCTTCCAGAGGTGATAATAGATAAGGCAACTTCCGACGACAGC 2296

Qy    682 GlyThrThrThrGluThrGluMetArgLysArgArg---SerSerSerPheHisValSer 700
Db   2297 GGCACGACT------AATCAGATGCGCAAAAAAAGGCTCTCTAGTTCTTACTTCTTGTCT 2350

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2351 GAGGACATGCTGAATGACCCGCATCTCAGGCAAAGGGCCATGAGCAGGGCGAGCATACTG 2410

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2411 ACCAACACTGTGGAAGAACTTGAAGAATCTAGACAAAAATGTCCACCATGGTGGTACAGA 2470

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2471 TTTGCTCACACATTTTTAATCTGGAATTGCTCTCCATATTGGATAAAATTCAAAAAGCTC 2530

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2531 ATCTATTTTATTGTGATGGATCCTTTTGTAGATCTTGCAATTACCATTTGCATAGTTTTA 2590

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2591 AACACCTTATTTATGGCTATGGAGCACCACCCAATGACTGAAGAATTCAAAAATGTCCTT 2650

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2651 GCAGTGGGGAACTTGATCTTTACAGGGATCTTCGCAGCTGAAATGGTACTGAAGTTAATA 2710

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2711 GCCATGGACCCCTATGAGTATTTCCAAGTAGGGTGGAATATTTTTGACAGCCTAATTGTG 2770

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2771 ACGCTGAGTTTGATAGAGCTTTTCCTAGCAGATGTGGAAGGATTATCAGTTCTGCGGTCA 2830

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2831 TTCAGATTGCTCCGAGTCTTCAAGTTGGCAAAGTCCTGGCCCACACTGAACATGCTCATT 2890

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2891 AAGATCATCGGCAACTCGGTGGGCGCACTGGGCAACCTGACCCTGGTGCTGGCCATCATC 2950

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2951 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTTGGAAAGAGCTACAAGGAGTGTGTC 3010

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   3011 TGCAAGATCAATGTGGACTGCAAGCTGCCGCGCTGGCACATGAACGACTTCTTCCACTCC 3070

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   3071 TTCCTCATCGTGTTCCGAGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGCATG 3130

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   3131 GAGGTCGCGGGCCAGACCATGTGCCTTATTGTTTACATGATGGTCATGGTGATTGGGAAC 3190

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   3191 CTTGTGGTCCTGAACCTGTTTCTGGCTCTTTGCTGAGTTCCTTTAGTTCTGACAATCTT 3250

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   3251 ACAGCAATTGAGGAAGACACCGATGCAAACAACCTCCAGATCGCAGTGGCCAGAATTAAG 3310

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3311 AGGGGAATCAATTACGTGAAACAGACCCTGCGTGAATTCATTCTAAAATCATTTTCCAAA 3370

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db   3371 AAGCCAAAGGGCTCCAAGGACACAAAACGAACAGCAGATCCCAACAACAAGAAAGAAAAC 3430

Qy   1061 CysMetSerAsnHisThr---***GluIleGlyLysAspLeuAspTyrLeuLysAspVal 1079
Db   3431 TATATTTCAAACCGTACCCTTGCGGAGATGAGCAAGGATCACAATTTCCTCAAAGAAAAG 3490

Qy   1080 AsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGlu 1099
Db   3491 GATAGGATCAGT---------GGTTATGGCAGCAGTCTAGACAAAAGCTTTATGGATGAA 3541

Qy   1100 SerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaVal 1119
Db   3542 AATGATTACCAGTCCTTTATCCATAACCCCAGCCTCACAGTGACAGTGCCAATTGCACCT 3601

Qy   1120 GlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGlu 1139
Db   3602 GGGGAGTCTGATTTGGAGATTATGAACACAGAAGAGCTTAGCAGTGACTCAGACAGTGAC 3661

Qy   1140 GluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIle 1159
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Db  3662 TACAGCAAAGAGAAACGGAACCGA---TCAAGCTCTTCTGAGTGCAGCACTGTTGACAAC 3718

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Db  3719 CCTCTGCCAGGAGAAGAGGAGGCTGAAGCAGAGCCCGTAAACGCAGATGAGCCTGAAGCC 3778

Qy  1180 CysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGly 1199
Db  3779 TGCTTTACAGATGGTTGTGTGAGGAGATTTCCATGCTGCCAAGTTAATGTAGACTCTGGG 3838

Qy  1200 ArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrp 1219
Db  3839 AAAGGGAAAGTTTGGTGGACCATCAGGAAGACGTGCTACAGGATAGTTGAACACAGCTGG 3898

Qy  1220 PheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAsp 1239
Db  3899 TTTGAAAGCTTCATCGTTCTCATGATCCTGCTCAGCAGTGGAGCTCTGGCTTTTGAAGAT 3958

Qy  1240 IleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPhe 1259
Db  3959 ATCTATATTGAAAAGAAAAAGACCATTAAGATTATCCTGGAGTATGCTGACAAGATATTC 4018

Qy  1260 ThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyr 1279
Db  4019 ACCTACATCTTCATTCTGGAAATGCTTCTAAAATGGGTCGCATATGGGTATAAAACATAT 4078

Qy  1280 PheThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeu 1299
Db  4079 TTCACTAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTGTCTCTAGTTACTTTA 4138

Qy  1300 ThrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArg 1319
Db  4139 GTAGCCAACACTCTTGGCTACTCAGACCTTGGCCCCATTAAATCTCTACGGACACTGAGG 4198

Qy  1320 AlaLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAla 1339
Db  4199 GCCCTAAGACCCCTAAGAGCCTTGTCTAGATTTGAAGGAATGAGGGTAGTGGTCAACGCA 4258

Qy  1340 LeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeu 1359
Db  4259 CTCATAGGAGCAATCCCTTCCATCATGAACGTGCTTCTCGTGTGCCTTATATTCTGGCTA 4318

Qy  1360 IlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThr 1379
Db  4319 ATATTTAGCATCATGGGAGTCAATCTGTTTGCTGGCAAGTTCTATGAGTGTGTCAACACC 4378

Qy  1380 ThrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeu 1399
Db  4379 ACCGATGGGTCACGATTTCCTACATCTCAAGTTGCAAACCGTTCTGAGTGTTTTGCCCTG 4438

Qy  1400 IleGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGly 1419
Db  4439 ATGAACGTTAGTGGAAATGTGCGATGGAAAAACCTGAAAGTAAACTTCGACAACGTTGGG 4498

Qy  1420 PheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyr 1439
Db  4499 CTTGGTTACCTGTCGCTGCTTCAAGTTGCAACATTCAAGGGCTGGATGGATATTATGTAT 4558

Qy  1440 AlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMet 1459
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Qy  1460 TyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIle 1479
Db  4619 TACATTTACTTTGTCATCTTCATCATCTTCGGCTCATTCTTCACGTTGAACCTGTTCATT 4678

Qy  1480 GlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePhe 1499
Db  4679 GGTGTCATCATAGATAATTTCAACCAACAGAAAAAAAAGCTTGGAGGTCAAGATATCTTT 4738

Qy  1500 MetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPro 1519

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Qy  1520 GlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThr 1539
Db  4799 CAAAAACCAATTCCAAGGCCAGGGAACAAATTCCAAGGATGTATATTTGACTTAGTGACA 4858

Qy  1540 ArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMet 1559
Db  4859 AACCAAGCTTTTGATATCACCATCATGGTTCTTATATGCCTCAACATGGTAACCATGATG 4918

Qy  1560 ValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuVal 1579
Db  4919 GTAGAAAAAGAGGGGCAAACTGAGTACATGGATTATGTTTTACACTGGATCAACATGGTC 4978

Qy  1580 PheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyr 1599
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Qy  1600 PheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMet 1619
Db  5039 TTCACTGTGGGTTGGAACATTTTTGATTTTGTGGTAGTGATCCTCTCCATTGTAGGAATG 5098

Qy  1620 PheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArg 1639
Db  5099 TTTCTCGCTGAGATGATAGAGAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTCATCCGC 5158

Qy  1640 LeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeu 1659
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Qy  1660 LeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeu 1679
Db  5219 CTCTTTGCTTTGATGATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCTG 5278

Qy  1680 ValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVal 1699
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Qy  1700 GlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGln 1719
Db  5339 GGAATTAATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCTTGTTCCAA 5398

Qy  1720 IleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProPro 1739
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Qy  1740 AspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPro 1759
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Qy  1780 MetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPro 1799
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Qy  1800 LeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAla 1819
Db  5639 CTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACCCTGACGCC 5698

Qy  1820 ThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeu 1839
Db  5699 ACTCAGTTCATAGAGTTCTGCAAGCTCTCTGACTTTGCAGCTGCCCTGGATCCTCCCCTC 5758

Qy  1840 AsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGly 1859
Db  5759 CTCATCGCAAAGCCAAACAAAGTCCAGCTCATTGCCATGGACCTGCCCATGGTGAGTGGA 5818

Qy  1860 AspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSer 1879
Db  5819 GACCGCATCCACTGCCTGGACATCTTGTTTGCTTTTACAAAGCGGGTCCTGGGTGAGGGT 5878
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Qy   1880 GlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSer 1899
          ||||||||||||:::||||||   ||||||||||||||||||||||:::::::|||||||||
Db   5879 GGAGAGATGGATTCTCTTCGTTCACAGATGGAAGAAAGGTTCATGTCAGCCAATCCTTCT 5938

Qy   1900 LysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAla 1919
          ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db   5939 AAAGTGTCCTATGAACCCATCACGACCACACTGAAGAGAAAACAAGAGGAGGTGTCCGCG 5998

Qy   1920 ValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSer 1939
          ||||||||||||||||||||||:::   |||::::::   ||||||      |||
Db   5999 ACTATCATTCAGCGTGCTTACAGACGGTATCGCCTCAGACAACACGTCAAGAATATATCG 6058

Qy   1940 PheThrTyrAsnLysAsnLysIleLysGlyGly---------AlaAsnLeuLeuIleLys 1956
               |||            ||||||  |||           :::|||      |||
Db   6059 AGTATATAC-----------ATAAAAGATGGAGACAGGGATGATGATTTGCCCAATAAA 6106

Qy   1957 GluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThr 1976
          ||||||   :::   |||   :::|||||||||||||      ||||||||||||:::|||
Db   6107 GAAGATACAGTTTTTGATAACGTGAACGAGAACTCAAGTCCGGAAAAGACAGATGTAACT 6166

Qy   1977 MetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLys 1996
          ||||||   :::   ||||||||||||||   ||||||||||||      ||||||
Db   6167 GCCTCAACCATCTCG---CCACCTTCCTATGACAGTGTCACAAAGCCAGATCAAGAGAAA 6223

Qy   1997 HisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
          :::|||   :::      :::::::::   |||   |||
Db   6224 TATGAAACAGACAAAACAGAGAAGGAAGACAAAGAGAAA 6262

RESULT 3
US-08-836-325-13
; Sequence 13, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
US-08-836-325-13

Alignment Scores:
Pred. No.:              0           Length:          6371
Score:                  7861.50     Matches:         1533
Percent Similarity:     85.60%      Conservative:    191
Best Local Similarity:  76.12%      Mismatches:      241
Query Match:            75.61%      Indels:          49
DB:                     3           Gaps:            14

US-09-930-871-12 (1-2009) x US-08-836-325-13 (1-6371)

Qy      2 GluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGluSer 21
          :::      :::|||   ||||||||||||   ||||||      |||||:::::|||
Db     46 AAGATGGCAATGTTGCCTCCCCCAGGACCTCAGAGCTTTGTCCATTTCACAAAACAGTCT 105

Qy     22 LeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLys 41
          ||||||   ||||||:::||||||||||||   |||:::|||   ||||||   :::|||
Db    106 CTTGCCCTCATTGAACAACGCATTGCTGAAAGAAAATCAAAGGAACCCAAAGAAGAAAAG 165

Qy     42 LysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
          ||||||||||||||      ||||||||:::||||||||||||||||||   |||
Db    166 AAAGATGATGATGAAGAAGCCCCAAAGCCAAGCAGTGACTTGGAAGCTGGCAAACAACTG 225

Qy     62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    226 CCCTTCATCTATGGGGACATTCCTCCCGGCATGGTGTCAGAGCCCCTGGAGGACTTGGAC 285

Qy     82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
          |||||||||   :::||||||||||||||||||||||||||||||||   |||||||||
Db    286 CCCTACTATGCAGACAAAAAGACTTTCATAGTATTGAACAAAGGGAAAACAATCTTCCGT 345

Qy    102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
          |||:::||||||   ||||||||||:::|||:::||||||:::||||||||||:::|||:::
Db    346 TTCAATGCCACACCTGCTTTATATATGCTTTCTCCTTTCAGTCCTCTAAGAAGAATATCT 405

Qy    122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 ATTAAGATTTTAGTACACTCCTTATTCAGCATGCTCATCATGTGCACTATTCTGACAAAC 465

Qy    142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
          |||:::||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db    466 TGCATATTTATGACCATGAATAACCCGCCGGACTGGACCAAAAATGTCGAGTACACTTTT 525

Qy    162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
          ||||||||||||||||||||||||||:::||||||||:::||||||||||||||||:::
Db    526 ACTGGAATATATACTTTTGAATCACTTGTAAAAATCCTTGCAAGAGGCTTCTGTGTAGGA 585

Qy    182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
          :::||||||||||||||||||||||||||||||||||||   ||||||   ||||||
Db    586 GAATTCACTTTTCTTCGTGACCCGTGGAACTGGCTGGATTTTGTCGTCATTGTTTTTGCG 645

Qy    202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
          |||:::||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db    646 TATTTAACAGAATTTGTAAACCTAGGCAATGTTTCAGCTCTTCGAACTTTCAGAGTATTG 705

Qy    222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 AGAGCTTTGAAAACTATTTCTGTAATCCCAGGCCTGAAGACAATTGTAGGGGCTTTGATC 765

Qy    242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 CAGTCAGTGAAGAAGCTTTCTGATGTCATGATCCTGACTGTGTTCTGTCTGAGTGTGTTT 825
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Qy    262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpPro 281
Db    826 GCACTAATTGGACTACAGCTGTTCATGGGAAACCTGAAGCATAAATGTTTTCGA------ 879

Qy    282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
Db    880 ----------------------AATTCACTTGAAAATAATGAAACATTAGAA------ 909

Qy    302 GlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAspSer 321
Db    910 ---AGCATAATGAATACCCTAGAGAGTGAAGAAGACTTTAGA----------------- 948

Qy    322 ArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSerAsp 341
Db    949 AAATATTTTTATTACTTGGAAGGATCCAAAGATGCTCTCCTTTGTGGTTTCAGCACAGAT 1008

Qy    342 AlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGly 361
Db   1009 TCAGGTCAGTGTCCAGAGGGGTACACCTGTGTGAAAATTGGCAGAAACCCTGATTATGGC 1068

Qy    362 TyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGln 381
Db   1069 TACACGAGCTTTGACACTTTCAGCTGGGCCTTCTTAGCCTTGTTTAGGCTAATGACCCAA 1128

Qy    382 AspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIle 401
Db   1129 GATTACTGGGAAAACCTTTACCAACAGACGCTGCGTGCTGCTGGCAAAACCTACATGATC 1188

Qy    402 PhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaVal 421
Db   1189 TTCTTTGTCGTAGTGATTTTCCTGGGCTCCTTTTATCTAATAAACTTGATCCTGGCTGTG 1248

Qy    422 ValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGlu 441
Db   1249 GTTGCCATGGCATATGAAGAACAGAACCAGGCAAACATTGAAGAAGCTAAACAGAAAGAA 1308

Qy    442 AlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGlnAla 461
Db   1309 TTAGAATTTCAACAGATGTTAGACCGTCTTAAAAAAGAGCAAGAAGAAGCTGAGGCAATT 1368

Qy    462 AlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSerAsp 481
Db   1369 GCAGCGGCAGCGGCTGAATATACAAGTATTAGGAGAAGCAGAATTATGGGCCTCTCAGAG 1428

Qy    482 SerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArgArg 501
Db   1429 AGTTCTTCTGAAACATCCAAACTGAGCTCTAAAAGTGCTAAAGAAAGAAGAAACAGAAGA 1488

Qy    502 LysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLys---AspGluAspGluPhe 520
Db   1489 AAGAAAAAGAATCAAAAGAAGCTCTCCAGTGGAGAGGAAAAGGGAGATGCTGAGAAATTG 1548

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1549 TCGAAATCAGAATCAGAGGACAGCATCAGAAGAAAAAGTTTCCACCTTGGTGTCGAAGGG 1608

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1609 CATAGGCGAGCACATGAAAAGAGGTTGTCTACCCCCAATCAGTCACCACTCAGCATTCGT 1668

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1669 GGCTCCTTGTTTTCTGCAAGGCGAAGCAGCAGAACAAGTCTTTTTAGTTTCAAAGGCAGA 1728

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1729 GGAAGAGATATAGGATCTGAGACTGAATTTGCCGATGATGAGCACAGCATTTTTGGAGAC 1788

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1789 AATGAGAGCAGAAGGGGCTCACTGTTTGTGCCCCACAGACCCCAGGAGCGACGCAGCAGT 1848

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
Db   1849 AACATCAGCCAAGCCAGTAGGTCCCCACCAATGCTG---------CCGGTGAACGGGAAA 1899

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1900 ATGCACAGTGCTGTGGACTGCAACGGTGTGGTCTCCCTGGTTGATGGACGCTCAGCCCTC 1959

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1960 ATGCTCCCCAATGGACAGCTTCTGCCAGAG---------------------------- 1989

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db   1990 ---GGCACGACCAATCAAATACAC---AAGAAAAGGCGTTGTAGTTCCTATCTCCTTTCA 2043

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2044 GAGGATATGCTGAATGATCCCAACCTCAGACAGAGAGCAATGAGTAGAGCAAGCATATTA 2103

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2104 ACAAACACTGTGGAAGAACTTGAAGAGTCCAGACAAAAATGTCCACCTTGGTGGTACAGA 2163

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2164 TTTGCACACAAATTCTTGATCTGGAATTGCTCTCCATATTGGATAAAATTCAAAAAGTGT 2223

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2224 ATCTATTTTATTGTAATGGATCCTTTTGTAGATCTTGCAATTACCATTTGCATAGTTTTA 2283

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2284 AACACATTATTTATGGCTATGGAACACCACCCAATGACTGAGGAATTCAAAAATGTACTT 2343

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2344 GCTATAGGAAATTTGGTCTTTACTGGAATCTTTGCAGCTGAAATGGTATTAAAACTGATT 2403

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2404 GCCATGGATCCATATGAGTATTTCCAAGTAGGCTGGAATATTTTTGACAGCCTTATTGTG 2463

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2464 ACTTTAAGTTTAGTGGAGCTCTTTCTAGCAGATGTGGAAGGATTGTCAGTTCTGCGATCA 2523

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2524 TTCAGACTGCTCCGAGTCTTCAAGTTGGCAAAATCCTGGCCAACATTGAACATGCTGATT 2583

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2584 AAGATCATTGGTAACTCAGTAGGGGCTCTAGGTAACCTCACCTTAGTGTTGGCCATCATC 2643

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2644 GTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGCTACAAAGAATGTGTC 2703

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2704 TGCAAGATCAATGATGACTGTACGCTCCCACGGTGGCACATGAACGACTTCTTCCACTCC 2763

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   2764 TTCCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACCATGTGGGACTGTATG 2823

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   2824 GAGGTCGCTGGTCAAGCTATGTGCCTTATTGTTTACATGATGGTCATGGTCATTGGAAAC 2883

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Qy   1719 GlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysPro 1738
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5092 CAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCTATTCTTAACAGTAAGCCA 5151

Qy   1739 ProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsn 1758
          ||||||||||||||| ||||||:::|||||||||||||||:::|||||||||||||||||
Db   5152 CCCGACTGTGACCCAAAAAAAGTTCATCCTGGAAGTTCAGTTGAAGGAGACTGTGGTAAC 5211

Qy   1759 ProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValVal 1778
          ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   5212 CCATCTGTTGGAATATTCTACTTTGTTAGTTATATCATCATATCCTTCCTGGTTGTGGTG 5271

Qy   1779 AsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGlu 1798
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db   5272 AACATGTACATTGCAGTCATACTGGAGAATTTTAGTGTTGCCACTGAAGAAAGTACTGAA 5331

Qy   1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAsp 1818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5332 CCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGAT 5391

Qy   1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProPro 1838
          |||||||||||||:::||||||   |||||||||   ||||||||||||||:::||||||
Db   5392 GCGACCCAGTTTATAGAGTTCTCTAAACTCTCTGATTTTGCAGCTGCCCTGGATCCTCCT 5451

Qy   1839 LeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSer 1858
          |||   :::   :::||||||||||:::||||||||||||||||||||||||||||||||||
Db   5452 CTTCTCATAGCAAAACCCAACAAAGTCCAGCTCATTGCCATGGATCTGCCCATGGTTAGT 5511

Qy   1859 GlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlu 1878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5512 GGTGACCGGATCCATTGTCTTGACATCTTATTTGCTTTTACAAAGCGTGTTTTGGGTGAG 5571

Qy   1879 SerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnPro 1898
          ||||||||||||||:::||||||   |||||||||||||||||||:::::|||||||||||
Db   5572 AGTGGGGAGATGGATTCTCTTCGTTCACAGATGGAAGAAAGGTTCATGTCTGCAAATCCT 5631

Qy   1899 SerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSer 1918
          ||||||||||||||:::||||||||||||||||||||||||||||||||:::||||||||||
Db   5632 TCCAAAGTGTCCTATGAACCCATCACAACCACACTAAAACGGAAACAAGAGGATGTGTCT 5691

Qy   1919 AlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAla 1938
          |||   :::||||||||||||||||||||:::   |||::::::   ||||||
Db   5692 GCTACTGTCATTCAGCGTGCTTATAGACGTTACCGCTTAAGGCAAAATGTCAAAAATATA 5751

Qy   1939 SerPheThrTyrAsnLysAsnLysIleLysGlyGly---------AlaAsnLeuLeuIle 1955
          |||   |||          ||||||   |||          :::||||||
Db   5752 TCAAGTATATAC------------ATAAAAGATGGAGACAGAGATGATGATTTACTCAAT 5799

Qy   1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975
          |||:::||||||      |||   :::||||||||||||      ||||||||||||
Db   5800 AAAAAAGATATGGCTTTTGATAATGTTAATGAGAACTCAAGTCCAGAAAAAACAGATGCC 5859

Qy   1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
          |||   ||||||   :::   ||||||||||||||   ||||||||||||      |||
Db   5860 ACTTCATCCACCACCTCT---CCACCTTCATATGATAGTGTAACAAAGCCAGACAAAGAG 5916

Qy   1996 LysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
          |||:::|||||:::     :::::::::   |||||||||
Db   5917 AAATATGAACAAGACAGAACAGAAAAGGAAGACAAAGGGAAA 5958

RESULT 4
US-09-024-020B-2
; Sequence 2, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-2

Alignment Scores:
Pred. No.:                0                 Length:          6007
Score:                    7755.50           Matches:         1538
Percent Similarity:       84.81%            Conservative:    187
Best Local Similarity:    75.61%            Mismatches:      227
Query Match:              74.59%            Indels:          83
DB:                       3                 Gaps:            24

US-09-930-871-12 (1-2009) x US-09-024-020B-2 (1-6007)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          |||         :::|||  ||||||||||||||||||||      ||||||  |||
Db     22 ATGGCAGCGCGGCTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAG 81

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysPro 39
          |||||||||  ||||||||||||||||||||  |||  |||      ||||||
Db     82 TCGCTGGCAAACATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCG 141

Qy     40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
          |||         ::::::||||||:::::::::  ||||||||||||||||||||||
Db    142 GATGGCAGCCACCGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAG 201

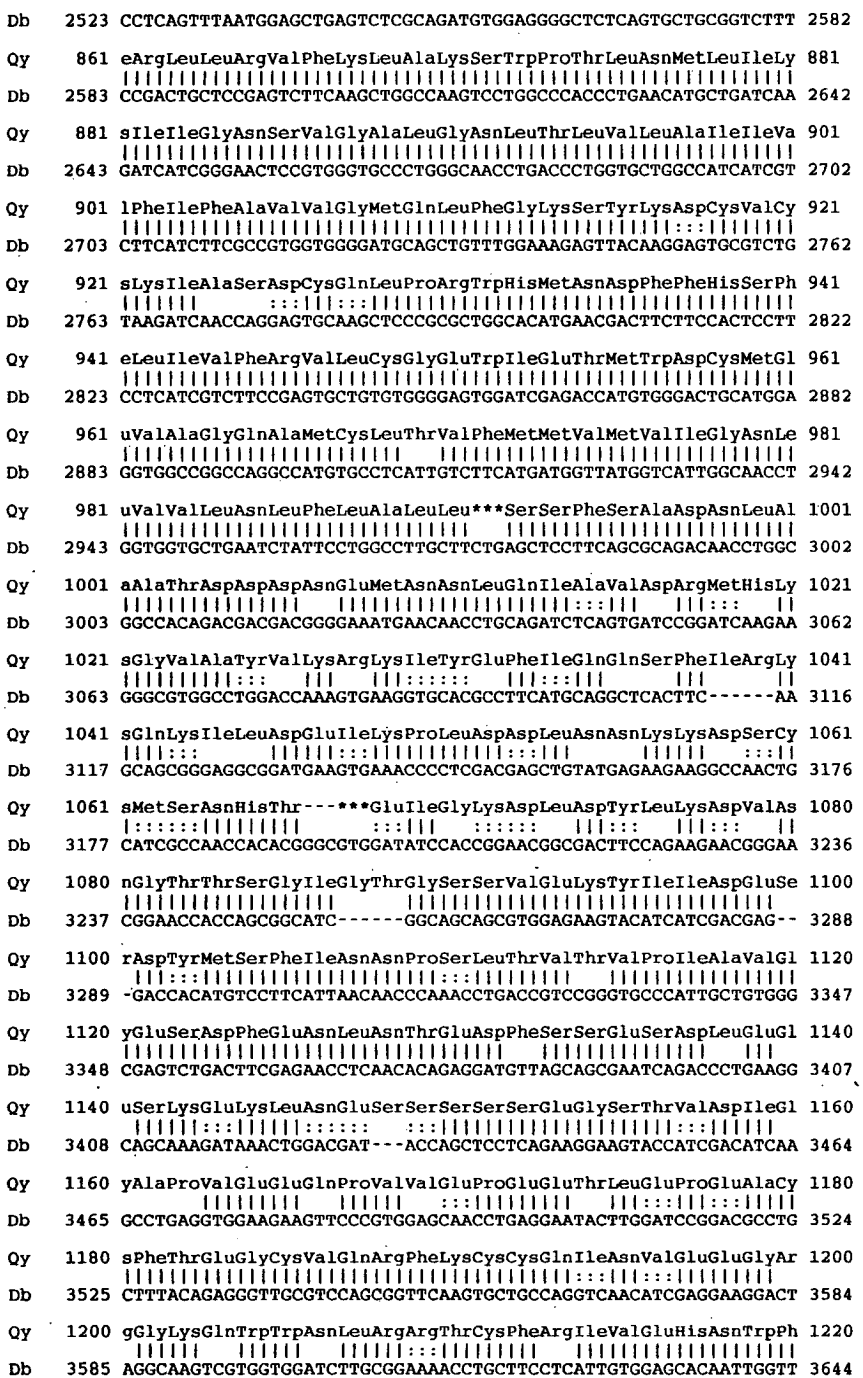
Qy     57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
          ||||||||||:::||||||||||||||||||||||||||||      :::|||:::  |||
Db    202 GCTGGGAAGAGTTTGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCC 261

Qy     77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
          |||||||||  ||||||||||||:::  :::||||||||||:::||||||||||:::|||
Db    262 CTGGAGGACTTTGACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG 321

Qy     97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
          |||   :::||||||||||||||||||  ||||||||||||||:::|||||||||
Db    322 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 381

Qy    117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
          :::|||:::||||||||||||||||||:::||||||:::||||||||||:::|||||||||
Db    382 ATAAGAAGAATAGCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGC 441
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Db 2523 CCTCAGTTTAATGGAGCTGAGTCTCGCAGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTT 2582
Qy 861 eArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLy 881
Db 2583 CCGACTGCTCCGAGTCTTCAAGCTGGCCAAGTCCTGGCCCACCCTGAACATGCTGATCAA 2642
Qy 881 sIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleVa 901
Db 2643 GATCATCGGGAACTCCGTGGGTGCCCTGGGCAACCTGACCCTGGTGCTGGCCATCATCGT 2702
Qy 901 lPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCy 921
Db 2703 CTTCATCTTCGCCGTGGTGGGGATGCAGCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTG 2762
Qy 921 sLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSerPh 941
Db 2763 TAAGATCAACCAGGAGTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTT 2822
Qy 941 eLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetGl 961
Db 2823 CCTCATCGTCTTCCGAGTGCTGTGTGGGGAGTGGATCGAGACCATGTGGGACTGCATGGA 2882
Qy 961 uValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsnLe 981
Db 2883 GGTGGCCGGCCAGGCCATGTGCCTCATTGTCTTCATGATGGTTATGGTCATTGGCAACCT 2942
Qy 981 uValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAl 1001
Db 2943 GGTGGTGCTGAATCTATTCCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAACCTGGC 3002
Qy 1001 aAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHisLy 1021
Db 3003 GGCCACAGACGACGACGGGGAAATGAACAACCTGCAGATCTCAGTGATCCGGATCAAGAA 3062
Qy 1021 sGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArgLy 1041
Db 3063 GGGCGTGGCCTGGACCAAAGTGAAGGTGCACGCCTTCATGCAGGCTCACTTC------AA 3116
Qy 1041 sGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCy 1061
Db 3117 GCAGCGGGAGGCGGATGAAGTGAAACCCCTCGACGAGCTGTATGAGAAGAAGGCCAACTG 3176
Qy 1061 sMetSerAsnHisThr---***GluIleGlyLysAspLeuAspTyrLeuLysAspValAs 1080
Db 3177 CATCGCCAACCACACGGGCGTGGATATCCACCGGAACGGCGACTTCCAGAAGAACGGGAA 3236
Qy 1080 nGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSe 1100
Db 3237 CGGAACCACCAGCGGCATC------GGCAGCAGCGTGGAGAAGTACATCATCGACGAG-- 3288
Qy 1100 rAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGl 1120
Db 3289 -GACCACATGTCCTTCATTAACAACCCAAACCTGACCGTCCGGGTGCCCATTGCTGTGGG 3347
Qy 1120 yGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGl 1140
Db 3348 CGAGTCTGACTTCGAGAACCTCAACACAGAGGATGTTAGCAGCGAATCAGACCCTGAAGG 3407
Qy 1140 uSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGl 1160
Db 3408 CAGCAAAGATAAACTGGACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAA 3464
Qy 1160 yAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCy 1180
Db 3465 GCCTGAGGTGGAAGAAGTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTG 3524
Qy 1180 sPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyAr 1200
Db 3525 CTTTACAGAGGGTTGCGTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACT 3584
Qy 1200 gGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPh 1220
Db 3585 AGGCAAGTCGTGGTGGATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTT 3644
Qy 1220 eGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIl 1240
Db 3645 TGAGACCTTCATCATCTTCATGATTCTGCTCAGCAGTGGCGCCCTGGCCTTTGAGGACAT 3704
Qy 1240 eTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheTh 1260
Db 3705 CTACATTGAGCAGAGGAAGACCATCCGCACCATCCTGGAGTATGCGGACAAGGTCTTCAC 3764
Qy 1260 rTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPh 1280
Db 3765 CTACATCTTCATCCTGGAGATGTTGCTCAAGTGGACAGCCTACGGCTTCGTCAAGTTCTT 3824
Qy 1280 eThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuTh 1300
Db 3825 CACCAATGCCTGGTGCTGGTTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTAT 3884
Qy 1300 rAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAl 1320
Db 3885 AGCTAATGCCCTGGGCTACTCGGAACTAGGTGCCATAAAGTCCCTTAGGACCCTAAGAGC 3944
Qy 1320 aLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLe 1340
Db 3945 TTTGAGACCCTTAAGAGCCTTATCACGATTTGAAGGGATGAGGGTGGTGGTGAATGCCTT 4004
Qy 1340 uLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIl 1360
Db 4005 GGTGGGCGCCATCCCCTCCATCATGAATGTGCTGCTGGTGTGTCTCATCTTCTGGCTGAT 4064
Qy 1360 ePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrTh 1380
Db 4065 TTTCAGCATCATGGGAGTTAACCTGTTTGCGGGGAAATACCACTACTGCTTTAATGAGAC 4124
Qy 1380 rThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIl 1400
Db 4125 TTCTGAAATCCGGTTCGAAATCGATATTGTCAACAATAAAACGGACTGTGAGAAGCTCAT 4184
Qy 1400 eGluArgAsnGluThr---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGl 1419
Db 4185 GGAGGGCAACAGCACGGAGATCCGATGGAAGAATGTCAAGATCAACTTTGACAATGTCGG 4244
Qy 1419 yPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTy 1439
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Qy 1439 rAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMe 1459
Db 4305 TGCGGCTGTAGATTCCCGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACAT 4364
Qy 1459 tTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIl 1479
Db 4365 GTACATCTACTTCGTCATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCAT 4424
Qy 1479 eGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePh 1499
Db 4425 CGGTGTCATCATCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTT 4484
Qy 1499 eMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPr 1519
Db 4485 CATGACAGAGGAACAGAAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCCAAGAAGCC 4544
Qy 1519 oGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValTh 1539
Db 4545 ACAGAAGCCCATCCCCCGACCCTTGAACAAAATCCAAGGGATTGTCTTTGATTTCGTCAC 4604
Qy 1539 rArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMe 1559
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Qy 1559 tValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuVa 1579
Db 4665 GGTGGAGACAGACACTCAGAGCAAGCAGATGGAGAACATTCTTTACTGGATTAATCTGGT 4724

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Qy   1579 lPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTy 1599
          ||||::::::   ||||||   ||||||||||||||:::   :::|||||||||||||||
Db   4725 CTTTGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGACACTACTA 4784

Qy   1599 rPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMe 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4785 TTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATCCTCTCCATTGTGGGAAT 4844

Qy   1619 tPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleAr 1639
          ||||||||||::::::||||||||||||||||||||||||||||||||||||||||||||
Db   4845 GTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCCCCAACCCTATTCCGAGTTATCCG 4904

Qy   1639 gLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLe 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4905 ATTGGCCCGTATTGGGCGCATCTTGCGTCTGATCAAGGGCGCCAAAGGGATCCGCACCCT 4964

Qy   1659 uLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLe 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4965 GCTCTTTGCCTTAATGATGTCGCTGCCCGCCCTGTTCAACATCGGCCTCCTGCTCTTCCT 5024

Qy   1679 uValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVa 1699
          ||||||||||||||:::::|||||||||||||||||||||||||||||||||   |||
Db   5025 CGTCATGTTCATCTTCTCCATTTTTGGCATGTCCAACTTCGCATACGTGAAGCACGAGGC 5084

Qy   1699 lGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGl 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5085 CGGCATTGACGACATGTTCAACTTCGAGACATTTGGCAACAGCATGATCTGTTTGTTCCA 5144

Qy   1719 nIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProPr 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5145 GATCACAACGTCTGCTGGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCC 5201

Qy   1739 oAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPr 1759
          |||||||      :::|||  :::||||||||||      ||||||||||||||||||||
Db   5202 TGACTGCAGCTTGGACAAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCC 5261

Qy   1759 oSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAs 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db   5262 CTCGGTGGGCATCTTCTTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAA 5321

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Db   5322 CATGTACATCGCCATCATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCC 5381

Qy   1799 oLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAl 1819
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Db   5382 TCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGC 5441

Qy   1819 aThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLe 1839
          ||||||||||:::|||:::   ||||||::   ||||||   |||||||||   |||||
Db   5442 CACCCAGTTCATCGAGTACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCT 5501

Qy   1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGl 1859
          |   :::|||:::||||||   ::::::||||||||||||||||||||||||||:::||
Db   5502 CCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGG 5561

Qy   1859 yAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSe 1879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||
Db   5562 AGATCGCATCCACTGCTTGGACATCCTTTTCGCCTTCACCAAGCGAGTCCTGGGAGACAG 5621

Qy   1879 rGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSe 1899
          |||||||:::|||   ||||||   ||||||||||||||||||:::|||||||||||||
Db   5622 TGGGGAGTTGGACATCCTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTC 5681

Qy   1899 rLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAl 1919
          ||||||||||||:::|||||||||||||||||:::||||||||||||||||||||||||
Db   5682 CAAAGTGTCTTACGAGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGC 5741

Qy   1919 aValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal---------Ly 1936
          ||||::::::|||||||||||||||   ||||||   :::|||              ||
Db   5742 AGTGGTCCTGCAGCGTGCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAA 5801

Qy   1936 sGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLy 1956
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          |   ||||||              ||||||::::::   |||
Db   5802 GATGGCCTCC--------------AACAAGCTGGAGAATGGA---------------- 5829

Qy   1956 sGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuTh 1976
                                                :::      :::|||   :::   ||
Db   5830 -------------------------------GGCACACACAGAGACAAGAAGGAGAGCAC 5858

Qy   1976 rMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLy 1996
          |   |||||||:::      ||||||||||||   ||||||||||||      |||||
Db   5859 CCCGTCCACAGCCTCCCTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAA 5915

Qy   1996 sHisGlu----~-GlnGluGlyLysAspGluLysAlaLys 2007
          |   :::      :::|||||:::   |||:::||||||
Db   5916 GCAGCAGCGTGCGGAGGAGGGCAGAAGGGAAAGAGCCAAG 5955

RESULT 5
US-09-425-043-2
; Sequence 2, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-2

Alignment Scores:
Pred. No.:                0          Length:          6007
Score:                 7755.50       Matches:         1538
Percent Similarity:     84.81%       Conservative:     187
Best Local Similarity:  75.61%       Mismatches:       227
Query Match:            74.59%       Indels:            83
DB:                     4            Gaps:              24
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Qy     702 pPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeuThrAs 722
Db    2103 CCAACTCGCCTCCTACGGACGGAAGGACAGAATCAACAGCATAATGAGCGTGGTCACAAA 2162

Qy     722 nThr---ValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLysPh 741
Db    2163 CACGCTAGTGGAAGAGCTGGAAGAGTCTCAGAGAAAGTGCCCACCGTGCTGGTATAAGTT 2222

Qy     741 eSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisValVa 761
Db    2223 TGCCAACACTTTCCTCATCTGGGAGTGTCACCCCTACTGGATAAAACTGAAGGAGATCGT 2282

Qy     761 lAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeuAs 781
Db    2283 GAACTTAATCGTCATGGACCCTTTTGTAGACTTAGCCATCACCATCTGCATCGTTCTGAA 2342

Qy     781 nThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeuTh 801
Db    2343 TACGCTATTTATGGCAATGGAGCACCATCCCATGACACCACAGTTCGAACACGTCTTGGC 2402

Qy     801 rValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIleAl 821
Db    2403 CGTAGGAAATCTGGTGTTCACCGGGATCTTCACGGCGGAAATGTTTCTGAAGCTCATAGC 2462

Qy     821 aMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleValTh 841
Db    2463 CATGGACCCCTACTATTATTTCCAAGAAGGCTGGAACATTTTTGACGGATTTATTGTCTC 2522

Qy     841 rLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSerPh 861
Db    2523 CCTCAGTTTAATGGAGCTGAGTCTCGCAGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTT 2582

Qy     861 eArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLy 881
Db    2583 CCGACTGCTCCGAGTCTTCAAGCTGGCCAAGTCCTGGCCCACCCTGAACATGCTGATCAA 2642

Qy     881 sIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleVa 901
Db    2643 GATCATCGGGAACTCCGTGGGTGCCCTGGGCAACCTGACCCTGGTGCTGGCCATCATCGT 2702

Qy     901 lPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCy 921
Db    2703 CTTCATCTTCGCCGTGGTGGGGATGCAGCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTG 2762

Qy     921 sLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSerPh 941
Db    2763 TAAGATCAACCAGGAGTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTT 2822

Qy     941 eLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetGl 961
Db    2823 CCTCATCGTCTTCCGAGTGCTGTGTGGGGAGTGGATCGAGACCATGTGGGACTGCATGGA 2882

Qy     961 uValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsnLe 981
Db    2883 GGTGGCCGGCCAGGCCATGTGCCTCATTGTCTTCATGATGGTTATGGTCATTGGCAACCT 2942

Qy     981 uValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAl 1001
Db    2943 GGTGGTGCTGAATCTATTCCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAACCTGGC 3002

Qy    1001 aAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHisLy 1021
Db    3003 GGCCACAGACGACGACGGGGAAATGAACAACCTGCAGATCTCAGTGATCCGGATCAAGAA 3062

Qy    1021 sGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArgLy 1041
Db    3063 GGGCGTGGCCTGGACCAAAGTGAAGGTGCACGCCTTCATGCAGGCTCACTTC------AA 3116

Qy    1041 sGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCy 1061
Db    3117 GCAGCGGGAGGCGGATGAAGTGAAACCCCTCGACGAGCTGTATGAGAAGAAGGCCAACTG 3176

Qy    1061 sMetSerAsnHisThr---***GluIleGlyLysAspLeuAspTyrLeuLysAspValAs 1080
Db    3177 CATCGCCAACCACACGGGCGTGGATATCCACCGGAACGGCGACTTCCAGAAGAACGGGAA 3236

Qy    1080 nGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSe 1100
Db    3237 CGGAACCACCAGCGGCATC------GGCAGCAGCGTGGAGAAGTACATCATCGACGAG-- 3288

Qy    1100 rAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGl 1120
Db    3289 -GACCACATGTCCTTCATTAACAACCCAAACCTGACCGTCCGGGTGCCCATTGCTGTGGG 3347

Qy    1120 yGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGl 1140
Db    3348 CGAGTCTGACTTCGAGAACCTCAACACAGAGGATGTTAGCAGCGAATCAGACCCTGAAGG 3407

Qy    1140 uSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGl 1160
Db    3408 CAGCAAAGATAAACTGGACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAA 3464

Qy    1160 yAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCy 1180
Db    3465 GCCTGAGGTGGAAGAAGTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTG 3524

Qy    1180 sPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyAr 1200
Db    3525 CTTTACAGAGGGTTGCGTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACT 3584

Qy    1200 gGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPh 1220
Db    3585 AGGCAAGTCGTGGTGGATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTT 3644

Qy    1220 eGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIl 1240
Db    3645 TGAGACCTTCATCATCTTCATGATTCTGCTCAGCAGTGGCGCCCTGGCCTTTGAGGACAT 3704

Qy    1240 eTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheTh 1260
Db    3705 CTACATTGAGCAGAGGAAGACCATCCGCACCATCCTGGAGTATGCGGACAAGGTCTTCAC 3764

Qy    1260 rTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPh 1280
Db    3765 CTACATCTTCATCCTGGAGATGTTGCTCAAGTGGACAGCCTACGGCTTCGTCAAGTTCTT 3824

Qy    1280 eThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuTh 1300
Db    3825 CACCAATGCCTGGTGCTGGTTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTAT 3884

Qy    1300 rAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAl 1320
Db    3885 AGCTAATGCCCTGGGCTACTCGGAACTAGGTGCCATAAAGTCCCTTAGGACCCTAAGAGC 3944

Qy    1320 aLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLe 1340
Db    3945 TTTGAGACCCTTAAGAGCCTTATCACGATTTGAAGGGATGAGGGTGGTGGTGAATGCCTT 4004

Qy    1340 uLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIl 1360
Db    4005 GGTGGGCGCCATCCCCTCCATCATGAATGTGCTGCTGGTGTGTCTCATCTTCTGGCTGAT 4064

Qy    1360 ePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrTh 1380
Db    4065 TTTCAGCATCATGGGAGTTAACCTGTTTGCGGGGAAATACCACTACTGCTTTAATGAGAC 4124

Qy    1380 rThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIl 1400
Db    4125 TTCTGAAATCCGGTTCGAAATCGATATTGTCAACAATAAAACGGACTGTGAGAAGCTCAT 4184

Qy    1400 eGluArgAsnGluThr---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGl 1419
Db    4185 GGAGGGCAACAGCACGGAGATCCGATGGAAGAATGTCAAGATCAACTTTGACAATGTCGG 4244

Qy    1419 yPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTy 1439
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Db   4245 AGCAGGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAAGGCTGGATGGACATCATGTA 4304

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Db   4305 TGCGGCTGTAGATTCCCGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACAT 4364

Qy   1459 tTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIl 1479
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Db   4365 GTACATCTACTTCGTCATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCAT 4424

Qy   1479 eGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePh 1499
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Db   4425 CGGTGTCATCATCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTT 4484

Qy   1499 eMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPr 1519
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Db   4485 CATGACAGAGGAACAGAAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCCAAGAAGCC 4544

Qy   1519 oGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValTh 1539
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Db   4545 ACAGAAGCCCATCCCCCGACCCTTGAACAAAATCCAAGGGATTGTCTTTGATTTCGTCAC 4604

Qy   1539 rArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMe 1559
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Db   4605 TCAACAAGCCTTTGACATTGTGATCATGATGCTCATCTGCCTTAACATGGTGACAATGAT 4664

Qy   1559 tValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuVa 1579
          ||||||||||||   ||||||:::   :::      ||||||      ||||||||||||
Db   4665 GGTGGAGACAGACACTCAGAGCAAGCAGATGGAGAACATTCTTTACTGGATTAATCTGGT 4724

Qy   1579 lPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTy 1599
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Db   4725 CTTTGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGACACTACTA 4784

Qy   1599 rPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMe 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4785 TTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATCCTCTCCATTGTGGGAAT 4844

Qy   1619 tPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleAr 1639
          ||||||||||::::::||||||||||||||||||||||||||||||||||||||||||||
Db   4845 GTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCCCCAACCCTATTCCGAGTTATCCG 4904

Qy   1639 gLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLe 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4905 ATTGGCCCGTATTGGGCGCATCTTGCGTCTGATCAAGGGCGCCAAAGGGATCCGCACCCT 4964

Qy   1659 uLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLe 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4965 GCTCTTTGCCTTAATGATGTCGCTGCCCGCCCTGTTCAACATCGGCCTCCTGCTCTTCCT 5024

Qy   1679 uValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVa 1699
          ||||||||||||::::::||||||||||||||||||||||||||||||||||   |||
Db   5025 CGTCATGTTCATCTTCTCCATTTTTGGCATGTCCAACTTCGCATACGTGAAGCACGAGGC 5084

Qy   1699 lGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGl 1719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5085 CGGCATTGACGACATGTTCAACTTCGAGACATTTGGCAACAGCATGATCTGTTTGTTCCA 5144

Qy   1719 nIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProPr 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5145 GATCACAACGTCTGCTGGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCC 5201

Qy   1739 oAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPr 1759
          |||||||      :::|||   :::|||||||||  .  ||||||||||||||||||||
Db   5202 TGACTGCAGCTTGGACAAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCC 5261

Qy   1759 oSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAs 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db   5262 CTCGGTGGGCATCTTCTTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAA 5321

Qy   1779 nMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPr 1799
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Db   5322 CATGTACATCGCCATCATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCC 5381

Qy   1799 oLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAl 1819
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Db   5382 TCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGC 5441

Qy   1819 aThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLe 1839
          ||||||||||:::|||:::  ||||||:::  ||||||  |||||||||  |||||
Db   5442 CACCCAGTTCATCGAGTACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCT 5501

Qy   1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGl 1859
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Db   5502 CCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGG 5561

Qy   1859 yAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSe 1879
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Db   5562 AGATCGCATCCACTGCTTGGACATCCTTTTCGCCTTCACCAAGCGAGTCCTGGGAGACAG 5621

Qy   1879 rGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSe 1899
          |||||||:::|||  ||||||  ||||||||||||||||||:::|||||||||||||||
Db   5622 TGGGGAGTTGGACATCCTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTC 5681

Qy   1899 rLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAl 1919
          ||||||||||||:::|||||||||||||||||:::|||||||||||||||||||||||||
Db   5682 CAAAGTGTCTTACGAGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGC 5741

Qy   1919 aValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal---------Ly 1936
          ||||:::::|||||||||||||||  ||||||  :::|||                ||
Db   5742 AGTGGTCCTGCAGCGTGCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAA 5801

Qy   1936 sGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLy 1956
          |  ||||||                  ||||||:::::  |||
Db   5802 GATGGCCTCC---------------AACAAGCTGGAGAATGGA---------------- 5829

Qy   1956 sGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuTh 1976
                                                :::     :::|||  :::  ||
Db   5830 ------------------------------GGCACACACAGAGACAAGAAGGAGAGCAC 5858

Qy   1976 rMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLy 1996
          |  ||||||||:::      ||||||||||||  ||||||||||      |||||
Db   5859 CCCGTCCACAGCCTCCCTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAA 5915

Qy   1996 sHisGlu------GlnGluGlyLysAspGluLysAlaLys 2007
          |   :::     :::|||||||:::   |||:::||||||
Db   5916 GCAGCAGCGTGCGGAGGAGGGCAGAAGGGAAAGAGCCAAG 5955

RESULT 6
US-09-024-020B-1
; Sequence 1, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-1

Alignment Scores:
Pred. No.:                0              Length:          5977
Score:                    7720.50        Matches:         1531
Percent Similarity:       84.46%         Conservative:     187
Best Local Similarity:    75.27%         Mismatches:       224
Query Match:              74.26%         Indels:            93
DB:                       3              Gaps:              24

US-09-930-871-12 (1-2009) x US-09-024-020B-1 (1-5977)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db      22 ATGGCAGCGCGGCTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAG 81

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysPro 39
           |||||||||   |||||||||||||||||||||   |||   |||      ||||||
Db      82 TCGCTGGCAAACATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCG 141

Qy      40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
           |||         ::::::||||||::::::::::   ||||||||||||||||||||||||
Db     142 GATGGCAGCCACCGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAG 201

Qy      57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
           |||||||||:::|||||||||||||||||||||||||||||      :::|||:::   |||
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Qy      77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
           |||||||||   ||||||||||||:::   :::||||||||||:::||||||||||:::|||
Db     262 CTGGAGGACTTTGACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG 321

Qy      97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
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Db     322 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 381

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Qy     137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsn 156
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Db     442 ACCATCCTGACCAACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAAT 501

Qy     157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg 176
           ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db     502 GTGGAGTACACATTCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGA 561

Qy     177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr 196
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Db     562 GGTTTCTGCATAGACGGCTTCACCTTCTTGCGAGACCCGTGGAACTGGTTAGACTTCAGT 621

Qy     197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216
           ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     622 GTCATCATGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGA 681

Qy     217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236
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Db     682 ACATTCAGGGTTCTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATC 741

Qy     237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     742 GTGGGCGCCCTAATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTC 801

Qy     257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     802 TGCCTGAGTGTTTTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAG 861

Qy     277 CysIleGlnTrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIle 296
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Db     862 TGTGTCGTGTGGCCC----------3---------------------------------- 876

Qy     297 ThrValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSer 316
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Db     877 ---ATAAACTTCAACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAA 933

Qy     317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCys 336
           ||||||  :::           |||  :::  |||  |||:::  |||||||||
Db     934 TATATCAACAATAAAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGC 993

Qy     337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356
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Db     994 GGGAACAGTTCTGATGCTGGGCAATGCCCAGAGGGATTCCAGTGCATGAAAGCAGGAAGG 1053

Qy     357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    1054 AACCCCAACTACGGTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTC 1113

Qy     377 ArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396
           ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db    1114 CGCCTTATGACCCAGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGG 1173

Qy     397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsn 416
           ||||||||||||||||||||||||||||||:::|||||||||||||||||||:::|||||
Db    1174 AAAACGTACATGATCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCTGGTGAAC 1233

Qy     417 LeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1234 TTGATCTTGGCTGTGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAG 1293

Qy     437 AlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGlu 456
           ||||||||||||||||||||||||::   |||:::||||||||||||||||||||||||||
Db    1294 GCAGAGCAAAAAGAGGCCGAGTTCAAGGCAATGCTGGAGCAACTCAAGAAGCAGCAGGAG 1353

Qy     457 AlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSer---------------- 470
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Db    1354 GAGGCACAGGCTGCTGCAATGGCCACCTC-AGCGGGCACTGTCTCGGAAGACGCCATTGA 1412

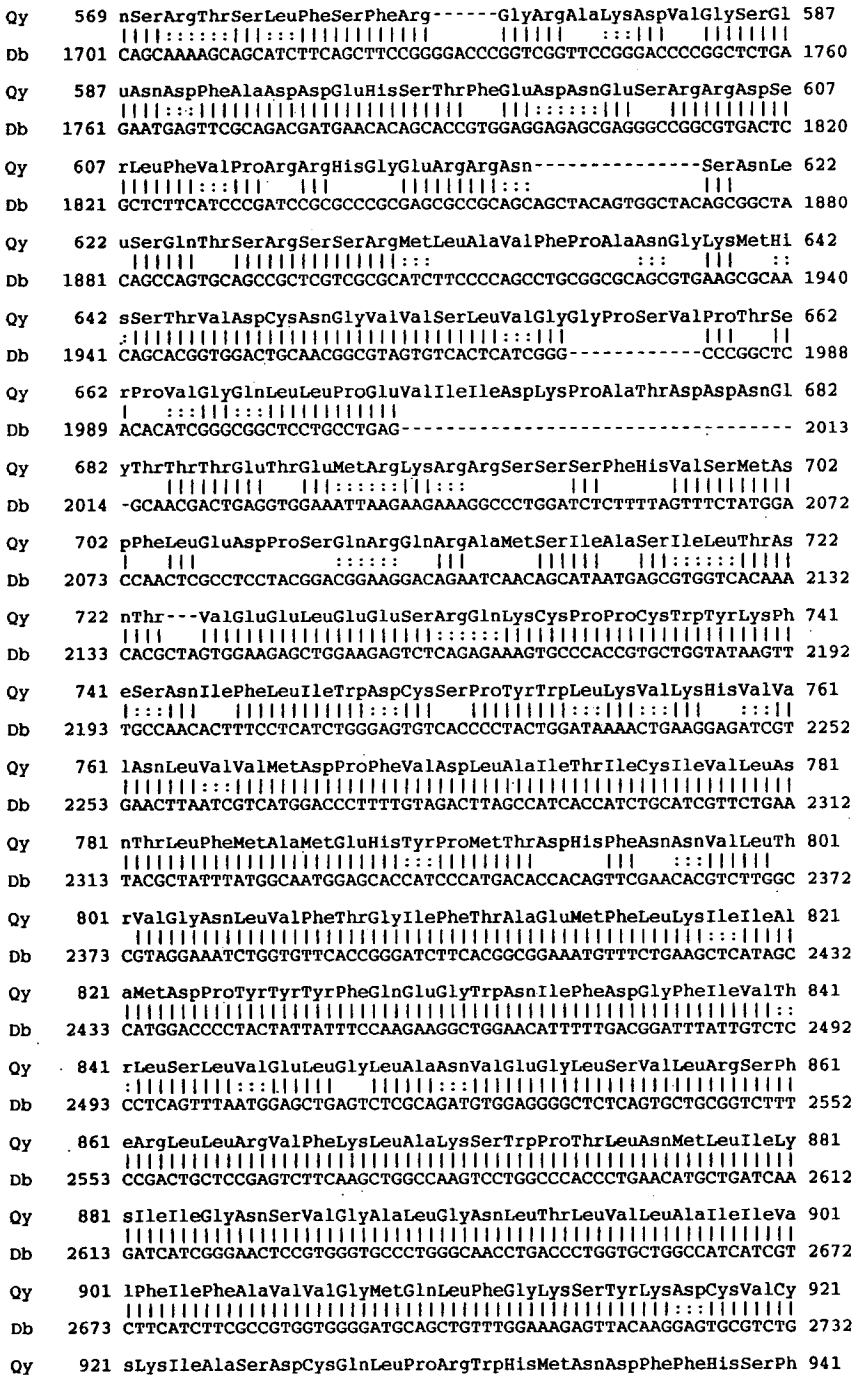
Qy     471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSe 490
           |||                |||||||||||::: ||||||||||   ||||||||||
Db    1413 AGAAGAAGGGGAAGATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAG 1472

Qy     490 rSerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSe 510
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db    1473 TTCCAAGAGCGCGAAGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTC 1532

Qy     510 rGlyGlyGluGluLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerIl 529
           |  ||||||||||||   |||  ::::::      ||||||||||||||||   ::
Db    1533 TGAAGGCGAGGAGAAAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAAGACGGTAT 1592

Qy     529 eArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTy 549
           :|||||||||  ||||||   :::      ||||||:::          ::::::::
Db    1593 GAGAAGGAAGGCCTTCCGG------CTGCCAGACAACAGGATA------GGGAGGAAGTT 1640

Qy     549 rSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569
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Db    1641 TTCCATCATGAATCAGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAA 1700
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Db 2073 CCAACTCGCCTCCTACGGACGGAAGGACAGAATCAACAGCATAATGAGCGTGGTCACAAA 2132
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Qy 781 nThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeuTh 801
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Qy 801 rValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIleAl 821
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Qy 861 eArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLy 881
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Qy 901 lPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCy 921
Db 2673 CTTCATCTTCGCCGTGGTGGGGATGCAGCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTG 2732
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Qy 1160 yAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCy 1180
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Qy 1400 eGluArgAsnGluThr---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGl 1419
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Qy 1439 rAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMe 1459
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Qy 1459 tTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIl 1479
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Qy 1579 lPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTy 1599
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Db 5352 TCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGC 5411
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Qy 1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGl 1859
Db 5472 CCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGG 5531
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Qy 1879 rGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSe 1899
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Qy 1899 rLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAl 1919
Db 5652 CAAAGTGTCTTACGAGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGC 5711
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Db 5800 ------------------------------GGCACACACAGAGACAAGAAGGAGAGCAC 5828
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Qy 1996 sHisGlu------GlnGluGlyLysAspGluLysAlaLys 2007
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RESULT 7
US-09-425-043-1
; Sequence 1, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-1

Alignment Scores:
Pred. No.:                0              Length:          5977
Score:                    7720.50        Matches:         1531
Percent Similarity:       84.46%         Conservative:    187
Best Local Similarity:    75.27%         Mismatches:      224
Query Match:              74.26%         Indels:          93
DB:                       4              Gaps:            24

US-09-930-871-12 (1-2009) x US-09-425-043-1 (1-5977)

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Qy     40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
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Qy     57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
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Qy    237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
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Db    742 GTGGGCGCCCTAATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTC 801

Qy    257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    277 CysIleGlnTrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIle 296
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Db    862 TGTGTCGTGTGGCCC---------------------------------------------- 876

Qy    297 ThrValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSer 316
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Db    877 ---ATAAACTTCAACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAA 933

Qy    317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCys 336
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Db    934 TATATCAACAATAAAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGC 993

Qy    337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356
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Db    994 GGGAACAGTTCTGATGCTGGGCAATGCCCAGAGGGATTCCAGTGCATGAAAGCAGGAAGG 1053

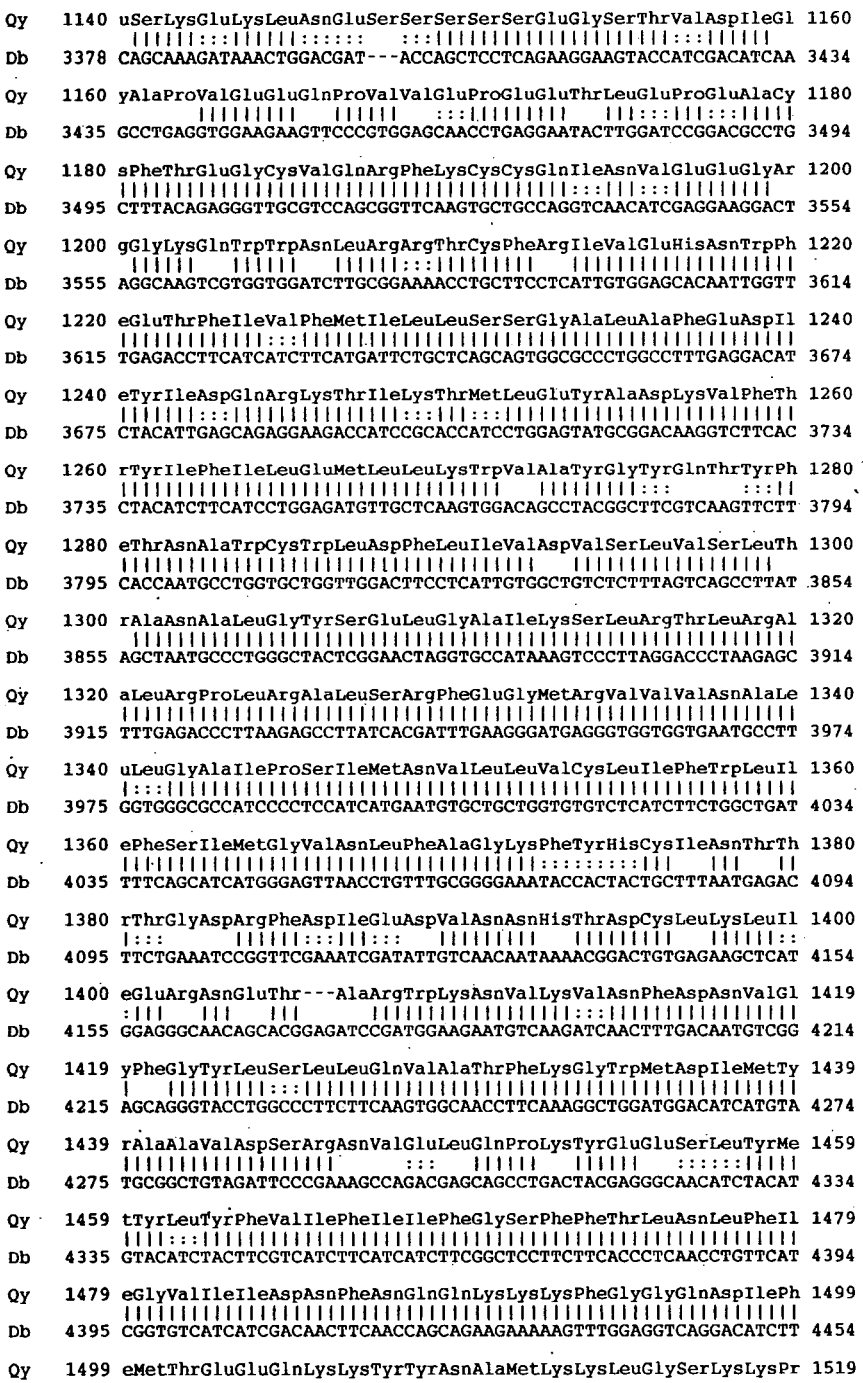
Qy    357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe 376
          ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   1054 AACCCCAACTACGGTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTC 1113

Qy    377 ArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396
          ||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db   1114 CGCCTTATGACCCAGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGG 1173

Qy    397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsn 416
          ||||||||||||||||||||||||||||||||||||:::|||||||||||||:::|||
Db   1174 AAAACGTACATGATCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCTGGTGAAC 1233

Qy    417 LeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 1140 uSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGl 1160
Db 3378 CAGCAAAGATAAACTGGACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAA 3434
Qy 1160 yAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCy 1180
Db 3435 GCCTGAGGTGGAAGAAGTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTG 3494
Qy 1180 sPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyAr 1200
Db 3495 CTTTACAGAGGGTTGCGTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACT 3554
Qy 1200 gGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPh 1220
Db 3555 AGGCAAGTCGTGGTGGATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTT 3614
Qy 1220 eGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIl 1240
Db 3615 TGAGACCTTCATCATCTTCATGATTCTGCTCAGCAGTGGCGCCCTGGCCTTTGAGGACAT 3674
Qy 1240 eTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheTh 1260
Db 3675 CTACATTGAGCAGAGGAAGACCATCCGCACCATCCTGGAGTATGCGGACAAGGTCTTCAC 3734
Qy 1260 rTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPh 1280
Db 3735 CTACATCTTCATCCTGGAGATGTTGCTCAAGTGGACAGCCTACGGCTTCGTCAAGTTCTT 3794
Qy 1280 eThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuTh 1300
Db 3795 CACCAATGCCTGGTGCTGGTTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTAT 3854
Qy 1300 rAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAl 1320
Db 3855 AGCTAATGCCCTGGGCTACTCGGAACTAGGTGCCATAAAGTCCCTTAGGACCCTAAGAGC 3914
Qy 1320 aLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLe 1340
Db 3915 TTTGAGACCCTTAAGAGCCTTATCACGATTTGAAGGGATGAGGGTGGTGGTGAATGCCTT 3974
Qy 1340 uLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIl 1360
Db 3975 GGTGGGCGCCATCCCCTCCATCATGAATGTGCTGCTGGTGTCTCATCTTCTGGCTGAT 4034
Qy 1360 ePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrTh 1380
Db 4035 TTTCAGCATCATGGGAGTTAACCTGTTTGCGGGGAAATACCACTACTGCTTTAATGAGAC 4094
Qy 1380 rThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIl 1400
Db 4095 TTCTGAAATCCGGTTCGAAATCGATATTGTCAACAATAAAACGGACTGTGAGAAGCTCAT 4154
Qy 1400 eGluArgAsnGluThr---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGl 1419
Db 4155 GGAGGGCAACAGCACGGAGATCCGATGGAAGAATGTCAAGATCAACTTTGACAATGTCGG 4214
Qy 1419 yPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTy 1439
Db 4215 AGCAGGGTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAAGGCTGGATGGACATCATGTA 4274
Qy 1439 rAlaAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMe 1459
Db 4275 TGCGGCTGTAGATTCCCGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACAT 4334
Qy 1459 tTyrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIl 1479
Db 4335 GTACATCTACTTCGTCATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCAT 4394
Qy 1479 eGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePh 1499
Db 4395 CGGTGTCATCATCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTT 4454
Qy 1499 eMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPr 1519
Db 4455 CATGACAGAGGAACAGAAGAAGTACTACAATGCCATGAAAAAGCTGGGCTCCAAGAAGCC 4514
Qy 1519 oGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValTh 1539
Db 4515 ACAGAAGCCCATCCCCCGACCCTTGAACAAAATCCAAGGGATTGTCTTTGATTTCGTCAC 4574
Qy 1539 rArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMe 1559
Db 4575 TCAACAAGCCTTTGACATTGTGATCATGATGCTCATCTGCCTTAACATGGTGACAATGAT 4634
Qy 1559 tValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuVa 1579
Db 4635 GGTGGAGACAGACACTCAGAGCAAGCAGATGGAGAACATTCTTTACTGGATTAATCTGGT 4694
Qy 1579 lPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTy 1599
Db 4695 CTTTGTCATCTTCTTCACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGACACTACTA 4754
Qy 1599 rPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMe 1619
Db 4755 TTTCACCATTGGCTGGAACATCTTTGACTTTGTGGTGGTCATCCTCTCCATTGTGGGAAT 4814
Qy 1619 tPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleAr 1639
Db 4815 GTTCCTGGCTGATATCATTGAGAAGTACTTCGTCTCCCCAACCCTATTCCGAGTTATCCG 4874
Qy 1639 gLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLe 1659
Db 4875 ATTGGCCCGTATTGGGCGCATCTTGCGTCTGATCAAGGGCGCCAAAGGGATCCGCACCCT 4934
Qy 1659 uLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLe 1679
Db 4935 GCTCTTTGCCTTAATGATGTCGCTGCCCGCCCTGTTCAACATCGGCCTCCTGCTCTTCCT 4994
Qy 1679 uValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluVa 1699
Db 4995 CGTCATGTTCATCTTCTCCATTTTTGGCATGTCCAACTTCGCATACGTGAAGCACGAGGC 5054
Qy 1699 lGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGl 1719
Db 5055 CGGCATTGACGACATGTTCAACTTCGAGACATTTGGCAACAGCATGATCTGTTTGTTCCA 5114
Qy 1719 nIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProPr 1739
Db 5115 GATCACAACGTCTGCTGGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCC 5171
Qy 1739 oAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPr 1759
Db 5172 TGACTGCAGCTTGGACAAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCC 5231
Qy 1759 oSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAs 1779
Db 5232 CTCGGTGGGCATCTTCTTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAA 5291
Qy 1779 nMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPr 1799
Db 5292 CATGTACATCGCCATCATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCC 5351
Qy 1799 oLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAl 1819
Db 5352 TCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGC 5411
Qy 1819 aThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLe 1839
Db 5412 CACCCAGTTCATCGAGTACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCT 5471
Qy 1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGl 1859
Db 5472 CCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGG 5531
Qy 1859 yAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSe 1879

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Db    5532 AGATCGCATCCACTGCTTGGACATCCTTTTCGCCTTCACCAAGCGAGTCCTGGGAGACAG 5591

Qy    1879 rGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSe 1899
           |||||||:::|||   ||||||   ||||||||||||||||||:::||||||||||||||||
Db    5592 TGGGGAGTTGGACATCCTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTC 5651

Qy    1899 rLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAl 1919
           ||||||||||||:::||||||||||||||||||:::||||||||||||||||||||||||
Db    5652 CAAAGTGTCTTACGAGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGC 5711

Qy    1919 aValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal---------Ly 1936
           ||||::::::||||||||||||||||   ||||||   :::|||              ||
Db    5712 AGTGGTCCTGCAGCGTGCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAA 5771

Qy    1936 sGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLy 1956
           |   ||||||                ||||||::::::   |||
Db    5772 GATGGCCTCC---------------AACAAGCTGGAGAATGGA----------------- 5799

Qy    1956 sGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuTh 1976
                                              :::      :::|||  :::   ||
Db    5800 ------------------------------GGCACACACAGAGACAAGAAGGAGAGCAC 5828

Qy    1976 rMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLy 1996
           |   ||||||||:::      ||||||||||||   ||||||||||||      |||||
Db    5829 CCCGTCCACAGCCTCCCTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAA 5885

Qy    1996 sHisGlu------GlnGluGlyLysAspGluLysAlaLys 2007
           |   :::      :::||||||:::   |||:::||||||
Db    5886 GCAGCAGCGTGCGGAGGAGGGCAGAAGGGAAAGAGCCAAG 5925

RESULT 8
US-09-024-020B-7
; Sequence 7, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-7

Alignment Scores:
Pred. No.:              0              Length:          6556
Score:                  7720.50        Matches:         1531
Percent Similarity:     84.46%         Conservative:    187
Best Local Similarity:  75.27%         Mismatches:      224
Query Match:            74.26%         Indels:          93
DB:                     3              Gaps:            24

US-09-930-871-12 (1-2009) x US-09-024-020B-7 (1-6556)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
            |||         :::|||   ||||||||||||||||||||||      ||||||  |||
Db    169 ATGGCAGCGCGGCTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAG 228

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysPro 39
           |||||||||   ||||||||||||||||||||   |||   |||      ||||||
Db    229 TCGCTGGCAAACATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCG 288

Qy     40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
           |||         ::::::|||||:::::::::   ||||||||||||||||||||||||
Db    289 GATGGCAGCCACCGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAG 348

Qy     57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
           |||||||||:::||||||||||||||||||||||||||||||      :::|||:::   |||
Db    349 GCTGGGAAGAGTTTGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCC 408

Qy     77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
           |||||||||   ||||||||||||:::   :::|||||||||:::||||||||||:::|||
Db    409 CTGGAGGACTTTGACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG 468

Qy     97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
           |||   :::||||||||||||||||||   ||||||||||||||:::|||||||||
Db    469 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 528

Qy    117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
           :::|||:::|||||||||||||||||||:::||||||:::|||||||||:::|||||||||
Db    529 ATAAGAAGAATAGCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGC 588

Qy    137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsn 156
           |||||||||||||||||||||||||||||   ||||||||||||:::|||:::||||||
Db    589 ACCATCCTGACCAACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAAT 648

Qy    157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg 176
           |||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    649 GTGGAGTACACATTCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGA 708

Qy    177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr 196
           |||||||||::::::   ||||||||||||||||||||||||||||||||||||||:::
Db    709 GGTTTCTGCATAGACGGCTTCACCTTCTTGCGAGACCCGTGGAACTGGTTAGACTTCAGT 768

Qy    197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216
           ||||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 GTCATCATGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGA 828

Qy    217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    829 ACATTCAGGGTTCTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATC 888

Qy    237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 GTGGGCGCCCTAATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTC 948

Qy    257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 TGCCTGAGTGTTTTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAG 1008

Qy    277 CysIleGlnTrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIle 296
           |||:::   ||||||
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Db    5262 GATCACAACGTCTGCTGGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCC 5318

Qy    1739 oAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnPr 1759
           |||||||       :::|||   :::||||||||||       ||||||||||||||||||||
Db    5319 TGACTGCAGCTTGGACAAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCC 5378

Qy    1759 oSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAs 1779
           ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db    5379 CTCGGTGGGCATCTTCTTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAA 5438

Qy    1779 nMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluPr 1799
           |||||||||||||:::||||||||||||||||||||||||||||||||||||||:::||
Db    5439 CATGTACATCGCCATCATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCC 5498

Qy    1799 oLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAl 1819
           ||||||||||||||||||||   |||||||||:::||||||||||||||||||||||||
Db    5499 TCTGAGTGAGGATGACTTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGC 5558

Qy    1819 aThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLe 1839
           ||||||||||:::|||:::   ||||||:::   ||||||   ||||||||   |||||
Db    5559 CACCCAGTTCATCGAGTACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCT 5618

Qy    1839 uAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGl 1859
           |   :::|||:::||||||   ::::::||||||||||||||||||||||||||||||||
Db    5619 CCGAGTACCCAAGCCCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGG 5678

Qy    1859 yAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSe 1879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||
Db    5679 AGATCGCATCCACTGCTTGGACATCCTTTTCGCCTTCACCAAGCGAGTCCTGGGAGACAG 5738

Qy    1879 rGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSe 1899
           |||||||:::|||   ||||||   ||||||||||||||||||:::||||||||||||||
Db    5739 TGGGGAGTTGGACATCCTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTC 5798

Qy    1899 rLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAl 1919
           ||||||||||||:::||||||||||||||||:::||||||||||||||||||||||||||
Db    5799 CAAAGTGTCTTACGAGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGC 5858

Qy    1919 aValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal---------Ly 1936
           ||||::::::|||||||||||||||   ||||||   :::|||                ||
Db    5859 AGTGGTCCTGCAGCGTGCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAA 5918

Qy    1936 sGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLy 1956
           |   ||||||                ||||||::::::   |||
Db    5919 GATGGCCTCC--------------AACAAGCTGGAGAATGGA---------------- 5946

Qy    1956 sGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuTh 1976
                                                :::      :::|||   :::   ||
Db    5947 ------------------------------GGCACACACAGAGACAAGAAGGAGAGCAC 5975

Qy    1976 rMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLy 1996
           |   |||||||||:::     ||||||||||||   ||||||||||||      |||||
Db    5976 CCCGTCCACAGCCTCCCTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAA 6032

Qy    1996 sHisGlu------GlnGluGlyLysAspGluLysAlaLys 2007
           |   :::      :::|||||||:::   |||:::||||||
Db    6033 GCAGCAGCGTGCGGAGGAGGGCAGAAGGGAAAGAGCCAAG 6072

RESULT 9
US-09-425-043-7
; Sequence 7, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-7

Alignment Scores:
Pred. No.:                0                Length:          6556
Score:                    7720.50          Matches:         1531
Percent Similarity:       84.46%           Conservative:    187
Best Local Similarity:    75.27%           Mismatches:      224
Query Match:              74.26%           Indels:          93
DB:                       4                Gaps:            24

US-09-930-871-12 (1-2009) x US-09-425-043-7 (1-6556)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db     169 ATGGCAGCGCGGCTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAG 228

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysPro 39
           |||||||||   ||||||||||||||||||||   |||   |||      ||||||
Db     229 TCGCTGGCAAACATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCG 288

Qy      40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
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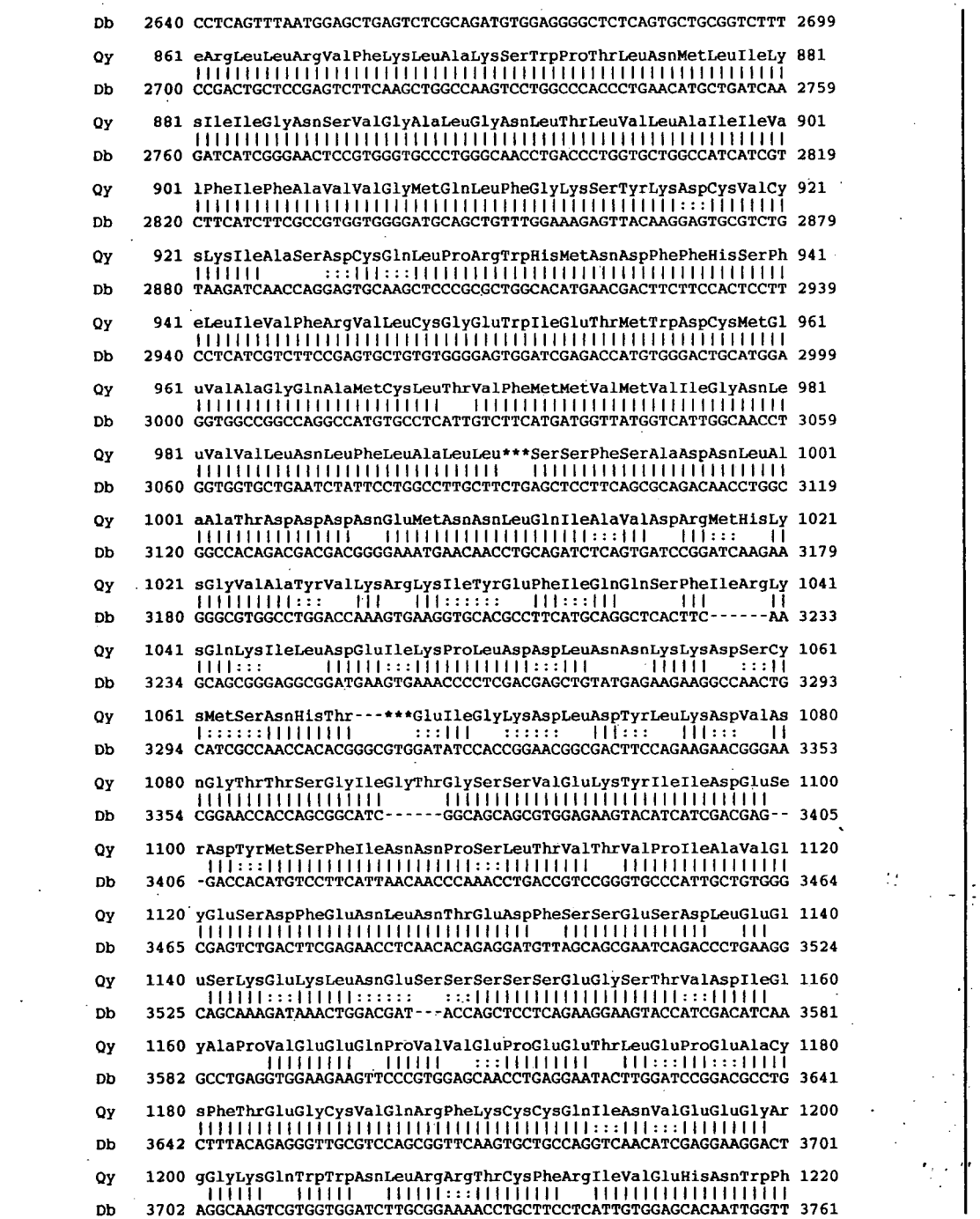
Qy      57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
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Db     349 GCTGGGAAGAGTTTGCCTTTCATCTACGGGGACATCCCGCCAAGGCCTGGTTGCGGTTCCC 408

Qy      77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
           |||||||||   ||||||||||||:::   :::||||||||||:::||||||||:::|||
Db     409 CTGGAGGACTTTGACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG 468

Qy      97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
           |||   :::||||||||||||||||||   |||||||||||||||:::|||||||||
Db     469 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 528

Qy     117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
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Db     529 ATAAGAAGAATAGCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGC 588
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Db 2640 CCTCAGTTTAATGGAGCTGAGTCTCGCAGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTT 2699
Qy 861 eArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLy 881
Db 2700 CCGACTGCTCCGAGTCTTCAAGCTGGCCAAGTCCTGGCCCACCCTGAACATGCTGATCAA 2759
Qy 881 sIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleVa 901
Db 2760 GATCATCGGGAACTCCGTGGGTGCCCTGGGCAACCTGACCCTGGTGCTGGCCATCATCGT 2819
Qy 901 lPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCy 921
Db 2820 CTTCATCTTCGCCGTGGTGGGGATGCAGCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTG 2879
Qy 921 sLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSerPh 941
Db 2880 TAAGATCAACCAGGAGTGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTT 2939
Qy 941 eLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetGl 961
Db 2940 CCTCATCGTCTTCCGAGTGCTGTGTGGGGAGTGGATCGAGACCATGTGGGACTGCATGGA 2999
Qy 961 uValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsnLe 981
Db 3000 GGTGGCCGGCCAGGCCATGTGCCTCATTGTCTTCATGATGGTTATGGTCATTGGCAACCT 3059
Qy 981 uValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAl 1001
Db 3060 GGTGGTGCTGAATCTATTCCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAACCTGGC 3119
Qy 1001 aAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHisLy 1021
Db 3120 GGCCACAGACGACGACGGGGAAATGAACAACCTGCAGATCTCAGTGATCCGGATCAAGAA 3179
Qy 1021 sGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArgLy 1041
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Qy 1041 sGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCy 1061
Db 3234 GCAGCGGGAGGCGGATGAAGTGAAACCCCTCGACGAGCTGTATGAGAAGAAGGCCAACTG 3293
Qy 1061 sMetSerAsnHisThr---***GluIleGlyLysAspLeuAspTyrLeuLysAspValAs 1080
Db 3294 CATCGCCAACCACACGGGCGTGGATATCCACCGGAACGGCGACTTCCAGAAGAACGGGAA 3353
Qy 1080 nGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSe 1100
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Qy 1100 rAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGl 1120
Db 3406 -GACCACATGTCCTTCATTAACAACCCAAACCTGACCGTCCGGGTGCCCATTGCTGTGGG 3464
Qy 1120 yGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGl 1140
Db 3465 CGAGTCTGACTTCGAGAACCTCAACACAGAGGATGTTAGCAGCGAATCAGACCCTGAAGG 3524
Qy 1140 uSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGl 1160
Db 3525 CAGCAAAGATAAACTGGACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAA 3581
Qy 1160 yAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCy 1180
Db 3582 GCCTGAGGTGGAAGAAGTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTG 3641
Qy 1180 sPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyAr 1200
Db 3642 CTTTACAGAGGGTTGCGTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACT 3701
Qy 1200 gGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPh 1220
Db 3702 AGGCAAGTCGTGGTGGATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTT 3761
Qy 1220 eGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIl 1240
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Db 4542 CGGTGTCATCATCGACAACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTT 4601
Qy 1499 eMetThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysPr 1519
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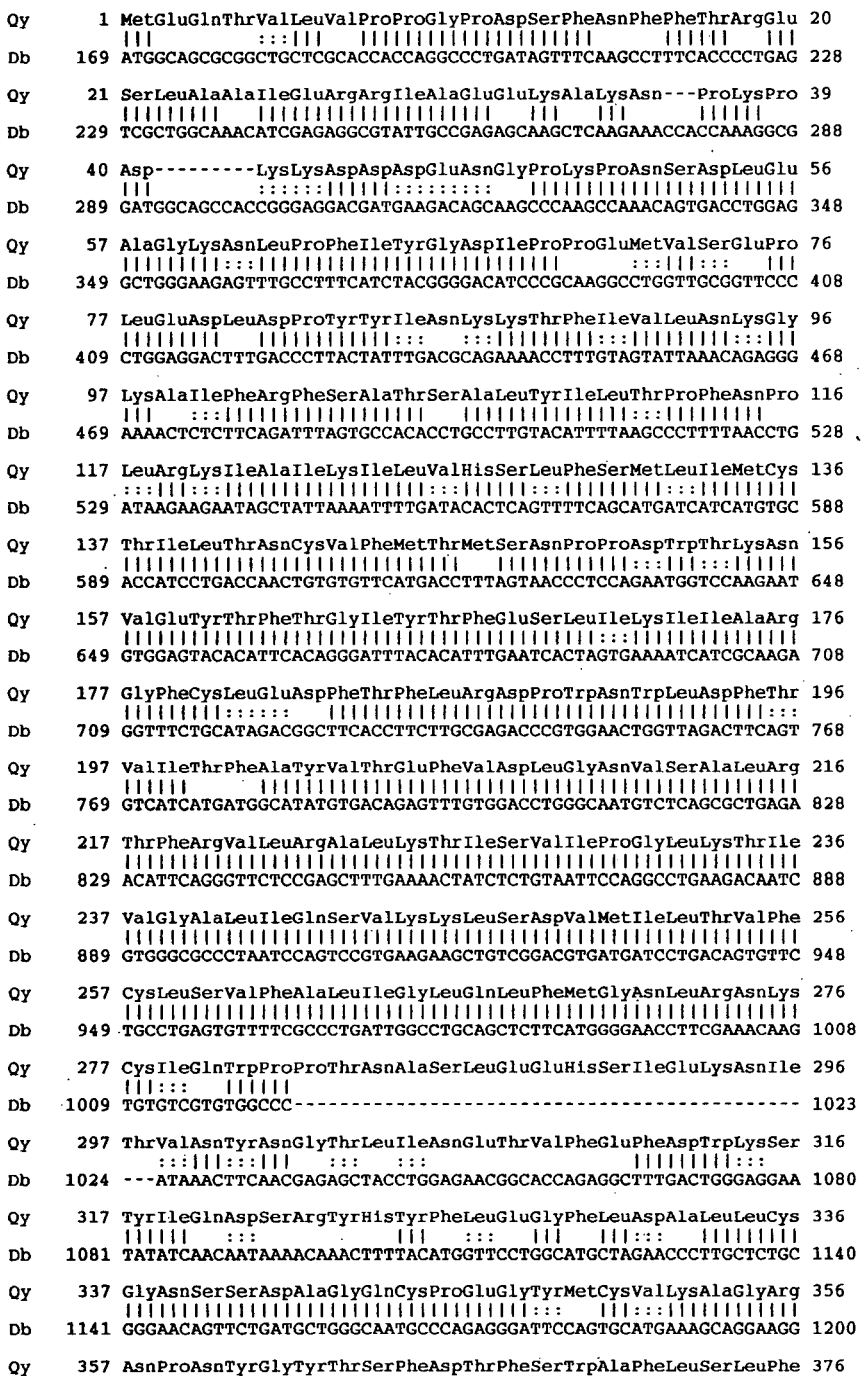
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RESULT 10
US-09-024-020B-43
; Sequence 43, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,020B
; FILING DATE: 16-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6586 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-024-020B-43

Alignment Scores:

Pred. No.:	0	Length:	6586
Score:	7712.50	Matches:	1533
Percent Similarity:	84.20%	Conservative:	188
Best Local Similarity:	75.00%	Mismatches:	221
Query Match:	74.18%	Indels:	103
DB:	3	Gaps:	26

US-09-930-871-12 (1-2009) x US-09-024-020B-43 (1-6586)


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Qy 40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
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Db 469 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 528
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Qy 197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216
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Qy 490 rSerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSe 510
Db 1620 TTCCAAGAGCGCGAAGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTC 1679
Qy 510 rGlyGlyGluGluLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerIl 529
Db 1680 TGAAGGCGAGGAGAAAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAAGACGGTAT 1739
Qy 529 eArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTy 549
Db 1740 GAGAAGGAAGGCCTTCCGG------CTGCCAGACAACAGGATA------GGGAGGAAGTT 1787
Qy 549 rSerSerProHisGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAs 569
Db 1788 TTCCATCATGAATCAGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAA 1847
Qy 569 nSerArgThrSerLeuPheSerPheArg-----GlyArgAlaLysAspValGlySerGl 587
Db 1848 CAGCAAAAGCAGCATCTTCAGCTTCCGGGGACCCGGTCGGTTCCGGGACCCCGGCTCTGA 1907
Qy 587 uAsnAspPheAlaAspAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSe 607
Db 1908 GAATGAGTTCGCAGACGATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTC 1967
Qy 607 rLeuPheValProArgArgHisGlyGluArgArgAsn----------SerAsnLe 622
Db 1968 GCTCTTCATCCCGATCCGCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTA 2027
Qy 622 uSerGlnThrSerArgSerSerArgMet----------LeuAlaValPh 635
Db 2028 CAGCCAGTGCAGCCGCTCGTCGCGTGAAAATAGATAAGGCAGCTACGGACAGCGCATCTT 2087
Qy 635 eProAla---------AsnGlyLysMetHisSerThrValAspCysAsnGlyValValSe 652
Db 2088 CCCCAGCCTGCGGCGCAGCGTGAAGCGCAACAGCACGGTGGACTGCAACGGCGTAGTGTC 2147
Qy 652 rLeuValGlyGlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIl 672
Db 2148 ACTCATCGGG----------CCCGGCTCACACATCGGGCGGCTCCTGCCTGAG----- 2190
Qy 672 eIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysAr 692
Db 2191 ----------GCAACGACTGAGGTGGAAATTAAGAAGAA 2219
Qy 692 gArgSerSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnAr 712



```
Qy   1429 aThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnValGluLe 1449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db   4422 AACCTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCCCGAAAGCCAGACGA 4481

Qy   1449 uGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIleIlePh 1469
          ||||||  ||||||  ::::::||||||||:::|||||||||||||||||||||||||||
Db   4482 GCAGCCTGACTACGAGGGCAACATCTACATGTACATCTACTTCGTCATCTTCATCATCTT 4541

Qy   1469 eGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAsnGlnGl 1489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4542 CGGCTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCATCATCGACAACTTCAACCAGCA 4601

Qy   1489 nLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTyrTyrAs 1509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4602 GAAGAAAAAGTTTGGAGGTCAGGACATCTTCATGACAGAGGAACAGAAGAAGTACTACAA 4661

Qy   1509 nAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLy 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db   4662 TGCCATGAAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCCCGACCCTTGAACAA 4721

Qy   1529 sPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIleMetIl 1549
          |  ||||||:::|||||||||||||||||||:::|||  |||||||||  |||||||::
Db   4722 AATCCAAGGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGACATTGTGATCATGAT 4781

Qy   1549 eLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGluTyrVa 1569
          :|||||||||||||||||||||||||||||||||||||||||||  ||||||:::  ::
Db   4782 GCTCATCTGCCTTAACATGGTGACAATGATGGTGGAGACAGACACTCAGAGCAAGCAGAT 4841

Qy   1569 lThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysVa 1589
          :    ||||||      ||||||||||||||||:::::   ||||||  ||||||||
Db   4842 GGAGAACATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTCACCTGCGAGTGTGT 4901

Qy   1589 lLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPh 1609
          ||||||||:::  :::|||||||||||||||||||||||||||||||||||||||||||||
Db   4902 GCTCAAAATGTTTGCCTTGAGACACTACTATTTCACCATTGGCTGGAACATCTTTGACTT 4961

Qy   1609 eValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPh 1629
          ||||||||||||||||||||||||||||||||||||||||||::::::|||||||||||||
Db   4962 TGTGGTGGTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTACTT 5021

Qy   1629 eValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLe 1649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5022 CGTCTCCCCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGGCGCATCTTGCGTCT 5081

Qy   1649 uIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAl 1669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5082 GATCAAGGGCGCCAAAGGGATCCGCACCCTGCTCTTTGCCTTAATGATGTCGCTGCCCGC 5141

Qy   1669 aLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMe 1689
          ||||||||||||||||||||||||||||||||||||||||||:::::|||||||||||||
Db   5142 CCTGTTCAACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTTCTCCATTTTTGGCAT 5201

Qy   1689 tSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluTh 1709
          ||||||||||||||||||||  |||  ||||||||||||||||||||||||||||||||
Db   5202 GTCCAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATGTTCAACTTCGAGAC 5261

Qy   1709 rPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLe 1729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5262 ATTTGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCTGGCTGGGATGGCCT 5321

Qy   1729 uLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysValAsnProGl 1749
          ||||  ||||||||||||  :::||||||||||||  :::|||  :::||||||
Db   5322 GCTGCTGCCAATCCTGAAC---CGCCCCCCTGACTGCAGCTTGGACAAAGAGCACCCAGG 5378

Qy   1749 ySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTy 1769
          ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5379 GAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTCTTCTTTGTGAGCTA 5438

Qy   1769 rIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPh 1789
          ||||||||||||||||||:::||||||||||||||||||:::||||||||||||||||||
Db   5439 CATCATCATCTCCTTCCTGATTGTGGTGAACATGTACATCGCCATCATCCTGGAGAACTT 5498

Qy   1789 eSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTy 1809
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db   5499 CAGCGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGACTTCGAGACTTTCTA 5558

Qy   1809 rGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSe 1829
          ||||:::|||||||||||||||||||||||||||||||||||||:::|||:::  |||||::
Db   5559 TGAGATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAGTACTGTAAGCTGGC 5618

Qy   1829 rGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLe 1849
          :  ||||||  |||||||||  ||||||  :::|||:::||||||  ::::::||
Db   5619 AGACTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCCAACACCATCGAGCT 5678

Qy   1849 uIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPh 1869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5679 CATCGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGCTTGGACATCCTTTT 5738

Qy   1869 eAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMe 1889
          ||||||||||||||||||||||||||:::|||||||||:::|||  ||||||  |||||
Db   5739 CGCCTTCACCAAGCGAGTCCTGGGAGACAGTGGGGAGTTGGACATCCTGCGGCAGCAGAT 5798

Qy   1889 tGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrTh 1909
          ||||||||||||:::|||||||||||||||||||||||||:::|||||||||||||||
Db   5799 GGAGGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACGAGCCTATCACAACCAC 5858

Qy   1909 rLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHi 1929
          ||||:::|||||||||||||||||||||||||||||:::::|||||||||||||||  ||
Db   5859 TCTGCGGCGCAAGCAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGTGCCTACAGGGGACA 5918

Qy   1929 sLeuLeuLysArgThrVal---------LysGlnAlaSerPheThrTyrAsnLysAsnLy 1946
          ||||  :::|||              |||  ||||||              |||||
Db   5919 CTTGGCTAGGCGGGGCTTCATCTGCAGAAAGATGGCCTCC--------------AACAA 5963

Qy   1946 sIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGl 1966
          |::::::  |||
Db   5964 GCTGGAGAATGGA---------------------------------------------- 5976

Qy   1966 uAsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTy 1986
               :::      :::|||  :::  |||  ||||||||::      ||||||||
Db   5977 -GGCACACACAGAGACAAGAAGGAGAGCACCCCGTCCACAGCCTCCCTC---CCCTCTTA 6032

Qy   1986 rAspArgValThrLysProIleValGluLysHisGlu------GlnGluGlyLysAspGl 2004
          ||||  ||||||||||||      ||||||  :::      :::||||||::  ||
Db   6033 CGACAGCGTCACAAAGCCAGACAAGGAGAAGCAGCAGCGTGCGGAGGAGGGCAGAAGGGA 6092

Qy   2004 uLysAlaLys 2007
          |:::|||||
Db   6093 AAGAGCCAAG 6102

RESULT 11
US-09-425-043-43
; Sequence 43, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6586 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-43

Alignment Scores:
Pred. No.:                0              Length:          6586
Score:                    7712.50        Matches:         1533
Percent Similarity:       84.20%         Conservative:    188
Best Local Similarity:    75.00%         Mismatches:      221
Query Match:              74.18%         Indels:          103
DB:                       4              Gaps:            26

US-09-930-871-12 (1-2009) x US-09-425-043-43 (1-6586)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
Db     169 ATGGCAGCGCGGCTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAG 228

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysPro 39
Db     229 TCGCTGGCAAACATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCG 288

Qy      40 Asp---------LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGlu 56
Db     289 GATGGCAGCCACCGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAG 348

Qy      57 AlaGlyLysAsnLeuProPheIleTyrGlyAspIleProProGluMetValSerGluPro 76
Db     349 GCTGGGAAGAGTTTGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCC 408

Qy      77 LeuGluAspLeuAspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGly 96
Db     409 CTGGAGGACTTTGACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG 468

Qy      97 LysAlaIlePheArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnPro 116
Db     469 AAAACTCTCTTCAGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTG 528

Qy     117 LeuArgLysIleAlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCys 136
Db     529 ATAAGAAGAATAGCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGC 588

Qy     137 ThrIleLeuThrAsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsn 156
Db     589 ACCATCCTGACCAACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAAT 648

Qy     157 ValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArg 176
Db     649 GTGGAGTACACATTCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGA 708

Qy     177 GlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThr 196
Db     709 GGTTTCTGCATAGACGGCTTCACCTTCTTGCGAGACCCGTGGAACTGGTTAGACTTCAGT 768

Qy     197 ValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArg 216
Db     769 GTCATCATGATGGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGA 828

Qy     217 ThrPheArgValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIle 236
Db     829 ACATTCAGGGTTCTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATC 888

Qy     237 ValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPhe 256
Db     889 GTGGGCGCCCTAATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTC 948

Qy     257 CysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLys 276
Db     949 TGCCTGAGTGTTTTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAG 1008

Qy     277 CysIleGlnTrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIle 296
Db    1009 TGTGTCGTGTGGCCC---------------------------------------------- 1023

Qy     297 ThrValAsnTyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSer 316
Db    1024 ---ATAAACTTCAACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAA 1080

Qy     317 TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCys 336
Db    1081 TATATCAACAATAAAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGC 1140

Qy     337 GlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArg 356
Db    1141 GGGAACAGTTCTGATGCTGGGCAATGCCCAGAGGGATTCCAGTGCATGAAAGCAGGAAGG 1200

Qy     357 AsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPhe 376
Db    1201 AACCCCAACTACGGTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTC 1260

Qy     377 ArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGly 396
Db    1261 CGCCTTATGACCCAGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGG 1320

Qy     397 LysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsn 416
Db    1321 AAAACGTACATGATCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCTGGTGAAC 1380

Qy     417 LeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGlu 436
Db    1381 TTGATCTTGGCTGTGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAG 1440

Qy     437 AlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGlu 456
Db    1441 GCAGAGCAAAAAGAGGCCGAGTTCAAGGCAATGCTGGAGCAACTCAAGAAGCAGCAGGAG 1500

Qy     457 AlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSer------------------ 470
Db    1501 GAGGCACAGGCTGCTGCAATGGCCACCTC-AGCGGGCACTGTCTCGGAAGACGCCATTGA 1559

Qy     471 ArgGluProSerAlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSe 490
Db    1560 AGAAGAAGGGGAAGATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAG 1619

Qy     490 rSerLysSerAlaLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSe 510
Db    1620 TTCCAAGAGCGCGAAGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTC 1679

Qy     510 rGlyGlyGluGluLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerIl 529
Db    1680 TGAAGGCGAGGAGAAAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAAGACGGTAT 1739

Qy     529 eArgArgLysGlyPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTy 549
Db    1740 GAGAAGGAAGGCCTTCCGG------CTGCCAGACAACAGGATA------GGGAGGAAGTT 1787
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Qy   1986 rAspArgValThrLysProIleValGluLysHisGlu------GlnGluGlyLysAspGl 2004
          ||||  ||||||||||||      ||||||   :::      :::|||||:::   ||
Db   6033 CGACAGCGTCACAAAGCCAGACAAGGAGAAGCAGCAGCGTGCGGAGGAGGGCAGAAGGGA 6092

Qy   2004 uLysAlaLys 2007
          |:::|||||
Db   6093 AAGAGCCAAG 6102

RESULT 12
US-09-024-020B-8
; Sequence 8, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6826 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-8

Alignment Scores:
Pred. No.:              0           Length:         6826
Score:                  7525.50     Matches:        1510
Percent Similarity:     83.74%      Conservative:   190
Best Local Similarity:  74.38%      Mismatches:     236
Query Match:            72.38%      Indels:         97
DB:                     3           Gaps:           25

US-09-930-871-12 (1-2009) x US-09-024-020B-8 (1-6826)

Qy      5 ValLeuValProProGlyProAspSerPheAsnPhePheThrArgGluSerLeuAlaAla 24
          :::|||   ||||||||||||||||||||      ||||||   ||||||||||||
Db     19 CTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAGTCGCTGGCAAAC 78

Qy     25 IleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysProAsp--------- 40
          ||||||||||||||||||||    |||   |||      ||||||   |||
Db     79 ATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCGGATGGCAGCCAC 138

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ::::::||||||:::::::::   ||||||||||||||||||||||||||||||||:::
Db    139 CGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAGGCTGGGAAGAGT 198

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||      :::|||:::   ||||||||||||
Db    199 TTGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTT 258

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||:::   :::|||||||||:::||||||||||:::||||||   :::|||
Db    259 GACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGGAAAACTCTCTTC 318

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||   ||||||||||||||:::|||||||||   :::|||:::|||
Db    319 AGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTGATAAGAAGAATA 378

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||:::||||||:::||||||||||:::||||||||||||||||||||
Db    379 GCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGCACCATCCTGACC 438

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||  ||||||||||||:::|||:::||||||||||||||||||
Db    439 AACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAATGTGGAGTACACA 498

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||:::
Db    499 TTCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGAGGTTTCTGCATA 558

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          :::  ||||||||||||||||||||||||||||||||||||||||:::||||||
Db    559 GACGGCTTCACCTTCTTACGAGACCCGTGGAACTGGTTAGACTTCAGTGTCATCATGATG 618

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 798

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||   |||||||||      :::|||:::   |||
Db    799 TTCGCCCTGATTGGCCTGCAGCTCTTTCATGGGAACCTTTCGAAACAGTGTGTCGTGTGG 858

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          |||                                                :::|||:::
Db    859 CCC-----------------------------------------------ATAAACTTC 870

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          |||   :::   :::                    |||||||||:::   ||||||   :::
Db    871 AACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAATATATCAACAAT 930

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
                |||   :::   |||   |||:::   ||||||||||||||||||||
Db    931 AAAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGCGGGAACAGTTCT 990

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||   |||||||:::   |||   ||||||||||||||||||||||||
Db    991 GATGCTGGGCAATGC---GAAGGATTCCAGTGCAGTAAAGCAGGAAGGAACCCCAACTAC 1047

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db   1048 GGTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTCCGCCTTATGACC 1107

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1108 CAGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGGAAAACGTACATG 1167
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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||:::|||||||||||||   :::||||||||||||||||
Db   1168 ATCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCCGGTGAACTTGATCTTGGCT 1227

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1228 GTGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAGGCAGAGCAAAAA 1287

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||:::   |||:::|||||||||||||||||||||||   ||||||
Db   1288 GAGGCCGAGTTCAAGGCAATGCTGGAGCAACTCAAGAAGCAGCAGGAGGAGGCACAGGCT 1347

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSer-----------------ArgGluProSer 474
          ||||||   ||||||   |||   |||                     |||
Db   1348 GCTGCAATGGCCACCTC-AGCGGGCACTGTCTCGGAAGACGCCATTGAAGAAGAAGGGGA 1406

Qy    475 AlaAlaGlyArgLeuSerAsp-SerSerSerGluAlaSerLysLeuSerSerLysSerAl 494
          ||||||||||||:: ||||||||||||   ||||||||||||||||||||||
Db   1407 AGATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAGTTCCAAGAGCGC 1466

Qy    494 aLysGluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGl 514
          ||||||||||||||||||||||||||||||||||||||   |||   ||||||||
Db   1467 GAAGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTCTGAAGGCGAGGA 1526

Qy    514 uLys---AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGl 533
          ||||   |||   ::::::      ||||||||||||||      :::||||||||||
Db   1527 GAAAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAATACGGTATGAGAAGGAAGGC 1586

Qy    533 yPheArgPheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHi 553
          ||||||      :::      |||||||:::         :::::::|||      ::
Db   1587 CTTCCGG------CTGCCAGACAACAGGATA------GGGAGGAAGTTTTCCATCATGAA 1634

Qy    553 sGlnSerLeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSe 573
          :||||||||||||||||||   ||||||   |||      |||   ||||||::::::||
Db   1635 TCAGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAACAGCAAAAGCAG 1694

Qy    573 rLeuPheSerPheArgGly---ArgAlaLysAspValGlySerGluAsnAspPheAlaAs 592
          |:::||||||||               :::|||   ||||||||||||:::||||||||
Db   1695 CATCTTCAGCTTCGGGGACCCGTCGGTTCGGGACCCCGGCTCTGAGAATGAGTTCGCAGA 1754

Qy    592 pAspGluHisSerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProAr 612
          ||||||||||||||||   |||:::::|||   ||||||||||||||||:::|||
Db   1755 CGATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTCGCTCTTCATCCCGAT 1814

Qy    612 gArgHisGlyGluArgArgAsn---------------SerAsnLeuSerGlnThrSerAr 627
          |||      |||||||||:::                 |||      ||||||   |||||
Db   1815 CCGCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTACAGCCAGTGCAGCCG 1874

Qy    627 gSerSerArgMetLeuAlaValPheProAlaAsnGlyLysMetHisSerThrValAspCy 647
          ||||||||||   ::::::         |||      :::   :::||||||||||||||
Db   1875 CTCGTCGCGC---ATCTCCCCAGCCTGCGCGCAGCGTGAAGCCAACAGCACGGTGGACTG 1931

Qy    647 sAsnGlyValValSerLeuValGlyGlyProSerValProThrSerProValGlyGlnLe 667
          ||||||||||||||||||:::|||           |||   |||   :::|||:::||
Db   1932 CAACGGCGTAGTGTCACTCATCGGG-----------CCCGGCTCACACATCGGGCGGCT 1979

Qy    667 uLeuProGluValIleIleAspLysProAlaThrAspAspAsnGlyThrThrThrGluTh 687
          ||||   |||                                        |||||||||
Db   1980 CCTGCT-GAG---------------------------------GCAACGACTGAGGT 2002

Qy    687 rGluMetArgLysArgArgSerSerSerPheHisValSerMetAspPheLeuGluAspPr 707
          |||:::::|||:::             |||   ||||||||||||   |||
Db   2003 GGAAATTAAGAAGAAAGGCCCTGGACTCTTTTA-GTTTCTATGGACCAACTCGCCTCCTA 2061

Qy    707 oSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeuThrAsnThrVal--GluGlu 726
          ::::::   |||      ||||||   |||:::::||||||||:::  ||||||
Db   2062 CGGACGGAAGGACAGAATCAACAGCATAATGAGCGTGGTCACAAACACGCTAGTGAAGAG 2121

Qy    727 LeuGluGluSerArgGlnLysCysProProCysTrpTyrLysPheSerAsnIlePheLeu 746
          ||||||||||||::::::|||||||||||||||||||||||||:::|||   ||||||
Db   2122 CTGGAAGAGTCTCAGAGAAAGTGCCCACCGTGCTGGTATAAGTTTGCCAACACTTTCCTC 2181

Qy    747 IleTrpAspCysSerProTyrTrpLeuLysValLysHisValValAsnLeuValValMet 766
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          ||||||:::|||   |||||||||:::|||:::|||   :::||||||||||:::||||||
Db   2182 ATCTGGGAGTGTCACCCCTACTGGATAAAACTGAAGGAGATCGTGAACTTAATCGTCATG 2241

Qy    767 AspProPheValAspLeuAlaIleThrIleCysIleValLeuAsnThrLeuPheMetAla 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2242 GACCCTTTTGTAGACTTAGCCATCACCATCTGCATCGTTCTGAATACGCTATTTATGGCA 2301

Qy    787 MetGluHisTyrProMetThrAspHisPheAsnAsnValLeuThrValGlyAsnLeuVal 806
          |||||||:::|||||||||      |||   :::||||||   ||||||||||||||||
Db   2302 ATGGAGCACCATCCCATGACACCACAGTTCGAACACGTCTTGGCCGTAGGAAATCTGGTG 2361

Qy    807 PheThrGlyIlePheThrAlaGluMetPheLeuLysIleIleAlaMetAspProTyrTyr 826
          ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db   2362 TTCACCGGGATCTTCACGGCGGAAATGTTTCTGAAGCTCATAGCCATGGACCCCTACTAT 2421

Qy    827 TyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleValThrLeuSerLeuValGlu 846
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||:::|||
Db   2422 TATTTCCAAGAAGGCTGGAACATTTTTGACGGATTTATTGTCTCCCTCAGTTTAATGGAG 2481

Qy    847 LeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSerPheArgLeuLeuArgVal 866
          |||   ||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   2482 CTGAGTCTCGCAGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTTCCGACTGCTCCGAGTC 2541

Qy    867 PheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIleLysIleIleGlyAsnSer 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2542 TTCAAGCTGGCCAAGTCCTGGCCCACCCTGAACATGCTGATCAAGATCATCGGGAACTCC 2601

Qy    887 ValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIleValPheIlePheAlaVal 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2602 GTGGGTGCCCTGGGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATCTTCGCCGTG 2661

Qy    907 ValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysValCysLysIleAlaSerAsp 926
          ||||||||||||||||||||||||||||||||:::|||||||||||||||      :::
Db   2662 GTGGGGATGCAGCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTGTAAGATCAACCAGGAG 2721

Qy    927 CysGlnLeuProArgTrpHisMetAsnAspPhePheHisSerPheLeuIleValPheArg 946
          |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2722 TGCAAGCTCCCGCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTCATCGTCTTCCGA 2781

Qy    947 ValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMetGluValAlaGlyGlnAla 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2782 GTGCTGTGTGGGGAGTGGATCGAGACCATGTGGGACTGCATGGAGGTGGCCGGCCAGGCC 2841

Qy    967 MetCysLeuThrValPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeu 986
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2842 ATGTGCCTCATTGTCTTCATGATGGTTATGGTCATTGGCAACCTGGTGGTGCTGAATCTA 2901

Qy    987 PheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAsp 1006
          ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db   2902 TTCCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAACCTGGCGGCCACAGACGACGAC 2961

Qy   1007 AsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrVal 1026
             ||||||||||||||||||:::|||   |||:::   ||||||||||||:::
Db   2962 GGGGAAATGAACAACCTGCAGATCTCAGTGATCCGGATCAAGAAGGGCGTGGCCTGGACC 3021

Qy   1027 LysArgLysIleTyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAsp 1046
          |||   |||::::::   |||:::|||      |||      |||||:::      |||
Db   3022 AAAGTGAAGGTGCACGCCTTCATGCAGGCTCACTTC------AAGCAGCGGGAGGCGGAT 3075

Qy   1047 GluIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr 1066
          |||:::|||||||||||:::|||      ||||||   :::|||:::::|||||||||
Db   3076 GAAGTGAAACCCCTCGACGAGCTGTATGAGAAGAAGGCCAACTGCATCGCCAACCACACG 3135

Qy   1067 ---***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGly 1085
             :::|||   ::::::   |||:::   |||:::   ||||||||||||||||||
Db   3136 GGCGTGGATATCCACCGGAACGGCGACTTCCAGAAGAACGGGAACGGAACCACCAGCGGC 3195

Qy   1086 IleGlyThrGlySerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPhe 1105
          |||      ||||||||||||||||||||||||||||||||   |||:::||||||||||
Db   3196 ATC------GGCAGCAGCGTGGAGAAGTACATCATCGACGAG---GACCACATGTCCTTC 3246

Qy   1106 IleAsnAsnProSerLeuThrValThrValProIleAlaValGlyGluSerAspPheGlu 1125
          ||||||||||||:::||||||||||   ||||||||||||||||||||||||||||||||
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Db   3247 ATTAACAACCCAAACCTGACCGTCCGGGTGCCCATTGCTGTGGGCGAGTCTGACTTCGAG 3306

Qy   1126 AsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeu 1145
          |||||||||||||||||   |||||||||||||||   |||   ||||||:::||||||
Db   3307 AACCTCAACACAGAGGATGTTAGCAGCGAATCAGACCCTGAAGGCAGCAAAGATAAACTG 3366

Qy   1146 AsnGluSerSerSerSerSerGluGlySerThrValAspIleGlyAlaProValGluGlu 1165
          ::::::   :::||||||||||||||||||||:::|||||||          |||||||||
Db   3367 GACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAAGCCTGAGGTGGAAGAA 3423

Qy   1166 GlnProValValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCys 1185
          ||||||   :::|||||||||   |||:::|||:::||||||||||||||||||||||||
Db   3424 GTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTGCTTTACAGAGGGTTGC 3483

Qy   1186 ValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrp 1205
          ||||||||||||||||||||||:::|||:::|||||||||   ||||||   ||||||
Db   3484 GTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACTAGGCAAGTCGTGGTGG 3543

Qy   1206 AsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleVal 1225
          ||||||:::|||||||||  ||||||||||||||||||||||||||||||||||||||::
Db   3544 ATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTTTGAGACCTTCATCATC 3603

Qy   1226 PheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArg 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   3604 TTCATGATTCTGCTCAGCAGTGGCGCCCTGGCCTTTGAGGACATCTACATTGAGCAGAGG 3663

Qy   1246 LysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeu 1265
          |||||||||:::|||:::||||||||||||||||||||||||||||||||||||||||||
Db   3664 AAGACCATCCGCACCATCCTGGAGTATGCGGACAAGGTCTTCACCTACATCTTCATCCTG 3723

Qy   1266 GluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCys 1285
          ||||||||||||||||  ||||||:::     :::||||||||||||||||||||||||
Db   3724 GAGATGTTGCTCAAGTGGACCACGTACGGCTTCGTCAAGTTCTTCACCAATGCCTGGTGC 3783

Qy   1286 TrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGly 1305
          ||||||||||||||||||  ||||||||||||||||  ||||||||||||||||||||||
Db   3784 TGGTTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTATAGCTAATGCCCTGGGC 3843

Qy   1306 TyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArg 1325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3844 TACTCGGAACTAGGTGCCATAAAGTCCCTTAGGACCCTAAGAGCTTTGAGACCCTTAAGA 3903

Qy   1326 AlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIlePro 1345
          ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db   3904 GCCTTATCACGATTTGAAGGGATGAGGGTGGTGGTGAATGCCTTGGTGGGTGCCATCCCC 3963

Qy   1346 SerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGly 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3964 TCCATCATGAATGTGCTGCTGGTGTGTCTCATCTTCTGGCTGATTTTCAGCATCATGGGA 4023

Qy   1366 ValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPhe 1385
          ||||||||||||||||||||:::::::::|||   |||   |||:::      ||||||
Db   4024 GTTAACCTGTTTGCGGGGAAATACCACTACTGCTTTAATGAGACTTCTGAAATCCGGTTC 4083

Qy   1386 AspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThr 1405
          :::|||:::   |||||||||   |||||||||   ||||||:::|||   |||   |||
Db   4084 GAAATCGATATTGTCAACAATAAAACGGACTGTGAGAAGCTCATGGAGGGCAACAGCACG 4143

Qy   1406 ---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSer 1424
             ||||||||||||||||||:::||||||||||||||||   ||||||||::
Db   4144 GAGATCCGATGGAAGAATGTCAAGATCAACTTTGACAATGTCGGAGCAGGGTACCTGGCC 4203

Qy   1425 LeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSer 1444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4204 CTTCTTCAAGTGGCAACCTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCC 4263

Qy   1445 ArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheVal 1464
          |||      :::   ||||||   ||||||   ::::::||||||||:::||||||||||
Db   4264 CGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACATGTACATCTACTTCGTC 4323

Qy   1465 IlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAsp 1484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4324 ATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCATCATCGAC 4383
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Qy   1485 AsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGln 1504
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4384 AACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTTCATGACAGAGGAACAG 4443

Qy   1505 LysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIlePro 1524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4444 AAGAAGTACTATAATGCCATGAAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCC 4503

Qy   1525 ArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAsp 1544
          ||||||   ||||||   ||||||:::||||||||||||||||:::|||   ||||||
Db   4504 CGACCCTTGAACAAAATCCAAGGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGAC 4563

Qy   1545 IleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAsp 1564
          |||   ||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   4564 ATTGTGATCATGATGCTCATCTGCCTTAACATGGTGACAATGATGGTGGAGACAGACACT 4623

Qy   1565 GlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPhe 1584
          ||||||:::   :::      ||||||      ||||||||||||||:::::   |||
Db   4624 CAGAGCAAGCAGATGGAGAACATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTC 4683

Qy   1585 ThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrp 1604
          |||   ||||||||||||||:::   :::||||||||||||||||||||||||||||||
Db   4684 ACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGACACTACTACTTCACCATTGGCTGG 4743

Qy   1605 AsnIlePheAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeu 1624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||::::::
Db   4744 AACATCTTTGACTTTGTGGTGGTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATC 4803

Qy   1625 IleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4804 ATTGAGAAGTACTTCGTCTCCCCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGG 4863

Qy   1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4864 CGCATCTTGCGTCTGATCAAGGGCGCCAAAGGGATCCGCACTCTGCTCTTTGCTCTGATG 4923

Qy   1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyr 1684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   4924 ATGTCGCTGCCCGCCCTGTTCAACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTTC 4983

Qy   1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMet 1704
          :::||||||||||||||||||||||||||||||||   |||   ||||||||||||||
Db   4984 TCCATTTTTGGCATGTCCAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATG 5043

Qy   1705 PheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAla 1724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5044 TTCAACTTCGAGACATTTGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCT 5103

Qy   1725 GlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsn 1744
          ||||||||||||||||  ||||||||||||  :::||||||||||||      :::
Db   5104 GGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCCTGACTGCAGCTTGGAC 5160

Qy   1745 LysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhe 1764
          |||   :::||||||||||      ||||||||||||||||||||||||||||||||||
Db   5161 AAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTC 5220

Qy   1765 PhePheValSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaVal 1784
          ||||||||||||||||||||||||||||||||||:::||||||||||   ||||||:::
Db   5221 TTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAACATGTGCATCGCCATC 5280

Qy   1785 IleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAsp 1804
          ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db   5281 ATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGAC 5340

Qy   1805 PheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGlu 1824
          ||||||   ||||||||::||||||||||||||||||||||||||||||||:::|||
Db   5341 TTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAG 5400

Qy   1825 PheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnPro 1844
          :::   ||||||:::   ||||||   |||||||||   ||||||   :::|||:::|||
Db   5401 TACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCC 5460
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Qy   1845 AsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCys 1864
          |||   ::::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 AACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGC 5520

Qy   1865 LeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAla 1884
          ||||||||||||||||||||||||||  |||||||||:::||||||||::|||
Db   5521 TTGGACATCCTTTTCGCCTTCACCAAGGCAGTCCTGGGAGACAGTGGGGAGTTGGACATC 5580

Qy   1885 LeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGln 1904
          ||||||   ||||||||||||||||||:::|||||||||||||||||||||||||||:::
Db   5581 CTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACGAA 5640

Qy   1905 ProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArg 1924
               ||||||||||:::|||   :::|||||||||||||||||||:::::::||||||
Db   5641 GCCTATCACACCACTCTGCGGCGCAACGAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGT 5700

Qy   1925 AlaTyrArgArgHisLeuLeuLysArgThrVal---------LysGlnAlaSerPheThr 1941
          |||||||||   ||||||   :::|||                |||   ||||||
Db   5701 GCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAAGATGGCCTCC------ 5754

Qy   1942 TyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIle 1961
               ||||||::::::   |||
Db   5755 ---------AACAAGCTGGAGAATGGA------------------------------- 5772

Qy   1962 AspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAla 1981
                         :::      :::|||   :::   |||   |||||:||||:::
Db   5773 ---------------GGCACACACAGAGACAAGAAGGAGAGCACCCCGTCCACAGCCTCC 5817

Qy   1982 CysProProSerTyrAspArgValThrLysProIleValGluLysHisGlu------Gln 1999
               ||||||||||||   ||||||||||||      ||||||   :::      :::
Db   5818 CTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAAGCAGCAGCGTGCGGAG 5874

Qy   2000 GluGlyLysAspGluLysAlaLys 2007
          ||||||:::   |||:::||||||
Db   5875 GAGGGCAGAAGGGAAAGAGCCAAG 5898

RESULT 13
US-09-425-043-8
; Sequence 8, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6826 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-8

Alignment Scores:
Pred. No.:                0                Length:                6826
Score:                    7525.50          Matches:               1510
Percent Similarity:       83.74%           Conservative:          190
Best Local Similarity:    74.38%           Mismatches:            236
Query Match:              72.38%           Indels:                97
DB:                       4                Gaps:                  25

US-09-930-871-12 (1-2009) x US-09-425-043-8 (1-6826)

Qy      5 ValLeuValProProGlyProAspSerPheAsnPhePheThrArgGluSerLeuAlaAla 24
          :::|||   |||||||||||||||||||||      ||||||   ||||||||||||
Db     19 CTGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAGTCGCTGGCAAAC 78

Qy     25 IleGluArgArgIleAlaGluGluLysAlaLysAsn---ProLysProAsp--------- 40
          ||||||||||||||||||||||   |||   |||      ||||||   |||
Db     79 ATCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCGGATGGCAGCCAC 138

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ::::::||||||:::::::::   |||||||||||||||||||||||||||||||:::
Db    139 CGGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAGGCTGGGAAGAGT 198

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||      :::|||:::   ||||||||||||
Db    199 TTGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTT 258

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||:::   :::|||||||||:::|||||||||:::||||||   :::|||
Db    259 GACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGGAAAACTCTCTTC 318

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    319 AGATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTGATAAGAAGAATA 378

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Db    379 GCTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGCACCATCCTGACC 438

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||   ||||||||||:::|||:::||||||||||||||||||||
Db    439 AACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAATGTGGAGTACACA 498

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||:::||||||||||||||||||||||||||:::
Db    499 TTCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGAGGTTTCTGCATA 558

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          :::   ||||||||||||||||||||||||||||||||||||||:::||||||
Db    559 GACGGCTTCACCTTCTTACGAGACCCGTGGAACTGGTTAGACTTCAGTGTCATCATGATG 618

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Qy     967 MetCysLeuThrValPheMetMetValMetValIleGlyAsnLeuValValLeuAsnLeu 986
           ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2842 ATGTGCCTCATTGTCTTCATGATGGTTATGGTCATTGGCAACCTGGTGGTGCTGAATCTA 2901

Qy     987 PheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeuAlaAlaThrAspAspAsp 1006
           ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db    2902 TTCCTGGCCTTGCTTCTGAGCTCCTTCAGCGCAGACAACCTGGCGGCCACAGACGACGAC 2961

Qy    1007 AsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHisLysGlyValAlaTyrVal 1026
              ||||||||||||||||||||:::|||   |||:::   ||||||||||||:::
Db    2962 GGGGAAATGAACAACCTGCAGATCTCAGTGATCCGGATCAAGAAGGGCGTGGCCTGGACC 3021

Qy    1027 LysArgLysIleTyrGluPheIleGlnGlnSerPheIleArgLysGlnLysIleLeuAsp 1046
           |||   |||::::::   |||:::|||       |||       |||||||::      |||
Db    3022 AAAGTGAAGGTGCACGCCTTCATGCAGGCTCACTTC------AAGCAGCGGGAGGCGGAT 3075

Qy    1047 GluIleLysProLeuAspAspLeuAsnAsnLysLysAspSerCysMetSerAsnHisThr 1066
           |||:::||||||||||||:::|||      ||||||   :::|||:::::|||||||||
Db    3076 GAAGTGAAACCCCTCGACGAGCTGTATGAGAAGAAGGCCAACTGCATCGCCAACCACACG 3135

Qy    1067 ---***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGly 1085
              :::|||   ::::::   |||:::   |||:::   ||||||||||||||||||
Db    3136 GGCGTGGATATCCACCGGAACGGCGACTTCCAGAAGAACGGGAACGGAACCACCAGCGGC 3195

Qy    1086 IleGlyThrGlySerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPhe 1105
           |||       ||||||||||||||||||||||||||||||||   |||:::|||||||||
Db    3196 ATC------GGCAGCAGCGTGGAGAAGTACATCATCGACGAG---GACCACATGTCCTTC 3246

Qy    1106 IleAsnAsnProSerLeuThrValThrValProIleAlaValGlyGluSerAspPheGlu 1125
           ||||||||||:::|||||||||   ||||||||||||||||||||||||||||||||||||
Db    3247 ATTAACAACCCAAACCTGACCGTCCGGGTGCCCATTGCTGTGGGCGAGTCTGACTTCGAG 3306

Qy    1126 AsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeu 1145
           ||||||||||||||||   ||||||||||||||   |||   ||||||:::||||||
Db    3307 AACCTCAACACAGAGGATGTTAGCAGCGAATCAGACCCTGAAGGCAGCAAAGATAAACTG 3366

Qy    1146 AsnGluSerSerSerSerSerGluGlySerThrValAspIleGlyAlaProValGluGlu 1165
           ::::::   :::|||||||||||||||||||:::||||||        |||||||||
Db    3367 GACGAT---ACCAGCTCCTCAGAAGGAAGTACCATCGACATCAAGCCTGAGGTGGAAGAA 3423

Qy    1166 GlnProValValGluProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCys 1185
           ||||||   :::||||||||||   |||:::|||:::||||||||||||||||||||||
Db    3424 GTTCCCGTGGAGCAACCTGAGGAATACTTGGATCCGGACGCCTGCTTTACAGAGGGTTGC 3483

Qy    1186 ValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrp 1205
           ||||||||||||||||||||||:::|||::::||||||||   ||||||   ||||||
Db    3484 GTCCAGCGGTTCAAGTGCTGCCAGGTCAACATCGAGGAAGGACTAGGCAAGTCGTGGTGG 3543

Qy    1206 AsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPheGluThrPheIleVal 1225
           ||||||:::|||||||||   ||||||||||||||||||||||||||||||||||:::
Db    3544 ATCTTGCGGAAAACCTGCTTCCTCATTGTGGAGCACAATTGGTTTGAGACCTTCATCATC 3603

Qy    1226 PheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArg 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db    3604 TTCATGATTCTGCTCAGCAGTGGCGCCCTGGCCTTTGAGGACATCTACATTGAGCAGAGG 3663

Qy    1246 LysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeu 1265
           |||||||||:::|||:::||||||||||||||||||||||||||||||||||||||||||
Db    3664 AAGACCATCCGCACCATCCTGGAGTATGCGGACAAGGTCTTCACCTACATCTTCATCCTG 3723

Qy    1266 GluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCys 1285
           ||||||||||||||||   |||||||::      :::||||||||||||||||||||||
Db    3724 GAGATGTTGCTCAAGTGGACCACGTACGGCTTCGTCAAGTTCTTCACCAATGCCTGGTGC 3783

Qy    1286 TrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGly 1305
           ||||||||||||||||||||   ||||||||||||||||   ||||||||||||||||||
Db    3784 TGGTTGGACTTCCTCATTGTGGCTGTCTCTTTAGTCAGCCTTATAGCTAATGCCCTGGGC 3843

Qy    1306 TyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArg 1325
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Db    3844 TACTCGGAACTAGGTGCCATAAAGTCCCTTAGGACCCTAAGAGCTTTGAGACCCTTAAGA 3903

Qy    1326 AlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIlePro 1345
           ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db    3904 GCCTTATCACGATTTGAAGGGATGAGGGTGGTGGTGAATGCCTTGGTGGGTGCCATCCCC 3963

Qy    1346 SerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGly 1365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3964 TCCATCATGAATGTGCTGCTGGTGTGTCTCATCTTCTGGCTGATTTTCAGCATCATGGGA 4023

Qy    1366 ValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPhe 1385
           ||||||||||||||||||||:::::::::|||   |||   |||:::      ||||||
Db    4024 GTTAACCTGTTTGCGGGGAAATACCACTACTGCTTTAATGAGACTTCTGAAATCCGGTTC 4083

Qy    1386 AspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThr 1405
           :::|||:::   |||||||||   |||||||||   ||||||:::|||   |||   |||
Db    4084 GAAATCGATATTGTCAACAATAAAACGGACTGTGAGAAGCTCATGGAGGGCAACAGCACG 4143

Qy    1406 ---AlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSer 1424
              ||||||||||||||||||:::|||||||||||||||||||   |||||||||:::
Db    4144 GAGATCCGATGGAAGAATGTCAAGATCAACTTTGACAATGTCGGAGCAGGGTACCTGGCC 4203

Qy    1425 LeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSer 1444
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4204 CTTCTTCAAGTGGCAACCTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCC 4263

Qy    1445 ArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheVal 1464
           |||       :::   ||||||   ||||||   ::::::|||||||||:::|||||||||
Db    4264 CGAAAGCCAGACGAGCAGCCTGACTACGAGGGCAACATCTACATGTACATCTACTTCGTC 4323

Qy    1465 IlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAsp 1484
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4324 ATCTTCATCATCTTCGGCTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCATCATCGAC 4383

Qy    1485 AsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGln 1504
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4384 AACTTCAACCAGCAGAAGAAAAAGTTTGGAGGTCAGGACATCTTCATGACAGAGGAACAG 4443

Qy    1505 LysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIlePro 1524
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Db    4444 AAGAAGTACTATAATGCCATGAAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCC 4503

Qy    1525 ArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAsp 1544
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Db    4504 CGACCCTTGAACAAAATCCAAGGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGAC 4563

Qy    1545 IleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAsp 1564
           |||   ||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db    4564 ATTGTGATCATGATGCTCATCTGCCTTAACATGGTGACAATGATGGTGGAGACAGACACT 4623

Qy    1565 GlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPhe 1584
           ||||||:::  :::      ||||||      ||||||||||||||:::::   |||
Db    4624 CAGAGCAAGCAGATGGAGAACATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTC 4683

Qy    1585 ThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrp 1604
           |||   ||||||||||||||:::   :::||||||||||||||||||||||||||||||
Db    4684 ACCTGCGAGTGTGTGCTCAAAATGTTTGCCTTGAGACACTACTACTTCACCATTGGCTGG 4743

Qy    1605 AsnIlePheAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeu 1624
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::::
Db    4744 AACATCTTTGACTTTGTGGTGGTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATC 4803

Qy    1625 IleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4804 ATTGAGAAGTACTTCGTCTCCCCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGG 4863

Qy    1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4864 CGCATCTTGCGTCTGATCAAGGGCGCCAAAGGGATCCGCACTCTGCTCTTTGCTCTGATG 4923

Qy    1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyr 1684
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db    4924 ATGTCGCTGCCCGCCCTGTTCAACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTTC 4983

Qy    1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMet 1704
           :::|||||||||||||||||||||||||||||||   |||   ||||||||||||||||
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Db   4984 TCCATTTTTGGCATGTCCAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATG 5043

Qy   1705 PheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAla 1724
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5044 TTCAACTTCGAGACATTTGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCT 5103

Qy   1725 GlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsn 1744
          |||||||||||||||||   ||||||||||||   :::||||||||||||      :::
Db   5104 GGCTGGGATGGCCTGCTGCTGCCAATCCTGAAC---CGCCCCCCTGACTGCAGCTTGGAC 5160

Qy   1745 LysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhe 1764
          |||   :::|||||||||      ||||||||||||||||||||||||||||||||||||
Db   5161 AAAGAGCACCCAGGGAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTC 5220

Qy   1765 PhePheValSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaVal 1784
          |||||||||||||||||||||||||||||||:::|||||||||||||   |||||||:::
Db   5221 TTCTTTGTGAGCTACATCATCATCTCCTTCCTGATTGTGGTGAACATGTGCATCGCCATC 5280

Qy   1785 IleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAsp 1804
          |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db   5281 ATCCTGGAGAACTTCAGCGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGAC 5340

Qy   1805 PheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGlu 1824
          ||||||   ||||||||||:::||||||||||||||||||||||||||||||:::|||
Db   5341 TTCGAGACTTTCTATGAGATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAG 5400

Qy   1825 PheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnPro 1844
          :::   ||||||:::   ||||||   |||||||||   ||||||   :::|||:::|||
Db   5401 TACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCC 5460

Qy   1845 AsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCys 1864
          |||   ::::::||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 AACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGC 5520

Qy   1865 LeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAla 1884
          ||||||||||||||||||||||   |||||||||:::||||||||:::|||
Db   5521 TTGGACATCCTTTTCGCCTTCACCAAGGCAGTCCTGGGAGACAGTGGGGAGTTGGACATC 5580

Qy   1885 LeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGln 1904
          ||||||   ||||||||||||||||||:::|||||||||||||||||||||||||:::
Db   5581 CTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACGAA 5640

Qy   1905 ProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArg 1924
                ||||||||:::|||   :::|||||||||||||||||||:::::|||||
Db   5641 GCCTATCACACCACTCTGCGGCGCAACGAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGT 5700

Qy   1925 AlaTyrArgArgHisLeuLeuLysArgThrVal---------LysGlnAlaSerPheThr 1941
          |||||||||   ||||||   :::|||                |||   ||||||
Db   5701 GCCTACAGGGGACACTTGGCTAGGCGGGGCTTCATCTGCAGAAAGATGGCCTCC------ 5754

Qy   1942 TyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIle 1961
                ||||||::::::   |||
Db   5755 ---------AACAAGCTGGAGAATGGA---------------------------------- 5772

Qy   1962 AspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAla 1981
                          :::    :::|||   :::   |||   ||||||||||:::
Db   5773 --------------GGCACACACAGAGACAAGAAGGAGAGCACCCCGTCCACAGCCTCC 5817

Qy   1982 CysProProSerTyrAspArgValThrLysProIleValGluLysHisGlu------Gln 1999
                ||||||||||||   ||||||||||||      ||||||  :::      :::
Db   5818 CTC---CCCTCTTACGACAGCGTCACAAAGCCAGACAAGGAGAAGCAGCAGCGTGCGGAG 5874

Qy   2000 GluGlyLysAspGluLysAlaLys 2007
          ||||||:::   |||:::||||||
Db   5875 GAGGGCAGAAGGGAAAGAGCCAAG 5898

RESULT 14
US-09-634-920-3
; Sequence 3, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
;  APPLICANT:  Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION:  ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE:  2323-155
;  CURRENT APPLICATION NUMBER: US/09/634,920
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/190,057
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  60/147,488
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6048
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(6048)
US-09-634-920-3

Alignment Scores:
Pred. No.:                0              Length:          6048
Score:                    6312.00        Matches:         1287
Percent Similarity:       72.72%         Conservative:    230
Best Local Similarity:    61.70%         Mismatches:      386
Query Match:              60.71%         Indels:          184
DB:                       4              Gaps:            30

US-09-930-871-12 (1-2009) x US-09-634-920-3 (1-6048)

Qy      6 LeuValProProGlyProAspSerPheAsnPhePheThrArgGluSerLeuAlaAlaIle 25
          |||:::|||   |||      ||||||      ||||||||||||||||||||||||||
Db     13 CTATTACCTCGGGGCACCAGCAGCTTCCGCAGGTTCACACGGGAGTCCCTGGCAGCCATC 72

Qy     26 GluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLysLysAsp------ 43
          |||:::|||:::||||||:::::|||:::                  ::::::
Db     73 GAGAAGCGCATGGCGGAGAAGCAAGCCCGCGGCTCAACCACCTTGCAGGAGAGCCGAGAG 132

Qy     44 ------AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
                :::|||      |||:::|||      ||||||:::|||   |||   |||
Db    133 GGGCTGCCCGAGGAGGAGGCTCCCCGGCCCCAGCTGGACCTGCAGGCCTCCAAAAAGCTG 192

Qy     62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
          |||   :::||||||:::   |||   |||::::::   ||||||||||||||||||||
Db    193 CCAGATCTCTATGGCAATCCACCCCAAGAGCTCATCGGAGAGCCCCTGGAGGACCTGGAC 252

Qy     82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
          |||:::|||      :::||||||||||||||||||||||||||||||   |||||||||
Db    253 CCCTTCTATAGCACCCAAAAGACTTTCATCGTACTGAATAAAGGCAAGACCATCTTCCGG 312

Qy    102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
          ||||||||||||:::|||||||||:::|||:::||||||:::|||:::|||:::   |||
Db    313 TTCAGTGCCACCAACGCCTTGTATGTCCTCAGTCCCTTCCACCCAGTTCGGAGAGCGGCT 372

Qy    122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
          :::||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db    373 GTGAAGATTCTGGTTCACTCGCTCTTCAACATGCTCATCATGTGCACCATCCTCACCAAC 432

Qy    142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
          ||||||||||||          :::||||||   |||||||   ||||||||||||||||
Db    433 TGCGTGTTCATGGCCCAGCACGACCCTCCACCCTGGACCAAGTATGTCGAGTACACCTTC 492

Qy    162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
          |||   ||||||||||||||||||||:::||||||:::||||||   ||||||||
Db    493 ACCGCCATTTACACCTTTGAGTCTCTGGTCAAGATTCTGGCTCGAGCTTTCTGCCTGCAC 552

Qy    182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
            ||||||||||||||||||||||||||||||||||||||:::||||||       |||
Db    553 GCGTTCACTTTCCTTCGGGACCCATGGAACTGGCTGGACTTTAGTGTGATTATCATGGCA 612

Qy    202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 TACACAACTGAATTTGTGGACCTGGGCAATGTCTCAGCCTTACGCACCTTCCGAGTCCTC 672
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Qy 222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
Db 673 CGGGCCCTGAAAACTATATCAGTCATTTCAGGGCTGAAGACCATCGTGGGGGCCCTGATC 732
Qy 242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
Db 733 CAGTCTGTGAAGAAGCTGGCTGATGTGATGGTCCTCACAGTCTTCTGCCTCAGCGTCTTT 792
Qy 262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpPro 281
Db 793 GCCCTCATCGGCCTGCAGCTCTTCATGGGCAACCTAAGGCACAAGTGTGTG--------- 843
Qy 282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
Db 844 ----------CGCAACTTCACAGCG---CTCAAC 864
Qy 302 GlyThrLeuIleAsnGluThrValPheGluPheAsp---------TrpLysSer------ 316
Db 865 GGCACC------AACGGCTCCGTG---GAGGCCGACGGCTTGGTCTGGGAATCCCTGGAC 915
Qy 317 ---TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeu 335
Db 916 CTTTACCTCAGTGATCCAGAAAATTACCTGCTCAAGAACGGCACCTCTGATGTGTTACTG 975
Qy 336 CysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGly 355
Db 976 TGTGGGAACAGCTCTGACGCTGGGACATGTCCGGAGGGCTACCGGTGCCTAAAGGCAGGC 1035
Qy 356 ArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeu 375
Db 1036 GAGAACCCCGACCACGGCTACACCAGCTTCGATTCCTTTGCCTGGGCCTTTCTTGCACTC 1095
Qy 376 PheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAla 395
Db 1096 TTCCGCCTGATGACGCAGGACTGCTGGGAGCGCCTCTATCAGCAGACCCTCAGGTCCGCA 1155
Qy 396 GlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIle 415
Db 1156 GGGAAGATCTACATGATCTTCTTCATGCTTGTCATCTTCCTGGGGTCCTTCTACCTGGTG 1215
Qy 416 AsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGlu 435
Db 1216 AACCTGATCCTGGCCGTGGTCGCAATGGCCTATGAGGAGCAAAACCAAGCCACCATCGCT 1275
Qy 436 GluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGln 455
Db 1276 GAGACCGAGGAGAAGGAAAAGCGCTTCCAGGAGGCCATGGAAATGCTCAAGAAAGAACAC 1335
Qy 456 GluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAla 475
Db 1336 GAGGCCCTCACCATCAGGGGTGTGGATACCGTGTCCCGT---------- 1374
Qy 476 AlaGlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLys 495
Db 1375 ----------AGCTCCTTGGAGATGTCCCCTTTGGCCCCAGTAAACAGCCAT 1416
Qy 496 GluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLys 515
Db 1417 GAGAGAAGAAGCAAGAGGAGAAAACGGATG---------TCTTCAGGAACTGAGGAGTGT 1467
Qy 516 AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db 1468 GGGGAGGACAGGCTCCCCAAGTCTGACTCAGAAGATGGTCCCAGAGCAATG--------- 1518
Qy 536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db 1519 ----------AATCATCTCAGCCTCACCCGTGGCCTCAGCAGGACTTCTATGAAG 1563
Qy 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db 1564 CCACGTTCCAGCCGCGGGAGCATTTTCACCTTTCGCAGG---------- 1602
Qy 576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db 1603 ----------CGAGACCTGGGTTCTGAAGCAGATTTTGCAGATGATGAAAAC 1644
Qy 596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db 1645 AGCACAGCGCGGGAGAGCGAGAGCCACCACACATCACTGCTGGTGCCC------TGGCCC 1698
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSer-ArgMetLeuAlaValPh 635
Db 1699 CTGCGCCGGACCAGTGCCCAGGGACAGCCCAGTCCCGGAACCTCGGCTCCTGGCCACG-- 1756
Qy 635 eProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGl 655
Db 1757 -CCCTC-CATGGCAAAAAGAACAGCACTGTGGACTGCAATGGGGTGGTCTCATTACTGGG 1814
Qy 655 y---GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAs 674
Db 1815 GGCAGGCGACCCAGAGGCCACATCCCCAGGAAGCCACCTCCTCCGCCCTGTGATGCTAGA 1874
Qy 674 pLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSe 694
Db 1875 GCACCCG------CCAGACACGACCACGCCATCGGAGGAGCCAGGCGGCCCCCAGATGCT 1928
Qy 694 rSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMe 714
Db 1929 GACCTCCCAGGCTCCGTGTGTAGATGGCTTCGAGGAGCCAGGAGCACGGCAGCGGGCCCT 1988
Qy 714 tSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCy 734
Db 1989 CAGCGCAGTCAGCGTCCTCACAAGCGCACTGGAAGAGTTAGAGGAGTCTCGCCACAAGTG 2048
Qy 734 sProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTr 754
Db 2049 TCCACCATGCTGGAACCGTCTCGCCCAGCGCTACCTGATCTGGGAGTGCTGCCCGCTGTG 2108
Qy 754 pLeuLysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIl 774
Db 2109 GATGTCCATCAAGCAGGGAGTGAAGTTGGTGGTCATGGACCCGTTTACTGACCTCACCAT 2168
Qy 774 eThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAs 794
Db 2169 CACTATGTGCATCGTACTCAACACACTCTTCATGGCGCTGGAGCACTACAACATGACAAG 2228
Qy 794 pHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGl 814
Db 2229 TGAATTCGAGGAGATGCTGCAGGTCGGAAACCTGGTCTTCACAGGGATTTTCACAGCAGA 2288
Qy 814 uMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIl 834
Db 2289 GATGACCTTCAAGATCATTGCCCTCGACCCCTACTACTACTTCCAACAGGGCTGGAACAT 2348
Qy 834 ePheAspGlyPheIleValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGl 854
Db 2349 CTTCGACAGCATCATCGTCATCCTTAGCCTCATGGAGCTGGGCCTGTCCCGCATGAGCAA 2408
Qy 854 yLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpPr 874
Db 2409 CTTGTCGGTGCTGCGCTCCTTCCGCCTGCTGCGGGTCTTCAAGCTGGCCAAATCATGGCC 2468
Qy 874 oThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuTh 894
Db 2469 CACCCTGAACACACTCATCAAGATCATCGGGAACTCAGTGGGGGCACTGGGGAACCTGAC 2528
Qy 894 rLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLy 914
Db 2529 ACTGGTGCTAGCCATCATCGTGTTCATCTTTGCTGTGGTGGGCATGCAGCTCTTTGGCAA 2588
Qy 914 sSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMe 934
Db 2589 GAACTACTCGGAG------CTGAGGGACAGCGACTCAGGCCTGCTGCCTCGCTGGCACAT 2642
Qy 934 tAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGl 954

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Db   2643 GATGGACTTCTTTCATGCCTTCCTAATCATCTTCCGCATCCTCTGTGGAGAGTGGATCGA 2702

Qy    954 uThrMetTrpAspCysMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMe 974
Db   2703 GACCATGTGGGACTGCATGGAGGTGTCGGGGCAGTCATTATGCCTGCTGGTCTTCTTGCT 2762

Qy    974 tValMetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSe 994
Db   2763 TGTTATGGTCATTGGCAACCTTGTGGTCCTGAATCTCTTCCTGGCCTTGCTGCTCAGCTC 2822

Qy    994 rPheSerAlaAspAsnLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIl 1014
Db   2823 CTTCAGTGCAGACAACCTCACAGCCCCTGATGAGGACAGAGAGATGAACAACCTCCAGCT 2882

Qy   1014 eAlaValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIl 1034
Db   2883 GGCCCTGGCCCGCATCCAGAGGGGCCTGCGCTTTGTCAAGCGGACCACCTGGGATTTCTG 2942

Qy   1034 eGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAsp---As 1053
Db   2943 CTGTGGTCTCCTGCGGCACCGGCCTCAG--------------AAGCCCGCAGCCCTTGC 2987

Qy   1053 pLeuAsnAsnLysLysAspSerCysMetSerAsn--------------------HisTh 1066
Db   2988 CGCCCAGGGCCAGCTGCCCAGCTGCATTGCCACCCCCTACTCCCCGCCACCCCCAGAGAC 3047

Qy   1066 r***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIl 1086
Db   3048 GGAGAAGGTGCCTCCCACCCGCAAGGAAACACAGTTTGAGGAAGGCGAGCAACCAGGCCA 3107

Qy   1086 eGlyThrGlySerSerValGluLysTyrIleIleAspGluSerAspTyrMetSerPheIl 1106
Db   3108 GGGCACCCCCGGGGATCCAGAG---------------------------------------- 3129

Qy   1106 eAsnAsnProSerLeuThrValThrValProIleAlaValGlyGluSerAspPheGluAs 1126
Db   3130 ----------------CCCGTGTGTGTGCCCATCGCTGTGGCCGAGTCAGACACAGATGA 3173

Qy   1126 nLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGluSerLysGluLysLeuAs 1146
Db   3174 C---CAAGAAGAGGATGAGGAGAACAGCCTGGGCACGGAGGAGGAGTCCAGCAAGCAGCA 3230

Qy   1146 nGluSer------------------------------------------------------ 1148
Db   3231 GGAATCCCAGCCTGTGTCCGGCTGGCCCAGAGGCCCTCCGGATTCCAGGACCTGGAGCCA 3290

Qy   1148 ------------------------------------------------------------ 1148

Db   3291 GGTGTCAGCGACTGCCTCCTCTGAGGCCGAGGCCAGTGCATCTCAGGCCGACTGGCGGCA 3350

Qy   1149 ----------------------------------------------SerSerSerSe 1152
Db   3351 GCAGTGGAAAGCGGAACCCCAGGCCCCAGGGTGCGGTGAGACCCCAGAGGACAGTTGCTC 3410

Qy   1152 rGluGlySerThrValAspIleGlyAlaProValGlu------GluGlnProValValGl 1170
Db   3411 CGAGGGCAGCACAGCAGACATGACCAACACCGCTGAGCTCCTGGAGCAGATCCCTGACCT 3470

Qy   1170 uProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLy 1190
Db   3471 CGGCCAGGATGTCAAGGACCCAGAGGACTGCTTCACTGAAGGCTGTGTCCGGCGCTGTCC 3530

Qy   1190 sCysCysGlnIleAsnValGluGluGlyArgGlyLysGlnTrpTrpAsnLeuArgArgTh 1210
Db   3531 CTGCTGTGCGGTGGACACCACACAGGCCCCAGGGAAGGTCTGGTGGCGGTTGCGCAAGAC 3590

Qy   1210 rCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLe 1230
Db   3591 CTGCTACCACATCGTGGAGCACAGCTGGTTCGAGACATTCATCATCTTCATGATCCTACT 3650

Qy   1230 uSerSerGlyAlaLeuAlaPheGluAspIleTyrIleAspGlnArgLysThrIleLysTh 1250
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Db   3651 CAGCAGTGGAGCGCTGGCCTTCGAGGACATCTACCTAGAGGAGCGGAAGACCATCAAGGT 3710

Qy   1250 rMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLeuLy 1270
Db   3711 TCTGCTTGAGTATGCCGACAAGATGTTCACATATGTCTTCGTGCTGGAGATGCTGCTCAA 3770

Qy   1270 sTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLe 1290
Db   3771 GTGGGTGGCCTACGGCTTCAAGAAGTACTTCACCAATGCCTGGTGCTGGCTCGACTTCCT 3830

Qy   1290 uIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGl 1310
Db   3831 CATCGTAGACGTCTCTCTGGTCAGCCTGGTGGCCAACACCCTGGGCTTTGCCGAGATGGG 3890

Qy   1310 yAlaIleLysSerLeuArgThrLeuArgAlaLeuArgProLeuArgAlaLeuSerArgPh 1330
Db   3891 CCCCATCAAGTCACTGCGGACGCTGCGTGCACTCCGTCCTCTGAGAGCTCTGTCACGATT 3950

Qy   1330 eGluGlyMetArgValValValAsnAlaLeuLeuGlyAlaIleProSerIleMetAsnVa 1350
Db   3951 TGAGGGCATGAGGGTGGTGGTCAATGCCCTGGTGGGCGCCATCCCGTCCATCATGAACGT 4010

Qy   1350 lLeuLeuValCysLeuIlePheTrpLeuIlePheSerIleMetGlyValAsnLeuPheAl 1370
Db   4011 CCTCCTCGTCTGCCTCATCTTCTGGCTCATCTTCAGCATCATGGGCGTGAACCTCTTTGC 4070

Qy   1370 aGlyLysPheTyrHisCysIleAsnThrThrThrGlyAsp---ArgPheAspIleGluAs 1389
Db   4071 GGGGAAGTTTGGGAGGTGCATCAACCAGACAGAGGGAGACTTGCCTTTGAACTACACCAT 4130

Qy   1389 pValAsnAsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThrAlaArg----- 1407
Db   4131 CGTGAACAACAAGAGCCAGTGTGAGTCCTTG---------AACTTGACCGGAGAATTGTA 4181

Qy   1408 -TrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeuLeuGl 1427
Db   4182 CTGGACCAAGGTGAAAGTCAACTTTGACAACGTGGGGGCCGGGTACCTGGCCCTTCTGCA 4241

Qy   1427 nValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArgAsnVa 1447
Db   4242 GGTGGCAACATTTAAAGGCTGGATGGACATTATGTATGCAGCTGTGGACTCCAGGGGGTA 4301

Qy   1447 lGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeuTyrPheValIlePheIl 1467
Db   4302 TGAAGAGCAGCCTCAGTGGGAATACAACCTCTACATGTACATCTATTTTGTCATTTTCAT 4361

Qy   1467 eIlePheGlySerPhePheThrLeuAsnLeuPheIleGlyValIleIleAspAsnPheAs 1487
Db   4362 CATCTTTGGGTCTTTCTTCACCCTGAACCTCTTTATTGGTGTCATCATTGACAACTTCAA 4421

Qy   1487 nGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMetThrGluGluGlnLysLysTy 1507
Db   4422 CCAACAGAAGAAAAAGTTAGGGGGCCAGGACATCTTCATGACAGAGGAGCAGAAGAAGTA 4481

Qy   1507 rTyrAsnAlaMetLysLysLeuGlySerLysLysProGlnLysProIleProArgProGl 1527
Db   4482 CTACAATGCCATGAAGAAGCTGGGCTCCAAGAAGCCCCAGAAGCCCATCCCACGGCCCCT 4541

Qy   1527 yAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIl 1547
Db   4542 GAACAAGTACCAGGGCTTCATATTCGACATTGTGACCAAGCAGGCCTTTGACGTCACCAT 4601

Qy   1547 eMetIleLeuIleCysLeuAsnMetValThrMetMetValGluThrAspAspGlnSerGl 1567
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Qy   1567 uTyrValThrThrIleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGl 1587
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Qy   1587 uCysValLeuLysLeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePh 1607
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Qy   1607 eAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLy 1627
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Db   4782 CGACTTCGTGGTTGTCATCCTCTCCATCGTGGGCACTGTGCTCTCGGACATCATCCAGAA 4841

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Qy   1827 sLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLe 1847
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Qy   1847 uGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIl 1867
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Db   5499 AAGCCTCATCAACATGGACCTGCCCATGGTGAGTGGGGACCGCATCCATTGCATGGACAT 5558

Qy   1867 eLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIl 1887
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Db   5559 TCTCTTTGCCTTCACCAAAAGGGTCCTGGGGGAGTCTGGGGAGATGGACGCCCTGAAGAT 5618

Qy   1887 eGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleTh 1907
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Db   5619 CCAGATGGAGGAGAAGTTCATGGCAGCCAACCCATCCAAGATCTCCTACGAGCCCATCAC 5678

Qy   1907 rThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrAr 1927
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Db   5679 CACCACACTCCGGCGCAAGCACGAAGAGGTGTCGGCCATGGTTATCCAGAGAGCCTTCCG 5738

Qy   1927 gArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIl 1947
          ||||||||||||||:::|||:::::::|||   |||||||||  :::  :::  :::
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Qy   1947 eLysGlyGlyAlaAsnLeuLeuIleLysGluAsp----------------MetIleIl 1961
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Qy   1978 rThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGl 1998
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Qy   1998 uGlnGluGlyLysAsp 2003
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Db   5967 GGTGCGGGGGTCTGAC 5982
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US-08-843-417-9
; Sequence 9, Application US/08843417
; Patent No. 6184349
;  GENERAL INFORMATION:
;    APPLICANT:  Herman, Ronald C
;    APPLICANT:  Delgado, Stephen G
;    APPLICANT:  Fish, Linda M
;    APPLICANT:  Sangameswaran, Lakshmi
;    APPLICANT:  Rabert, Douglas K
;    TITLE OF INVENTION:  CLONED PERIPHERAL NERVE
;    TITLE OF INVENTION:  TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Heller Ehrman White & McAuliffe
;      STREET:  525 University Ave
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/843,417
;      FILING DATE:  April 15, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  28340-P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415)-324-7041
;      TELEFAX:  (415)-324-0638
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5874 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-843-417-9

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DB:                     4              Gaps:            31

US-09-930-871-12 (1-2009) x US-08-843-417-9 (1-5874)

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Qy   1479 IleGlyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIle 1498
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Qy   1519 ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal 1538
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Qy   1916 GluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal 1935
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Qy   1936 LysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIle 1955
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Qy   1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975
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Qy   1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
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Copyright (c) 1993 - 2003 Compugen Ltd.

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	10197	98.1	5922	10	US-09-930-871-13	Sequence 13, Appl
4	10124.5	97.4	5889	10	US-09-930-871-3	Sequence 3, Appli
5	8448.5	81.3	6822	10	US-09-917-800A-1604	Sequence 1604, Ap
6	7511	72.2	4362	10	US-09-930-871-15	Sequence 15, Appl
7	7438.5	71.5	4329	10	US-09-930-871-5	Sequence 5, Appli
8	7181	69.1	4179	10	US-09-930-871-17	Sequence 17, Appl
9	7108.5	68.4	4146	10	US-09-930-871-7	Sequence 7, Appli
10	7105.5	68.3	4197	10	US-09-930-871-19	Sequence 19, Appl
11	7033	67.6	4164	10	US-09-930-871-9	Sequence 9, Appli
12	6312	60.7	6048	10	US-09-840-125-3	Sequence 3, Appli
13	6310	60.7	6048	9	US-09-896-994-1	Sequence 1, Appli
c 14	2037	19.6	1992	10	US-09-864-761-10189	Sequence 10189, A
c 15	1967.5	18.9	1194	10	US-09-864-761-18334	Sequence 18334, A
c 16	1933.5	18.6	1178	10	US-09-864-761-26829	Sequence 26829, A
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19	1555	15.0	7193	9	US-10-029-413A-17	Sequence 17, Appl
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21	1526.5	14.7	5565	9	US-10-029-413A-1	Sequence 1, Appli
22	1520.5	14.6	6816	10	US-09-935-541-1	Sequence 1, Appli
23	1520.5	14.6	6855	10	US-09-935-541-3	Sequence 3, Appli
24	1517	14.6	6160	9	US-10-029-413A-11	Sequence 11, Appl
25	1517	14.6	6160	9	US-10-029-413A-13	Sequence 13, Appl
26	1510.5	14.5	6503	10	US-09-935-541-12	Sequence 12, Appl
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32	1408.5	13.5	7364	10	US-09-954-456-1179	Sequence 1179, Ap
33	1408.5	13.5	7364	12	US-10-033-026-5	Sequence 5, Appli
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35	1364.5	13.1	6615	9	US-10-029-413A-9	Sequence 9, Appli
36	992.5	9.5	5562	10	US-09-030-482B-18	Sequence 18, Appl
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39	533	5.1	343	10	US-09-030-482B-17	Sequence 17, Appl
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45	409	3.9	465	10	US-09-864-761-10437	Sequence 10437, A

ALIGNMENTS

RESULT 1
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; Sequence 11, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polyr
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-11

Alignment Scores:

Pred. No.:	0	Length:	6030
Score:	10393.00	Matches:	2009
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 99.96% Indels: 0
DB: 10 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-11 (1-6030)

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Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
Db    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

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Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

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Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

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Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
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RESULT 2
US-09-930-871-1
; Sequence 1, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc.
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5997
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-1

Alignment Scores:

Pred. No.:	0	Length:	5997
Score:	10320.50	Matches:	1998
Percent Similarity:	99.45%	Conservative:	0
Best Local Similarity:	99.45%	Mismatches:	0
Query Match:	99.26%	Indels:	11

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DB:                 10          Gaps:          1

US-09-930-871-12 (1-2009) x US-09-930-871-1 (1-5997)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287
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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   5968 GGCAAAGATGAAAAAGCCAAAGGGAAA 5994
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RESULT 3
US-09-930-871-13
; Sequence 13, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polyr
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5922
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-13

Alignment Scores:

Pred. No.:	0	Length:	5922
Score:	10197.00	Matches:	1972
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.08%	Indels:	0
DB:	10	Gaps:	0

US-09-930-871-12 (1-2009) x US-09-930-871-13 (1-5922)

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Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu  20
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA  60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp  40
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Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn  60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu  80
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Db    481 TTCACAGGAATATATACTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
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Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
          ||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5916

RESULT 4
US-09-930-871-3
; Sequence 3, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 5889
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-3

Alignment Scores:
Pred. No.:              0              Length:          5889
Score:                  10124.50        Matches:         1961
Percent Similarity:     99.44%         Conservative:    0
Best Local Similarity:  99.44%         Mismatches:      0
Query Match:            97.38%         Indels:          11
DB:                     10             Gaps:            1

US-09-930-871-12 (1-2009) x US-09-930-871-3 (1-5889)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
           ||||||||||||||||||||||||||||||
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy     721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy     741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
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RESULT 5
US-09-917-800A-1604
; Sequence 1604, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5038-US
;  CURRENT APPLICATION NUMBER: US/09/917,800A
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 1740
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1604
;   LENGTH: 6822
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013119
US-09-917-800A-1604

Alignment Scores:
Pred. No.:              0              Length:         6822
Score:                  8448.50        Matches:        1648
Percent Similarity:     88.49%         Conservative:   136
Best Local Similarity:  81.75%         Mismatches:     153
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Query Match:          81.26%      Indels:        79
DB:                   10          Gaps:          12

US-09-930-871-12 (1-2009) x US-09-917-800A-1604 (1-6822)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
Db     474 TCTCTTGCTGCTATCGAAAAGCGTGCTGCAGAAGAGAAAGCCAAGAAACCCAAGAAAGAG 533

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
Db     894 TTCACTGGGATCTATACCTTTGAGTCACTTATAAAGATCTTGGCAAGAGGGTTTTGCTTA 953

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
Db     954 GAAGATTTCACTTTCCTCCGTGACCCATGGAACTGGCTGGATTTCAGTGTCATCGTGATG 1013

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
Db    1194 TTTGCTCTAATCGGGCTGCAGCTCTTCATGGGCAACCTGAGGAATAAATGCTCGCAGTGG 1253

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLys---AsnIleThrValAsn 299
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Qy     300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
Db    1314 TCAAATGGGACATTTGTTAATGTAACAATGAGCACTTTCAACTGGAAGGATTATATCGCA 1373

Qy     320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
Db    1374 GATGACAGTCACTTTTATGTCTTGGATGGACAAAAAGATCCTTTACTCTGTGGAAATGGC 1433

Qy     340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
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Qy     360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
Db    1494 TACGGCTACACAAGCTTTGACACCTTCAGCTGGGCCTTCTTGTCCCTGTTTCGACTCATG 1553

Qy     380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
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Qy     420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
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Qy     440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
Db    1734 AAGGAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAGCAGCAGGAGGAGGCTCAG 1793

Qy     460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSer---------AlaAla 476
Db    1794 ------GCAGTGGCTGCAGCCTCCGCGGCATCCAGAGACTTCAGTGGAATAGGAGGGTTA 1847

Qy     477 GlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGlu 496
Db    1848 GGAGAACTTCTGGAGAGTTCTTCAGAAGCTTCCAAGTTGAGCTCCAAGAGTGCTAAGGAG 1907

Qy     497 ArgArgAsnArgArgLysLysArgLysGlnLysGluGln---SerGlyGlyGluGluLys 515
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Qy     516 AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db    1968 GATGGAGACAGGTTTCCCAAGTCGGAATCGGAAGACAGTGTCAAACGAAGAAGCTTCCTG 2027

Qy     536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db    2028 CTCTCCCTGGATGGCAACCCGCTGACTGGTGACAAGAAGCTGTGCTCTCCCCACCAGTCT 2087

Qy     556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db    2088 CTCTTGAGTATCCGTGGCTCCCTGTTTTCCCCAAGACGCAATAGCAAAACGAGCATTTTC 2147

Qy     576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db    2148 AGCTTCAGAGGTCGGGCGAAGGACGTGGGGTCTGAGAATGACTTTGCAGACGATGAGCAC 2207

Qy     596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db    2208 AGCACCTTCGAGGACAGCGAGAGCAGGAGAGACTCCCTGTTTGTGCCGCACAGACCTGGA 2267

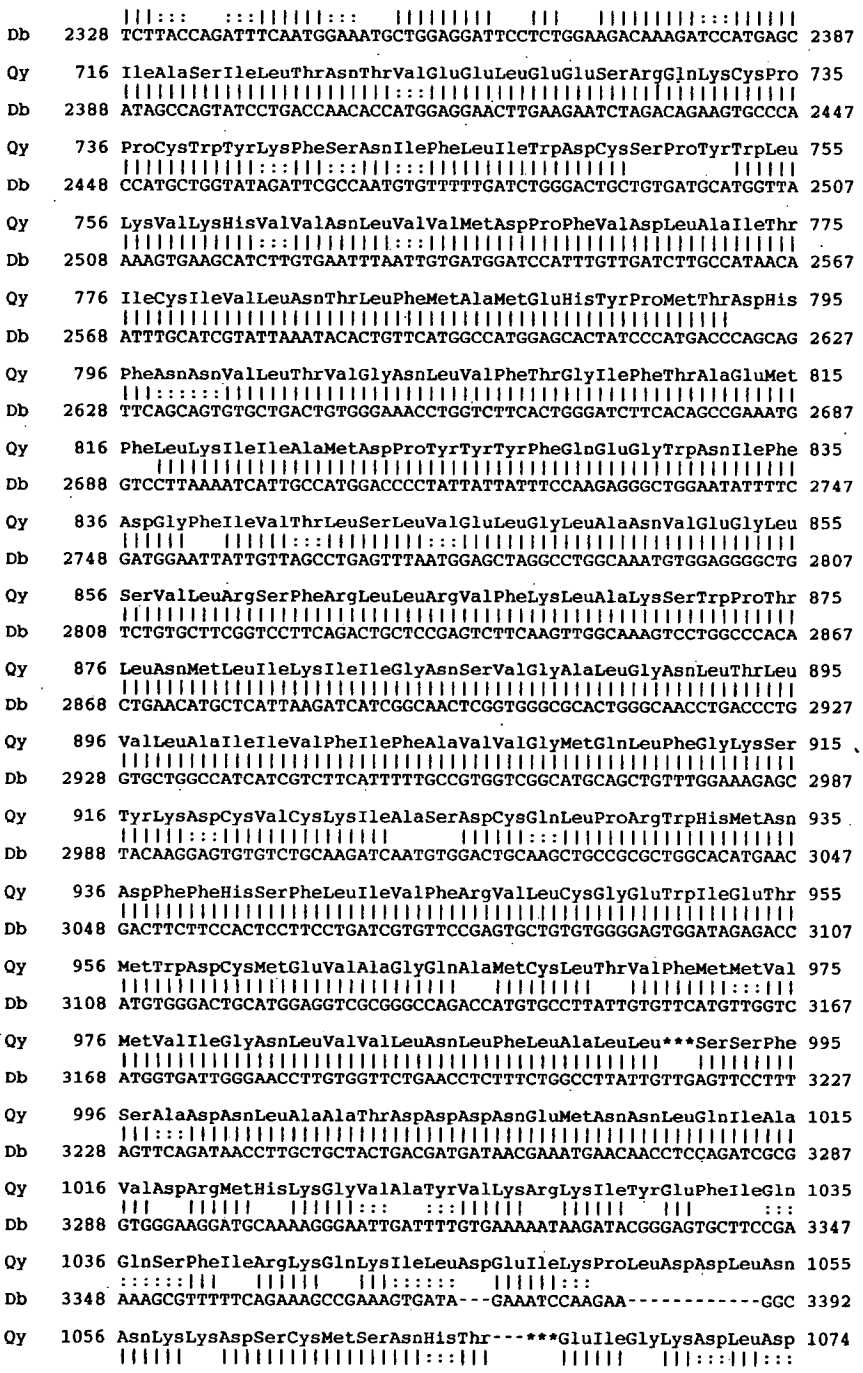
Qy     616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPhe 635
Db    2268 GAGCGACGCAACAGT---------------------------------------------- 2282

Qy     636 ProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGly 655
Db    2282 ---------------------------------------------------------- 2282

Qy     656 GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLys 675
Db    2282 ---------------------------------------------------------- 2282

Qy     676 ProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSer 695
Db    2283 --------------AACGGTACCACCACTGAAACGGAAGTCAGGAAGAGAAGGCTAAGT 2327

Qy     696 SerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSer 715
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Db 2328 TCTTACCAGATTTCAATGGAAATGCTGGAGGATTCCTCTGGAAGACAAAGATCCATGAGC 2387
Qy 716 IleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysPro 735
Db 2388 ATAGCCAGTATCCTGACCAACACCATGGAGGAACTTGAAGAATCTAGACAGAAGTGCCCA 2447
Qy 736 ProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeu 755
Db 2448 CCATGCTGGTATAGATTCGCCAATGTGTTTTTGATCTGGGACTGCTGTGATGCATGGTTA 2507
Qy 756 LysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIleThr 775
Db 2508 AAAGTGAAGCATCTTGTGAATTTAATTGTGATGGATCCATTTGTTGATCTTGCCATAACA 2567
Qy 776 IleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHis 795
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Qy 796 PheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMet 815
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Qy 816 PheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePhe 835
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Db 2928 GTGCTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTTGGAAAGAGC 2987
Qy 916 TyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsn 935
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Qy 936 AspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThr 955
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Qy 976 MetValIleGlyAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPhe 995
Db 3168 ATGGTGATTGGGAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTGTTGAGTTCCTTT 3227
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Qy 1016 ValAspArgMetHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGln 1035
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Db 3348 AAAGCGTTTTTCAGAAAGCCGAAAGTGATA---GAAATCCAAGAA-----------GGC 3392
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Db 3990 TATGCAGACAAGGTCTTCACGTACATCTTCATCCTGGAGATGCTCCTCAAATGGGTGGCC 4049
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Qy   1514 LeuGlySerLysLysProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMet 1533
          ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5061 CTCTCGATTGTAGGAATGTTTCTCGCAGAGCTGATAGAGAAGTATTTCGTGTCCCCTACC 5120

Qy   1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5121 CTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC 5180

Qy   1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5181 AAGGGGATCCGCACTCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGCTGTTCAACATC 5240

Qy   1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5241 GGCCTCCTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 5300

Qy   1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713
          |||||||||:::|||   ||||||||||||||||||||||||||||||||||||||||||
Db   5301 TATGTTAAAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGC 5360

Qy   1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIle 1733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5361 ATGATCTGCTTGTTCCAAATCACCACCTCTGCCGGCTGGGACGGACTGCTGGCCCCCATC 5420

Qy   1734 LeuAsnSerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLys 1753
          ||||||||   ||||||||||||||||||:::   ::::::||||||||||||||||||
Db   5421 CTCAACAGCGCACCTCCCGACTGTGACCCCGATGCAATTCACCCTGGAAGCTCGGTGAAG 5480

Qy   1754 GlyAspCysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSer 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5481 GGGGACTGTGGGAACCCATCCGTGGGGATTTTCTTTTTTGTCAGCTACATCATCATATCC 5540

Qy   1774 PheLeuValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThr 1793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5541 TTCCTGGTGGTGGTGAACATGTACATCGCTGTCATCCTGGAGAACTTCAGCGTCGCCACC 5600

Qy   1794 GluGluSerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGlu 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5601 GAAGAAAGTGCAGAGCCCCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAG 5660

Qy   1814 LysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAla 1833
          ||||||||||||||||||||||||||:::||||||   |||||||||   |||||||||
Db   5661 AAGTTCGACCCTGACGCCACTCAGTTCATAGAGTTCTGCAAGCTTTCTGACTTTGCAGCT 5720

Qy   1834 AlaLeuGluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAsp 1853
          ||||||:::|||||||||   :::   :::||||||||||:::|||||||||||||||||
Db   5721 GCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACAAAGTCCAGCTCATTGCCATGGAC 5780

Qy   1854 LeuProMetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLys 1873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5781 CTGCCCATGGTGAGTGGAGACCGCATCCACTGCCTGGACATCTTGTTTGCTTTTACAAAG 5840

Qy   1874 ArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPhe 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   5841 CGGGTCCTGGGCGAGAGTGGAGAGATGGACGCTCTTCGAATCCAGATGGAAGATCGCTTC 5900

Qy   1894 MetAlaSerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLys 1913
          ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db   5901 ATGGCTTCCAACCCCTCCAAGGTCTCTTATGAGCCCATTACCACCACCCTGAAACGGAAA 5960

Qy   1914 GlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArg 1933
          ||||||||||||||||||   ||||||||||||   ||||||   :::|||||||||:::
Db   5961 CAAGAGGAGGTGTCTGCTGCTATCATTCAGCGTAATTATAGATGTTATCTTTTAAAGCAA 6020

Qy   1934 ThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeu 1953
             :::|||      |||      |||:::|||      |||||||||      :::|||
Db   6021 CGGTTAAAAAACATATCGAGTAAATACGACAAAGAGACAATCAAGGGAAGGATTGACTTG 6080

Qy   1954 LeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThr 1973
          ||||||   |||||||:::||||||::::::|||   ||||||      |||||||||
Db   6081 CCTATAAAAGGAGATATGGTTATTGACAAATTGAATGGGAATTCCACCCCAGAAAAGACG 6140

Qy   1974 AspLeuThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIle 1993
          |||   :::   ||||||   :::   ||||||||||||||||   ||||||||||||
Db   6141 GATGGGAGTTCCTCCACAACCTCT---CCTCCTTCCTATGACAGTGTAACAAAACCAGAT 6197

Qy   1994 ValGluLysHisGluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
             ||||||   |||::::::      :::::::::   |||||||||
Db   6198 AAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAATCAAAGGGAAA 6245

RESULT 6
US-09-930-871-15
; Sequence 15, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucl
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 4362
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-15

Alignment Scores:
Pred. No.:              0              Length:          4362
Score:                  7511.00        Matches:         1446
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            72.24%         Indels:          0
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DB:                    10          Gaps:          0

US-09-930-871-12 (1-2009) x US-09-930-871-15 (1-4362)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu  20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA  60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp  40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu  80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
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Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   1441 AlaValAspSerArgAsn 1446
          |||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAAT 4338

RESULT 7
US-09-930-871-5
; Sequence 5, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4329
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-5

Alignment Scores:
Pred. No.:                0              Length:          4329
Score:                    7438.50        Matches:         1435
Percent Similarity:       99.24%         Conservative:    0
Best Local Similarity:    99.24%         Mismatches:      0
Query Match:              71.54%         Indels:          11
DB:                       10             Gaps:            1

US-09-930-871-12 (1-2009) x US-09-930-871-5 (1-4329)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240

Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807
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Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsn 1446
          |||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAAT 4305

RESULT 8
US-09-930-871-17
; Sequence 17, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 4179
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-17

Alignment Scores:
Pred. No.:              0              Length:          4179
Score:                  7181.00        Matches:         1392
Percent Similarity:     96.87%         Conservative:    0
Best Local Similarity:  96.87%         Mismatches:      1
Query Match:            69.07%         Indels:          45
DB:                     10             Gaps:            1

US-09-930-871-12 (1-2009) x US-09-930-871-17 (1-4179)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy    1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy    1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy    1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy    1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy    1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy    1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy    1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy    1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy    1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy    1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy    1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy    1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy    1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy    1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
           ||||||||||||
Db    4141 ACTGGTGACAGGCC---------------------------------------------- 4154

Qy    1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db    4154 ---------------------------------------------------------- 4154

Qy    1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIle 1437
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Db    4155 --------------------------ACATTCAAAGGATGGATGGATATA 4178

RESULT 9
US-09-930-871-7
; Sequence 7, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 4146
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-7

Alignment Scores:
Pred. No.:                0              Length:          4146
Score:                    7108.50        Matches:         1381
Percent Similarity:       96.10%         Conservative:    0
Best Local Similarity:    96.10%         Mismatches:      1
Query Match:              68.37%         Indels:          56
DB:                       10             Gaps:            2

US-09-930-871-12 (1-2009) x US-09-930-871-7 (1-4146)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240

Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260

Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280

Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

Db   4108 ACTGGTGACAGGCC---------------------------------------------- 4121

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db   4121 ---------------------------------------------------------- 4121

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIle 1437

Db   4122 ----------------------------ACATTCAAAGGATGGATGGATATA 4145

RESULT 10
US-09-930-871-19
; Sequence 19, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 4197
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-19

Alignment Scores:
Pred. No.:              0           Length:          4197
Score:                  7105.50     Matches:         1377
Percent Similarity:     98.43%      Conservative:    0
Best Local Similarity:  98.43%      Mismatches:      0
Query Match:            68.34%      Indels:          22
DB:                     10          Gaps:            1

US-09-930-871-12 (1-2009) x US-09-930-871-19 (1-4197)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20

Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40

Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg---------------- 1334
          ||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGATAATCTTGCTCCAACT 4020

Qy   1335 ----------------------------------------------ValValValAsnAl 1339
                                                         ||||||||||||
Db   4021 TGGATGGGGTGGAGCGCTGGTTCCTCCCCTGAGCCCTTTATTATGGGTGGTTGTGAATGC 4080

Qy   1339 aLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLe 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4140

Qy   1359 uIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIle 1377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATT 4195
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RESULT 11
US-09-930-871-9
; Sequence 9, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4164
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-9

Alignment Scores:

Pred. No.:	0	Length:	4164
Score:	7033.00	Matches:	1366
Percent Similarity:	97.64%	Conservative:	0
Best Local Similarity:	97.64%	Mismatches:	0
Query Match:	67.64%	Indels:	33
DB:	10	Gaps:	2

US-09-930-871-12 (1-2009) x US-09-930-871-9 (1-4164)

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Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
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Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg---------------------- 1334
          ||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGATAATCTTGCTCCAACT 3987

Qy   1335 ----------------------------------------------ValValValAsnAl 1339
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Db   3988 TGGATGGGGTGGAGCGCTGGTTCCTCCCCTGAGCCCTTTATTATGGGTGGTTGTGAATGC 4047

Qy   1339 aLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLe 1359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4107

Qy   1359 uIlePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIle 1377
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Db   4108 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATT 4162
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RESULT 12
US-09-840-125-3
; Sequence 3, Application US/09840125
; Patent No. US20020061524A1
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME

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;  FILE REFERENCE: 2323-155
;  CURRENT APPLICATION NUMBER: US/09/840,125
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: 09/634,920
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,488
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6048
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(6048)
US-09-840-125-3

Alignment Scores:
Pred. No.:                0              Length:          6048
Score:                    6312.00        Matches:         1287
Percent Similarity:       72.72%         Conservative:    230
Best Local Similarity:    61.70%         Mismatches:      386
Query Match:              60.71%         Indels:          184
DB:                       10             Gaps:            30

US-09-930-871-12 (1-2009) x US-09-840-125-3 (1-6048)

Qy      6 LeuValProProGlyProAspSerPheAsnPhePheThrArgGluSerLeuAlaAlaIle 25
          |||:::|||   |||      ||||||      ||||||||||||||||||||||||||||
Db     13 CTATTACCTCGGGGCACCAGCAGCTTCCGCAGGTTCACACGGGAGTCCCTGGCAGCCATC 72

Qy     26 GluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLysLysAsp------ 43
          |||:::|||:::||||||:::::::|||:::                 ::::::
Db     73 GAGAAGCGCATGGCGGAGAAGCAAGCCCGCGGCTCAACCACCTTGCAGGAGAGCCGAGAG 132

Qy     44 ------AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
                ::::|||      |||:::|||      ||||||:::|||   |||   |||
Db    133 GGGCTGCCCGAGGAGGAGGCTCCCCGGCCCCAGCTGGACCTGCAGGCCTCCAAAAAGCTG 192

Qy     62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
          |||   :::|||||:::   |||   |||::::::   ||||||||||||||||||||||
Db    193 CCAGATCTCTATGGCAATCCACCCCAAGAGCTCATCGGAGAGCCCCTGGAGGACCTGGAC 252

Qy     82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
          |||:::|||      :::||||||||||||||||||||||||||||||   |||||||||
Db    253 CCCTTCTATAGCACCCAAAAGACTTTCATCGTACTGAATAAAGGCAAGACCATCTTCCGG 312

Qy    102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
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Db    313 TTCAGTGCCACCAACGCCTTGTATGTCCTCAGTCCCTTCCACCCAGTTCGGAGAGCGGCT 372

Qy    122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
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Db    373 GTGAAGATTCTGGTTCACTCGCTCTTCAACATGCTCATCATGTGCACCATCCTCACCAAC 432

Qy    142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
          ||||||||||||         :::||||||   |||||||||   ||||||||||||||||
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Qy    162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
          |||   ||||||||||||||||||||||:::||||||::||||||   |||||||||
Db    493 ACCGCCATTTACACCTTTGAGTCTCTGGTCAAGATTCTGGCTCGAGCTTTCTGCCTGCAC 552

Qy    182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
             ||||||||||||||||||||||||||||||||||||||:::||||||      |||
Db    553 GCGTTCACTTTCCTTCGGGACCCATGGAACTGGCTGGACTTTAGTGTGATTATCATGGCA 612

Qy    202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 TACACAACTGAATTTGTGGACCTGGGCAATGTCTCAGCCTTACGCACCTTCCGAGTCCTC 672

Qy    222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
          |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db    673 CGGGCCCTGAAAACTATATCAGTCATTTCAGGGCTGAAGACCATCGTGGGGGCCCTGATC 732

Qy    242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
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Qy    282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
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Qy    317 ---TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeu 335
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Db    916 CTTTACCTCAGTGATCCAGAAAATTACCTGCTCAAGAACGGCACCTCTGATGTGTTACTG 975

Qy    336 CysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGly 355
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Qy    416 AsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGlu 435
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Db   1216 AACCTGATCCTGGCCGTGGTCGCAATGGCCTATGAGGAGCAAAACCAAGCCACCATCGCT 1275

Qy    436 GluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGln 455
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Db   1336 GAGGCCCTCACCATCAGGGGTGTGGATACCGTGTCCCGT---------------------- 1374

Qy    476 AlaGlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLys 495
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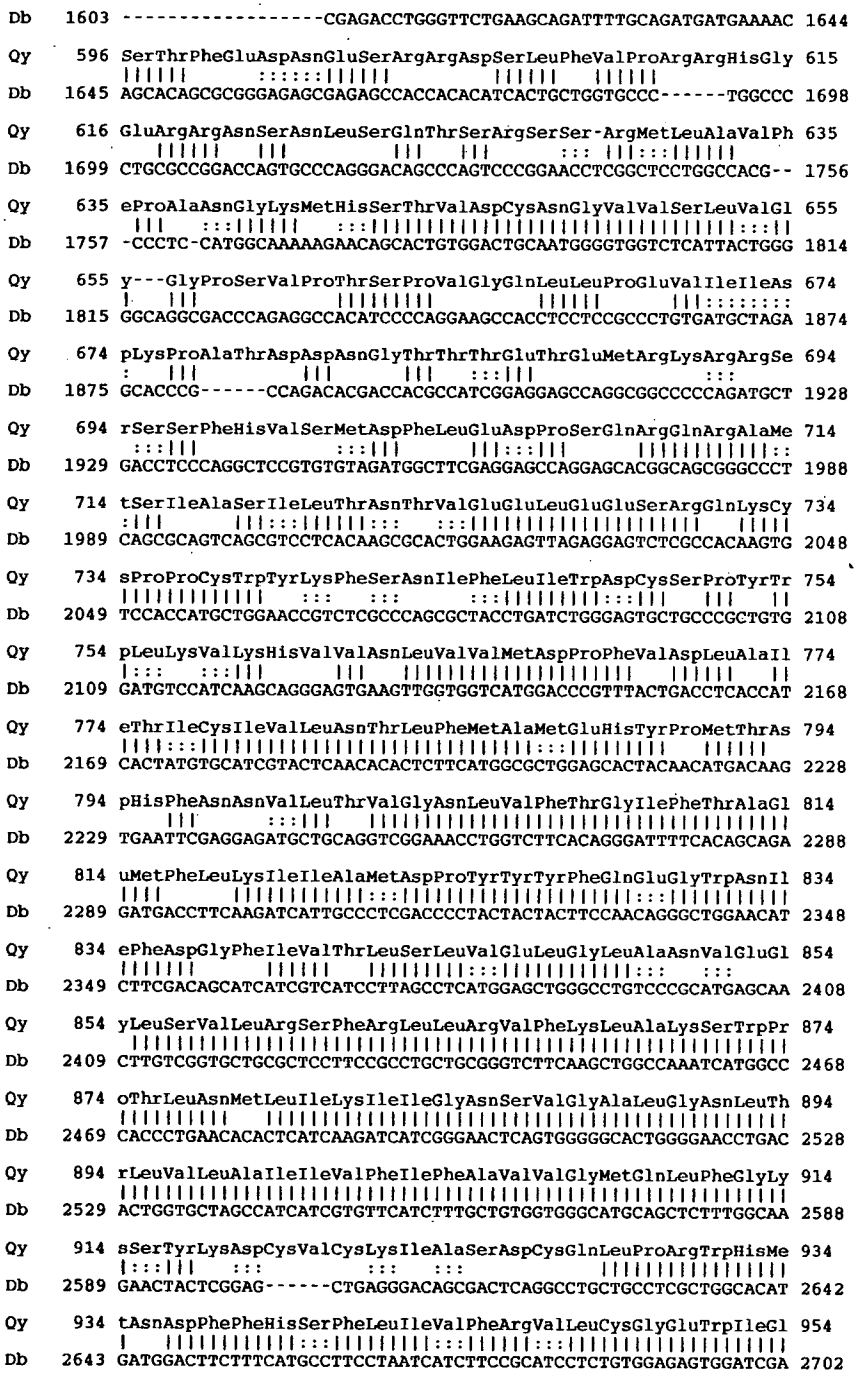
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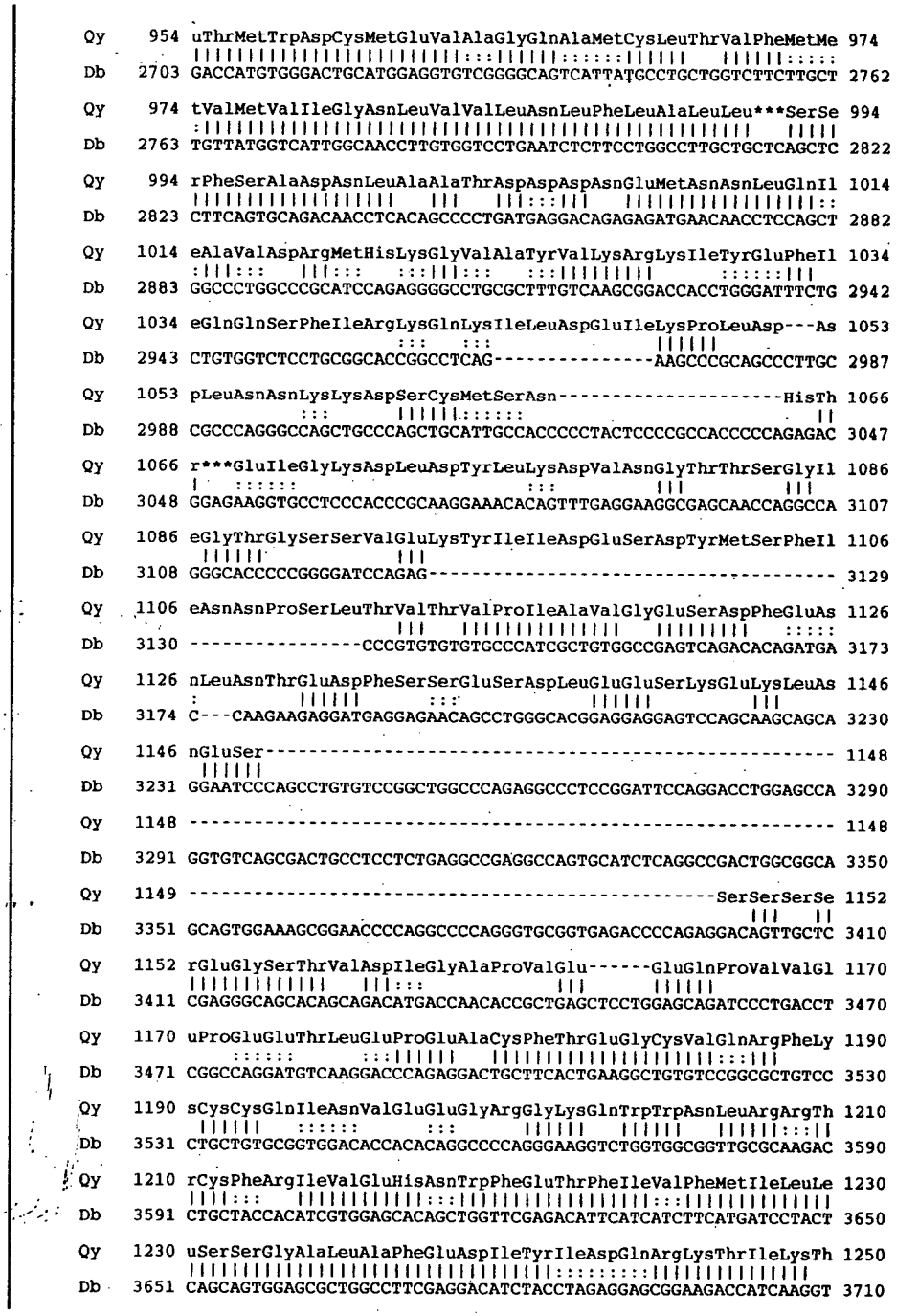
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Db 1645 AGCACAGCGCGGGAGAGCGAGAGCCACCACACATCACTGCTGGTGCCC------TGGCCC 1698
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSer-ArgMetLeuAlaValPh 635
Db 1699 CTGCGCCGGACCAGTGCCCAGGGACAGCCCAGTCCCGGAACCTCGGCTCCTGGCCACG-- 1756
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RESULT 13
US-09-896-994-1
; Sequence 1, Application US/09896994
; Publication No. US20030074024A1
;   GENERAL INFORMATION:
;        APPLICANT: Ken Stokes
;                   Jos e Morissette
;        TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                            SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/896,994
;             FILING DATE: 02-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/514,907
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul K. Legaard
;             REGISTRATION NUMBER: 38,534
;             REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 568-3100
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;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6048 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-896-994-1

Alignment Scores:
Pred. No.:                0              Length:          6048
Score:                    6310.00        Matches:         1286
Percent Similarity:       72.72%         Conservative:    231
Best Local Similarity:    61.65%         Mismatches:      386
Query Match:              60.69%         Indels:          184
DB:                       9              Gaps:            30

US-09-930-871-12 (1-2009) x US-09-896-994-1 (1-6048)

Qy      6 LeuValProProGlyProAspSerPheAsnPhePheThrArgGluSerLeuAlaAlaIle 25
          |||:::|||   |||      ||||||     |||||||||||||||||||||||||||
Db     13 CTATTACCTCGGGGCACCAGCAGCTTCCGCAGGTTCACACGGGAGTCCCTGGCAGCCATC 72

Qy     26 GluArgArgIleAlaGluGluLysAlaLysAsnProLysProAspLysLysAsp------ 43
          |||:::|||:::||||||::::::|||:::             ::::::
Db     73 GAGAAGCGCATGGCGGAGAAGCAAGCCCGCGGCTCAACCACCTTGCAGGAGAGCCGAGAG 132

Qy     44 ------AspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsnLeu 61
                  :::|||     |||:::|||     ||||||:::|||   |||   |||
Db    133 GGGCTGCCCGAGGAGGAGGCTCCCCGGCCCCAGCTGGACCTGCAGGCCTCCAAAAAGCTG 192

Qy     62 ProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeuAsp 81
          |||   :::||||||:::   |||   |||::::::   ||||||||||||||||||||
Db    193 CCAGATCTCTATGGCAATCCACCCCAAGAGCTCATCGGAGAGCCCCTGGAGGACCTGGAC 252

Qy     82 ProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePheArg 101
          |||:::|||      :::||||||||||||||||||||||||||||||||   |||||||||
Db    253 CCCTTCTATAGCACCCAAAAGACTTTCATCGTACTGAATAAAGGCAAGACCATCTTCCGG 312

Qy    102 PheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIleAla 121
          ||||||||||||:::||||||||:::|||:::||||||:::|||:::|||   |||
Db    313 TTCAGTGCCACCAACGCCTTGTATGTCCTCAGTCCCTTCCACCCAGTTCGGAGAGCGGCT 372

Qy    122 IleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThrAsn 141
          :::||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db    373 GTGAAGATTCTGGTTCACTCGCTCTTCAACATGCTCATCATGTGCACCATCCTCACCAAC 432

Qy    142 CysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThrPhe 161
          ||||||||||||          :::||||||   |||||||||   ||||||||||||||||
Db    433 TGCGTGTTCATGGCCCAGCACGACCCTCCACCCTGGACCAAGTATGTCGAGTACACCTTC 492

Qy    162 ThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeuGlu 181
          |||   ||||||||||||||||||:::||||||:::||||||   |||||||||
Db    493 ACCGCCATTTACACCTTTGAGTCTCTGGTCAAGATTCTGGCTCGAGCTTTCTGCCTGCAC 552

Qy    182 AspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPheAla 201
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Db    553 GCGTTCACTTTCCTTCGGGACCCATGGAACTGGCTGGACTTTAGTGTGATTATCATGGCA 612

Qy    202 TyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgValLeu 221
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613 TACACAACTGAATTTGTGGACCTGGGCAATGTCTCAGCCTTACGCACCTTCCGAGTCCTC 672

Qy    222 ArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeuIle 241
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    673 CGGGCCCTGAAAACTATATCAGTCATTTCAGGGCTGAAGACCATCGTGGGGGCCCTGATC 732

Qy    242 GlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerValPhe 261
          ||||||||||||||||||:::||||||||||:::||||||||||||||||||||||||||
Db    733 CAGTCTGTGAAGAAGCTGGCTGATGTGATGGTCCTCACAGTCTTCTGCCTCAGCGTCTTT 792

Qy    262 AlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrpPro 281
          |||||||||||||||||||||||||||||||||||||:::||||||:::
Db    793 GCCCTCATCGGCCTGCAGCTCTTCATGGGCAACCTAAGGCACAAGTGTGTG--------- 843

Qy    282 ProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyrAsn 301
                                              :::|||   |||         |||
Db    844 ----------------------------------CGCAACTTCACAGCG---CTCAAC 864

Qy    302 GlyThrLeuIleAsnGluThrValPheGluPheAsp---------TrpLysSer------ 316
          ||||||      |||   :::|||   |||   |||         |||:::|||
Db    865 GGCACC------AACGGCTCCGTG---GAGGCCGACGGCTTGGTCTGGGAATCCCTGGAC 915

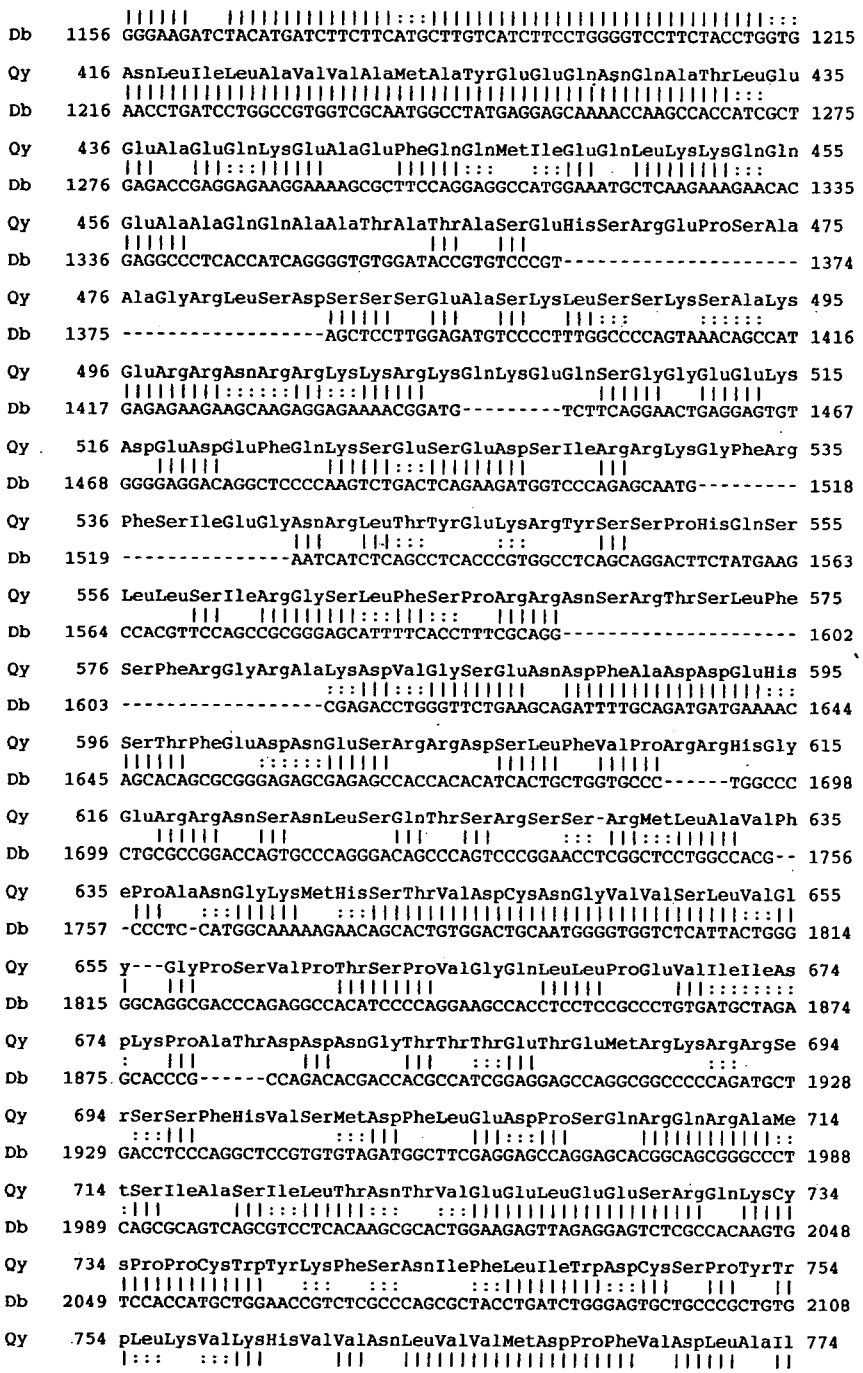
Qy    317 ---TyrIleGlnAspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeu 335
             |||:::  |||         :::            |||      |||  ||||||
Db    916 CTTTACCTCAGTGATCCAGAAAATTACCTGCTCAAGAACGGCACCTCTGATGTGTTACTG 975

Qy    336 CysGlyAsnSerSerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGly 355
          ||||||||||||||||||||||   ||||||||||||||   |||:::|||||||||
Db    976 TGTGGGAACAGCTCTGACGCTGGGACATGTCCGGAGGGCTACCGGTGCCTAAAGGCAGGC 1035

Qy    356 ArgAsnProAsnTyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeu 375
          ||||||:::::|||||||||||||:::|||:::|||||||||||:::|||
Db   1036 GAGAACCCCGACCACGGCTACACCAGCTTCGATTCCTTTGCCTGGGCCTTTCTTGCACTC 1095

Qy    376 PheArgLeuMetThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAla 395
          ||||||||||||||||||   ||||||   |||||||||   |||||||||:::|||
Db   1096 TTCCGCCTGATGACGCAGGACTGCTGGGAGCGCCTCTATCAGCAGACCCTCAGGTCCGCA 1155

Qy    396 GlyLysThrTyrMetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIle 415
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Db 1156 GGGAAGATCTACATGATCTTCTTCATGCTTGTCATCTTCCTGGGGTCCTTCTACCTGGTG 1215
Qy 416 AsnLeuIleLeuAlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGlu 435
Db 1216 AACCTGATCCTGGCCGTGGTCGCAATGGCCTATGAGGAGCAAAACCAAGCCACCATCGCT 1275
Qy 436 GluAlaGluGlnLysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGln 455
Db 1276 GAGACCGAGGAGAAGGAAAAGCGCTTCCAGGAGGCCATGGAAATGCTCAAGAAAGAACAC 1335
Qy 456 GluAlaAlaGlnGlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAla 475
Db 1336 GAGGCCCTCACCATCAGGGGTGTGGATACCGTGTCCCGT---------- 1374
Qy 476 AlaGlyArgLeuSerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLys 495
Db 1375 ----------AGCTCCTTGGAGATGTCCCCTTTGGCCCCAGTAAACAGCCAT 1416
Qy 496 GluArgArgAsnArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLys 515
Db 1417 GAGAGAAGAAGCAAGAGGAGAAAACGGATG---------TCTTCAGGAACTGAGGAGTGT 1467
Qy 516 AspGluAspGluPheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArg 535
Db 1468 GGGGAGGACAGGCTCCCCAAGTCTGACTCAGAAGATGGTCCCAGAGCAATG--------- 1518
Qy 536 PheSerIleGluGlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSer 555
Db 1519 --------------AATCATCTCAGCCTCACCCGTGGCCTCAGCAGGACTTCTATGAAG 1563
Qy 556 LeuLeuSerIleArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPhe 575
Db 1564 CCACGTTCCAGCCGCGGGAGCATTTTCACCTTTCGCAGG---------- 1602
Qy 576 SerPheArgGlyArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHis 595
Db 1603 ----------CGAGACCTGGGTTCTGAAGCAGATTTTGCAGATGATGAAAAC 1644
Qy 596 SerThrPheGluAspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGly 615
Db 1645 AGCACAGCGCGGGAGAGCGAGAGCCACCACACATCACTGCTGGTGCCC------TGGCCC 1698
Qy 616 GluArgArgAsnSerAsnLeuSerGlnThrSerArgSerSer-ArgMetLeuAlaValPh 635
Db 1699 CTGCGCCGGACCAGTGCCCAGGGACAGCCCAGTCCCGGAACCTCGGCTCCTGGCCACG-- 1756
Qy 635 eProAlaAsnGlyLysMetHisSerThrValAspCysAsnGlyValValSerLeuValGl 655
Db 1757 -CCCTC-CATGGCAAAAAGAACAGCACTGTGGACTGCAATGGGGTGGTCTCATTACTGGG 1814
Qy 655 y---GlyProSerValProThrSerProValGlyGlnLeuLeuProGluValIleIleAs 674
Db 1815 GGCAGGCGACCCAGAGGCCACATCCCCAGGAAGCCACCTCCTCCGCCCTGTGATGCTAGA 1874
Qy 674 pLysProAlaThrAspAspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSe 694
Db 1875 GCACCCG------CCAGACACGACCACGCCATCGGAGGAGCCAGGCGGCCCCCAGATGCT 1928
Qy 694 rSerSerPheHisValSerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMe 714
Db 1929 GACCTCCCAGGCTCCGTGTGTAGATGGCTTCGAGGAGCCAGGAGCACGGCAGCGGGCCCT 1988
Qy 714 tSerIleAlaSerIleLeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCy 734
Db 1989 CAGCGCAGTCAGCGTCCTCACAAGCGCACTGGAAGAGTTAGAGGAGTCTCGCCACAAGTG 2048
Qy 734 sProProCysTrpTyrLysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTr 754
Db 2049 TCCACCATGCTGGAACCGTCTCGCCCAGCGCTACCTGATCTGGGAGTGCTGCCCGCTGTG 2108
Qy 754 pLeuLysValLysHisValValAsnLeuValValMetAspProPheValAspLeuAlaIl 774
Db 2109 GATGTCCATCAAGCAGGGAGTGAAGTTGGTGGTCATGGACCCGTTTACTGACCTCACCAT 2168
Qy 774 eThrIleCysIleValLeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAs 794
Db 2169 CACTATGTGCATCGTACTCAACACACTCTTCATGGCGCTGGAGCACTACAACATGACAAG 2228
Qy 794 pHisPheAsnAsnValLeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGl 814
Db 2229 TGAATTCGAGGAGATGCTGCAGGTCGGAAACCTGGTCTTCACAGGGATTTTCACAGCAGA 2288
Qy 814 uMetPheLeuLysIleIleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIl 834
Db 2289 GATGACCTTCAAGATCATTGCCCTCGACCCCTACTACTACTTCCAACAGGGCTGGAACAT 2348
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Qy 854 yLeuSerValLeuArgSerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpPr 874
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Qy 874 oThrLeuAsnMetLeuIleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuTh 894
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Qy 894 rLeuValLeuAlaIleIleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLy 914
Db 2529 ACTGGTGCTAGCCATCATCGTGTTCATCTTTGCTGTGGTGGGCATGCAGCTCTTTGGCAA 2588
Qy 914 sSerTyrLysAspCysValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMe 934
Db 2589 GAACTACTCGGAG------CTGAGGGACAGCGACTCAGGCCTGCTGCCTCGCTGGCACAT 2642
Qy 934 tAsnAspPhePheHisSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGl 954
Db 2643 GATGGACTTCTTTCATGCCTTCCTAATCATCTTCCGCATCCTCTGTGGAGAGTGGATCGA 2702
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Db 2763 TGTTATGGTCATTGGCAACCTTGTGGTCCTGAATCTCTTCCTGGCCTTGCTGCTCAGCTC 2822
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Qy 1034 eGlnGlnSerPheIleArgLysGlnLysIleLeuAspGluIleLysProLeuAsp---As 1053
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Qy 1066 r***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsnGlyThrThrSerGlyIl 1086
Db 3048 GGAGAAGGTGCCTCCCACCCGCAAGGAAACACAGTTTGAGGAAGGCGAGCAACCAGGCCA 3107
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Qy 1170 uProGluGluThrLeuGluProGluAlaCysPheThrGluGlyCysValGlnArgPheLy 1190
Db 3471 CGGCCAGGATGTCAAGGACCCAGAGGACTGCTTCACTGAAGGCTGTGTCCGGCGCTGTCC 3530
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Qy 1210 rCysPheArgIleValGluHisAsnTrpPheGluThrPheIleValPheMetIleLeuLe 1230
Db 3591 CTGCTACCACATCGTGGAGCACAGCTGGTTCGAGACATTCATCATCTTCATGATCCTACT 3650
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Qy 1250 rMetLeuGluTyrAlaAspLysValPheThrTyrIlePheIleLeuGluMetLeuLeuLy 1270
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Qy 1270 sTrpValAlaTyrGlyTyrGlnThrTyrPheThrAsnAlaTrpCysTrpLeuAspPheLe 1290
Db 3771 GTGGGTGGCCTACGGCTTCAAGAAGTACTTCACCAATGCCTGGTGCTGGCTCGACTTCCT 3830
Qy 1290 uIleValAspValSerLeuValSerLeuThrAlaAsnAlaLeuGlyTyrSerGluLeuGl 1310
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Db 3951 TGAGGGCATGAGGGTGGTGGTCAATGCCCTGGTGGGCGCCATCCCGTCCATCATGAACGT 4010
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Qy 1527 yAsnLysPheGlnGlyMetValPheAspPheValThrArgGlnValPheAspIleSerIl 1547
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Db 4722 GTGTATTGTCAAGCTGGCTGCCCTGCGCCACTACTACTTCACCAACAGCTGGAATATCTT 4781
Qy 1607 eAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLy 1627
Db 4782 CGACTTCGTGGTTGTCATCCTCTCCATCGTGGGCACTGTGCTCTCGGACATCATCCAGAA 4841
Qy 1627 sTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLe 1647
Db 4842 GTACTTCTTCTCCCCGACGCTCTTCCGAGTCATCCGCCTGGCCCGAATAGGCCGCATCCT 4901
Qy 1647 uArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLe 1667
Db 4902 CAGACTGATCCGAGGGGCCAAGGGGATCCGCACGCTGCTCTTTGCCCTCATGATGTCCCT 4961
Qy 1667 uProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePh 1687
Db 4962 GCCTGCCCTCTTCAACATCGGGCTGCTGCTCTTCCTCGTCATGTTCATCTACTCCATCTT 5021
Qy 1687 eGlyMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPh 1707
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Db 5142 TGGCCTCCTCAGCCCCATCCTCAACACTGGGCCGCCCTACTGCGACCCCACTCTGCCCAA 5201
Qy 1747 nProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePheVa 1767
Db 5202 CAGCAATGGCTCT---CGGGGGGACTGCGGGAGCCCAGCCGTGGGCATCCTCTTCTTCAC 5258
Qy 1767 lSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeuGl 1787
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Qy 1787 uAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGluMe 1807

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Db   5319 GAACTTCAGCGTGGCCACGGAGGAGAGCACCGAGCCCCTGAGTGAGGACGACTTCGATAT 5378

Qy   1807 tPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGluLy 1827

Db   5379 GTTCTATGAGATCTGGGAGAAATTTGACCCAGAGGCCACTCAGTTTATTGAGTATTCGGT 5438

Qy   1827 sLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLysLe 1847

Db   5439 CCTGTCTGACTTTGCCGACGCCCTGTCTGAGCCACTCCGTATCGCCAAGCCCAACCAGAT 5498

Qy   1847 uGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAspIl 1867

Db   5499 AAGCCTCATCAACATGGACCTGCCCATGGTGAGTGGGGACCGCATCCATTGCATGGACAT 5558

Qy   1867 eLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArgIl 1887

Db   5559 TCTCTTTGCCTTCACCAAAAGGGTCCTGGGGGAGTCTGGGGAGATGGACGCCCTGAAGAT 5618

Qy   1887 eGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIleTh 1907

Db   5619 CCAGATGGAGGAGAAGTTCATGGCAGCCAACCCATCCAAGATCTCCTACGAGCCCATCAC 5678

Qy   1907 rThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrAr 1927

Db   5679 CACCACACTCCGGCGCAAGCACGAAGAGGTGTCGGCCATGGTTATCCAGAGAGCCTTCCG 5738

Qy   1927 gArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLysIl 1947

Db   5739 CAGGCACCTGCTGCAACGCTCTTTGAAGCATGCCTCCTTCCTCTTCCGTCAGCAGGCGGG 5798

Qy   1947 eLysGlyGlyAlaAsnLeuLeuIleLysGluAsp----------MetIleIl 1961

Db   5799 CAGCGGC----------CTCTCCGAAGAGGATGCCCCTGAGCGAGAGGGCCTCATCGC 5846

Qy   1961 eAspArgIleAsnGluAsn---------SerIleThrGluLysThrAspLeuThrMetSe 1978

Db   5847 CTACGTGATGAGTGAGAACTTCTCCCGACCCCTTGGCCCACCCTCCAGCTCCTCCATCTC 5906

Qy   1978 rThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGl 1998

Db   5907 CTCCACTTCCTTCCCACCCTCCTATGACAGTGTCACTAGAGCCACCAGCGATAACCTCCA 5966

Qy   1998 uGlnGluGlyLysAsp 2003

Db   5967 GGTGCGGGGGTCTGAC 5982

RESULT 14
US-09-864-761-10189/c
; Sequence 10189, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10189
;  LENGTH: 1992
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: MAP TO AC010127.3
;  OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
;  OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-10189

Alignment Scores:
Pred. No.:                1.1e-201      Length:          1992
Score:                    2037.00       Matches:         442
Percent Similarity:       70.74%        Conservative:    27
Best Local Similarity:    66.67%        Mismatches:      79
Query Match:              19.59%        Indels:          116
DB:                       10            Gaps:            12

US-09-930-871-12 (1-2009) x US-09-864-761-10189 (1-1992)

Qy   1371 GlyLysPheTyrHisCysIleAsnThrThrThrGlyAspArgPheAspIleGluAspVal 1390

Db   1984 GGATCCTTTCAGAAATGCACCAGAACATACATAAATGAGTATATAAAAATATTAGAGTGG 1925

Qy   1391 Asn---------------AsnHisThrAspCysLeuLysLeuIleGluArgAsnGluThr 1405

Db   1924 AATTTAAGTAAGTACCAAGATCATGGGGAGATGAAAGTAGCATCAAAAGCTACCAATACT 1865

Qy   1406 AlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPheGlyTyrLeuSerLeu 1425

Db   1864 TTCAGATGGAAAAGGAGTAAATAGAGAATTTAGAATATGGCAATT-------------- 1820

Qy   1426 LeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAlaAlaValAspSerArg 1445

Db   1820 ------------------------------------------------------------ 1820

Qy   1446 AsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyrLeu------------ 1461

Db   1819 ----------------------TCAGAAAAAGTCACTGTATACATATAAACTTGTACC 1784

Qy   1462 TyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPhe---IleGly 1480

Db   1783 TATACTGTTGGGCTGCTACTGTTCGGCCAAATGTGCATTTTTAACTTATTTTCTTTTTAA 1724

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500

Db   1723 ATTCTGACTTGGGACTTTACATAAACTAAAAGTAGTTTATAAACATCT------------ 1676
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Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAla------MetLysLysLeuGlySerLysLys 1518
          :::::::::|||||||||||||||||         :::|||   |||  :::
Db   1675 CTTAAAGATAAAAAAAAGTACTATAATCC-TTATAATTGAAATTATTGCTGAAT------ 1623

Qy   1519 ProGlnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheVal 1538

Db   1623 ------------------------------------------------------------ 1623

Qy   1539 ThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMet 1558
                   |||   |||   |||      ::::::|||
Db   1622 -----------TTCAAAATTAAGATTTATAATATATTATGT----------------- 1593

Qy   1559 MetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeu 1578
                                                |||||:::     :::   :::
Db   1592 ----------------------------------ACAATTATATATATATTATATATA 1569

Qy   1579 ValPheIleValLeuPheThrGlyGluCysValLeuLysLeu----------------- 1592
          |||   |||        ||||||         |||   |||
Db   1568 GTTGTCATATTTAATATAACTGGGTTCAGGACTCTGAACCTTACCTTGGAGCTTTAGAAG 1509

Qy   1593 ---------IleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsn---------Ile 1606
                       |||   |||   :::||||||   ||||||              :::
Db   1508 AAACATATGTTTATTTTAACGCATGATTTCTTCACT---GGTTGGTATTCTCATTGTTTA 1452

Qy   1607 PheAspPheValValValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGlu 1626
          |||                          :::||||||||||||||||||||||||||||
Db   1451 TTC--------------------------ATAGGTATGTTTCTTGCCGAGCTGATAGAA 1419

Qy   1627 LysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIle 1646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 AAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATC 1359

Qy   1647 LeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSer 1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 CTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCC 1299

Qy   1667 LeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIle 1686
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 CTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATC 1239

Qy   1687 PheGlyMetSerAsnPheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsn 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 TTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAAC 1179

Qy   1707 PheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrp 1726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 TTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGG 1119

Qy   1727 AspGlyLeuLeuAlaProIleLeuAsnSerLysProProAspCysAspProAsnLysVal 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 GATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTT 1059

Qy   1747 AsnProGlySerSerValLysGlyAspCysGlyAsnProSerValGlyIlePhePhePhe 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 AACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTT 999

Qy   1767 ValSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAlaValIleLeu 1786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 GTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTG 939

Qy   1787 GluAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAspAspPheGlu 1806
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 GAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAG 879

Qy   1807 MetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGlu 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 ATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAA 819

Qy   1827 LysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLys 1846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 AAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAA 759

Qy   1847 LeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAsp 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 CTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGAT 699

Qy   1867 IleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArg 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 ATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGA 639

Qy   1887 IleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIle 1906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 ATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATC 579

Qy   1907 ThrThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIleGlnArgAlaTyr 1926
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 ACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTAC 519

Qy   1927 ArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyrAsnLysAsnLys 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 AGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAAACAAA 459

Qy   1947 IleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAspArgIleAsnGlu 1966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 ATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGACAGAATAAATGAA 399

Qy   1967 AsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAlaCysProProSerTyr 1986
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 AACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGTCCACCTTCCTAT 339

Qy   1987 AspArgValThrLysProIleValGluLysHisGluGlnGluGlyLysAspGluLysAla 2006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 GACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAAGATGAAAAAGCC 279

Qy   2007 LysGlyLys 2009
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Db    278 AAAGGGAAA 270
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RESULT 15
US-09-864-761-18334/c
; Sequence 18334, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

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;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18334
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
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;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
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;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
;   OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
US-09-864-761-18334

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Score:                    1967.50         Matches:        390
Percent Similarity:       96.56%          Conservative:   3
Best Local Similarity:    95.82%          Mismatches:     1
Query Match:              18.92%          Indels:         13
DB:                       10              Gaps:           3

US-09-930-871-12 (1-2009) x US-09-864-761-18334 (1-1194)

Qy   1599 TyrPheThrIleGlyTrpAsn---------IlePheAspPheValValValIleLeuSer 1615
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Db   1191 TTCTTCACT---GGTTGGTATTCTCATTGTTTATTC---------------------- 1159

Qy   1616 IleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPhe 1635
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Db   1158 ---ATAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTC 1102

Qy   1636 ArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGly 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101 CGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGG 1042

Qy   1656 IleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeu 1675
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Db   1041 ATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTC 982

Qy   1676 LeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrVal 1695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981 CTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTT 922

Qy   1696 LysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIle 1715
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Db    921 AAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATC 862

Qy   1716 CysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsn 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 TGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAAC 802

Qy   1736 SerLysProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAsp 1755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 AGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGAC 742

Qy   1756 CysGlyAsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeu 1775
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Db    741 TGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTG 682

Qy   1776 ValValValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGlu 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 GTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAA 622

Qy   1796 SerAlaGluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPhe 1815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 AGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTT 562

Qy   1816 AspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeu 1835
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Db    561 GATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTT 502

Qy   1836 GluProProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuPro 1855
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Db    501 GAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCC 442

Qy   1856 MetValSerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgVal 1875
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Db    441 ATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTT 382

Qy   1876 LeuGlyGluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAla 1895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 CTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCT 322

Qy   1896 SerAsnProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGlu 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 TCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAG 262

Qy   1916 GluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrVal 1935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 GAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTA 202

Qy   1936 LysGlnAlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIle 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 AAACAAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATA 142

Qy   1956 LysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeu 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 AAAGAAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTG 82

Qy   1976 ThrMetSerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGlu 1995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 ACCATGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAA 22

Qy   1996 LysHisGluGlnGluGlyLys 2002
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Db     21 AAACATGAGCAAGAAGGCAAA 1

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Job time : 651 secs
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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 23, 2003, 02:49:16 ; Search time 7546 Seconds
(without alignments)
7748.150 Million cell updates/sec

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106490

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1970	98.1	5922	6	AX391142	AX391142 Sequence
3	1733	86.3	8378	6	AX164171	AX164171 Sequence
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13	701	34.9	4146	6	AX391136	AX391136 Sequence
14	670	33.3	4164	6	AX391138	AX391138 Sequence
15	403	20.1	1269	9	HSSCN1A	X65362 Homo sapien
16	403	20.1	1269	9	HUMSODCHAA	M91803 Human sodiu
c 17	392	19.5	190066	9	AC010127	AC010127 Homo sapi
18	392	19.5	191194	2	AC021673	AC021673 Homo sapi
19	375	18.7	8398	10	RNSCPIR	X03638 Rat brain m
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21	329	16.4	164928	2	AC129458	AC129458 Rattus no
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23	318	15.8	3403	6	AX164202	AX164202 Sequence
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25	161	8.0	1531	10	MUSSOCHA	L42341 Mus musculu
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ALIGNMENTS

RESULT 1

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LOCUS       AX391140               6030 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 11 from Patent WO0214498.
ACCESSION   AX391140
VERSION     AX391140.1  GI:19584237
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 11 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT     1786 a   1190 c   1345 g   1706 t      3 others
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Alignment Scores:
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Score:                    2007.00       Matches:         2009
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              99.90%        Indels:          0
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US-09-930-871-12 (1-2009) x AX391140 (1-6030)

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Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

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RESULT 2
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AX391142
LOCUS       AX391142               5922 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 13 from Patent WO0214498.
ACCESSION   AX391142
VERSION     AX391142.1  GI:19584238
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 13 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1746 a   1166 c   1320 g   1687 t      3 others
ORIGIN

Alignment Scores:
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Score:                    1970.00    Matches:        1972
Percent Similarity:       100.00%    Conservative:   0
Best Local Similarity:    100.00%    Mismatches:     0
Query Match:              98.06%     Indels:         0
DB:                       6          Gaps:           0

US-09-930-871-12 (1-2009) x AX391142 (1-5922)

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Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Qy   601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Qy   821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Qy   841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Qy   921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Qy  1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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RESULT 3
AX164171
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DEFINITION  Sequence 1 from Patent WO0138564.
ACCESSION   AX164171
VERSION     AX164171.1  GI:14545110
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 8378)
AUTHORS Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and Ragsdale,D.
TITLE Loci for idiopathic generalized epilepsy, mutations thereof and method using same to assess, diagnose, prognose or treat epilepsy
JOURNAL Patent: WO 0138564-A 1 31-MAY-2001;
McGill University (CA)
FEATURES Location/Qualifiers
source 1. .8378
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/db_xref="taxon:9606"
BASE COUNT 2496 a 1575 c 1782 g 2525 t
ORIGIN

Alignment Scores:

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Score:	1733.00	Matches:	2006
Percent Similarity:	99.75%	Conservative:	0
Best Local Similarity:	99.75%	Mismatches:	3
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US-09-930-871-12 (1-2009) x AX164171 (1-8378)

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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065
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Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2186 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2245

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2246 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2305

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2306 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2365

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2366 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2425

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2426 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2485

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2546 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2605

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2606 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2665

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Db   2666 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2725

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Db   2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Db   2966 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3025

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db   3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Db   3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAsnLe 1000
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Db   3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACAACCT 3264

Qy   1000 uAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHi 1020
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Db   3265 TGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCA 3324

Qy   1020 sLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleAr 1040
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Db   3325 CAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAG 3384

Qy   1040 gLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSe 1060
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Db   3385 GAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAG 3444

Qy   1060 rCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspValA 1080
          ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db   3445 TTGTATGTCCAATCATACAGC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAA 3503

Qy   1080 snGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluS 1100
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Db   3504 ATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAA 3563

Qy   1100 erAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValG 1120
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Db   3564 GTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAG 3623

Qy   1120 lyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluG 1140
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Db   3624 GAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAG 3683

Qy   1140 luSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG 1160
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Db   3684 AAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCG 3743

Qy   1160 lyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaC 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3744 GCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTT 3803

Qy   1180 ysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyA 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3804 GTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCA 3863

Qy   1200 rgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpP 1220
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Db   3864 GAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGT 3923

Qy   1220 heGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspI 1240
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Db   3924 TTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCG-GCATTTGAAGATA 3982

Qy   1240 leTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheT 1260
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Db   3983 TATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCA 4042

Qy   1260 hrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrP 1280
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Db   4043 CTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATT 4102

Qy   1280 heThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuT 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4103 TCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAA 4162

Qy   1300 hrAlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgA 1320
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Db   4163 CAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAG 4222

Qy   1320 laLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaL 1340
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Db   4223 CTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCC 4282

Qy   1340 euLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuI 1360
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Qy   1360 lePheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrT 1380
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Db   4343 TTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCA 4402

Qy   1380 hrThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuI 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4403 CAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAA 4462

Qy   1400 leGluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyP 1420
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Db   4463 TAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGAT 4522

Qy   1420 heGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrA 1440
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Db   4523 TTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATG 4582

Qy   1440 laAlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetT 1460
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Db   4583 CAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGT 4642

Qy   1460 yrLeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleG 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4643 ATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTG 4702

Qy   1480 lyValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheM 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4703 GTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTA 4762

Qy   1500 etThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProG 1520
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Db   4763 TGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGC 4822

Qy   1520 lnLysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrA 1540
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Qy   1540 rgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetV 1560
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Qy   1560 alGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValP 1580
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Qy   1580 heIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrP 1600
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Db   5003 TCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATT 5062

Qy   1600 heThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetP 1620
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Qy   1620 heLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgL 1640
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Qy   1640 euAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuL 1660
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Qy   1660 euPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuV 1680
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Qy   1680 alMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValG 1700
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Qy   1700 lyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnI 1720
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Qy   1720 leThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProA 1740
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Qy   1740 spCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProS 1760
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Qy   1760 erValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnM 1780
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Db   5543 CTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACA 5602

Qy   1780 etTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProL 1800
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Qy   1800 euSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaT 1820
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Qy   1820 hrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuA 1840
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Qy   1840 snLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyA 1860
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Qy   1860 spArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerG 1880
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Qy   1880 lyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerL 1900
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Db   5903 GAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCA 5962

Qy   1900 ysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaV 1920
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Db   5963 AGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTG 6022

Qy   1920 alIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerP 1940
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Db   6023 TCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCT 6082

Qy   1940 heThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetI 1960
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Qy   1960 leIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrA 1980
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Qy   1980 laAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnG 2000
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Qy   2000 luGlyLysAspGluLysAlaLysGlyLys 2009
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Db   6263 AAGGCAAAGATGAAAAAGCCAAAGGGAAA 6291

RESULT 4
AX164172
LOCUS       AX164172               8378 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138564.
ACCESSION   AX164172
VERSION     AX164172.1  GI:14545111
KEYWORDS    .
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 2 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT     2498 a   1571 c   1775 g   2534 t
ORIGIN

Alignment Scores:
Pred. No.:                0          Length:          8378
Score:                 1447.00       Matches:         2002
Percent Similarity:     99.40%       Conservative:    0
Best Local Similarity:  99.40%       Mismatches:      7
Query Match:            72.03%       Indels:          12
DB:                     6            Gaps:            0

US-09-930-871-12 (1-2009) x AX164172 (1-8378)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db    446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Db    626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy    201 AlaTyr-ValThrGluPheValAsp-LeuGlyAsnVal-SerAlaLeuArgThrPheArg 219
          |||   ||||||||||||||||   |||||||||   ||||||||||||||||||||||
Db    866 GCGTT-TGTAACAGAATTTGTAAA-CCTAGGCAATTT-TTCAGCTCTTCGCACTTTCAGA 922

Qy    220 ValLeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAla 239
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Db    923 GTCTTGAGAGCTTTGAAAACTATTTCGGTAATTCCAGGCCTGAAAACCATTGTGGGAGCC 982

Qy    240 LeuIleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSer 259
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Qy    260 ValPheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGln 279
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Db   1043 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 1102

Qy    280 TrpProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsn 299
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Db   1103 TGGCCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAAT 1162

Qy    300 TyrAsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGln 319
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Qy    320 AspSerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSer 339
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Qy    340 SerAspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsn 359
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Qy    360 TyrGlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMet 379
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Db   1343 TATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATG 1402

Qy    380 ThrGlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyr 399
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Db   1403 ACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTAC 1462

Qy    400 MetIlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeu 419
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Db   1463 ATGATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTG 1522

Qy    420 AlaValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGln 439
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Db   1523 GCTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAG 1582

Qy    440 LysGluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGln 459
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Qy    460 GlnAlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeu 479
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Db   1643 CAGGCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTC 1702

Qy    480 SerAspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsn 499
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Db   1703 TCAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAAT 1762

Qy    500 ArgArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGlu 519
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Db   1763 CGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAA 1822

Qy    520 PheGlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGlu 539
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Db   1823 TTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAA 1882

Qy    540 GlyAsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIle 559
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Db   1883 GGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATC 1942

Qy    560 ArgGlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGly 579
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Db   1943 CGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGG 2002

Qy    580 ArgAlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGlu 599
          ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db   2003 CGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCC-AGCACCTTTGAG 2061
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Qy    600 AspAsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsn 619
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Db   2062 GATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAAC 2121

Qy    620 SerAsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGly 639
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Db   2122 AGCAACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGG 2181

Qy    640 LysMetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProServal 659
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Db   2182 AAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTT 2241

Qy    660 ProThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAsp 679
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Db   2242 CCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGAT 2301

Qy    680 AspAsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisVal 699
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Qy    700 SerMetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIle 719
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Qy    720 LeuThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyr 739
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Db   2422 CTAACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTAT 2481

Qy    740 LysPheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHis 759
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Qy    760 ValValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleVal 779
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Db   2542 GTTGTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTC 2601

Qy    780 LeuAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnVal 799
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Qy    800 LeuThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIle 819
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Db   2662 CTTACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATT 2721

Qy    820 IleAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIle 839
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Qy    840 ValThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArg 859
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Db   2782 GTGACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGT 2841

Qy    860 SerPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeu 879
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Db   2842 TCATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTA 2901

Qy    880 IleLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIle 899
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Db   2902 ATAAAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATC 2961

Qy    900 IleValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCys 919
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Qy    920 ValCysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHis 939
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Qy    960 MetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGly 979
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Db   3142 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 3201

Qy    980 AsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAs 999
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Db   3202 AACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACAA 3260

Qy    999 nLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMe 1019
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Db   3261 CCTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGAT 3320

Qy   1019 tHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIl 1039
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Qy   1039 eArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAs 1059
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Qy   1059 pSerCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspV 1079
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Db   3441 CAGTTGTATGTCCAATCATACAGC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATG 3499

Qy   1079 alAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspG 1099
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Qy   1119 alGlyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuG 1139
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Qy   1139 luGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspI 1159
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Qy   1159 leGlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluA 1179
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Db   3740 TCGGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAG 3799

Qy   1179 laCysPheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluG 1199
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Qy   1199 lyArgGlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnT 1219
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Qy   1219 rpPheGluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluA 1239
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Qy   1239 spIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValP 1259
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Db   3980 ATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTT 4039

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Db   4219 GAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATG 4278

Qy   1339 laLeuLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpL 1359

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Qy   1419 lyPheGlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetT 1439

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DEFINITION  Sequence 15 from Patent WO0214498.
ACCESSION   AX391144
VERSION     AX391144.1  GI:19584239
KEYWORDS    .
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SOURCE      human.
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REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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                     /db_xref="taxon:9606"
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ORIGIN

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Percent Similarity:    100.00%       Conservative:    0
Best Local Similarity: 100.00%       Mismatches:      0
Query Match:           71.88%        Indels:          0
DB:                    6             Gaps:            0

US-09-930-871-12 (1-2009) x AX391144 (1-4362)

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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440

Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsn 1446

Db   4321 GCAGTTGATTCCAGAAAT 4338

RESULT 6
AX391146
LOCUS       AX391146               4179 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 17 from Patent WO0214498.
ACCESSION   AX391146
VERSION     AX391146.1  GI:19584240
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 17 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .4179
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1239 a     815 c     958 g    1164 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          4179
Score:                    1382.00        Matches:         1384
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              68.79%         Indels:          0
DB:                       6              Gaps:            0

US-09-930-871-12 (1-2009) x AX391146 (1-4179)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20

Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40

Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100

Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120

Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160

Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180

Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200

Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220

Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240

Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

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Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Qy    1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db    3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy    1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db    3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy    1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy    1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy    1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db    3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy    1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db    3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy    1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy    1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db    3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy    1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy    1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy    1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy    1381 ThrGlyAspArg 1384
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Db    4141 ACTGGTGACAGG 4152

RESULT 7
AX391148
LOCUS       AX391148               4197 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 19 from Patent WO0214498.
ACCESSION   AX391148
VERSION     AX391148.1  GI:19584241
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 19 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .4197
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1232 a    821 c    965 g   1176 t      3 others
ORIGIN
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Alignment Scores:
Pred. No.:                0          Length:          4197
Score:                    1332.00    Matches:         1334
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              66.30%     Indels:          0
DB:                       6          Gaps:            0

US-09-930-871-12 (1-2009) x AX391148 (1-4197)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

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Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

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Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

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Qy    1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Qy    1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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RESULT 8
AX391130
LOCUS       AX391130               5997 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 1 from Patent WO0214498.
ACCESSION   AX391130
VERSION     AX391130.1  GI:19584232
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 1 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1773 a    1185 c    1338 g    1698 t      3 others
ORIGIN

Alignment Scores:
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Score:                    1326.00        Matches:         1992
Percent Similarity:       99.15%         Conservative:    0
Best Local Similarity:    99.15%         Mismatches:      17
Query Match:              66.00%         Indels:          17
DB:                       6              Gaps:            0

US-09-930-871-12 (1-2009) x AX391130 (1-5997)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

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Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

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Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967
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Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

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Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
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Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
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Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Qy    1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Qy    1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Qy    1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Db    5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy    1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db    5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy    1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Qy    1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Qy    1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Qy    1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Qy    1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Qy    1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Db    5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy    2001 GlyLysAspGluLysAlaLysGlyLys 2009
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RESULT 9
AX391132
LOCUS       AX391132               5889 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 3 from Patent WO0214498.
ACCESSION   AX391132
VERSION     AX391132.1  GI:19584233
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 3 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .5889
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1733 a    1161 c    1313 g    1679 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:                0              Length:          5889
Score:                    1289.00        Matches:         1955
Percent Similarity:       99.14%         Conservative:    0
Best Local Similarity:    99.14%         Mismatches:      17
Query Match:              64.16%         Indels:          17
DB:                       6              Gaps:            0

US-09-930-871-12 (1-2009) x AX391132 (1-5889)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640

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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

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Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

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Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

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Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

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Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

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Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

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Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

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Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
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Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Qy     1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Qy     1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db     5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy     1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Qy     1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Qy     1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
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Qy     1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Qy     1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db     5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy     1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
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Qy     1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Qy     1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db     5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy     1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db     5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy     1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
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RESULT 10
AY043484

```
LOCUS       AY043484                6046 bp    mRNA    linear   PRI 24-APR-2002
DEFINITION  Homo sapiens voltage-gated sodium channel type I mRNA, complete
            cds.
ACCESSION   AY043484
VERSION     AY043484.1  GI:15421161
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimomura,J.,
            Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa,K.
  TITLE     Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy
  JOURNAL   Neurology 58 (7), 1122-1124 (2002)
  MEDLINE   21938587
   PUBMED   11940708
REFERENCE   2  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
            mRNA
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,
            Wako, Saitama 351-0198, Japan
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                     FTGIYTFESLIKIIARGFCLEDFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTF
                     RVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNK
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                     SAEPLSEDDFEMFYEVWEKFDPDATQFMEFEKLSQFAALEPPLNLPQPNKLQLIAMD
                     LPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKVSYQPITTTLK
                     RKQEEVSAVIIQRAYRRHLLKRTVKQASFTYNKNKIKGGANLLIKEDMIIDRINENSI
                     TEKTDLTMSTAACPPSYDRVTKPIVEKHEQEGKDEKAKGK"
BASE COUNT     1808 a   1188 c   1345 g   1704 t      1 others
ORIGIN
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Alignment Scores:

Pred. No.:	0	Length:	6046
Score:	1126.00	Matches:	1990
Percent Similarity:	98.96%	Conservative:	0
Best Local Similarity:	98.96%	Mismatches:	19
Query Match:	56.05%	Indels:	21
DB:	9	Gaps:	0

US-09-930-871-12 (1-2009) x AY043484 (1-6046)

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Qy        1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db        1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy       21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100

Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120

Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160

Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGARTACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180

Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200

Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220

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Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

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Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTGGATGCACTACTATGTGGAAATAGCTCT 1020

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Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

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Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

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Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

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Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

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Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

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Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640

Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db    1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db    2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db    2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy     721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db    2128 ACAAATACAGTGGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy     741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspAsnLe 1000
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Qy   1000 uAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHi 1020
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Qy   1020 sLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleAr 1040
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Qy   1040 gLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSe 1060
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Qy   1060 rCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAspValA 1080
          ||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||
Db   3147 TTGTATGTCCAATCATACAAC-AGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAA 3205

Qy   1080 snGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluS 1100
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Qy   1100 erAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValG 1120
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Db   3266 GTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAG 3325

Qy   1120 lyGluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluG 1140
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Qy   1140 luSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleG 1160
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Qy   1320 laLeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaL 1340
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Qy   1340 euLeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuI 1360
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AF225985
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DEFINITION  Homo sapiens voltage-gated sodium channel alpha subunit SCN1A
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ACCESSION   AF225985
VERSION     AF225985.1  GI:12642269
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Cloning of cDNA for human voltage-gated sodium channel alpha
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Department of Neurology, University of
            Tokyo, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo
            113-8655, Japan
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BASE COUNT     2453 a    1530 c    1719 g    2422 t      7 others
ORIGIN

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Score:                    947.00         Matches:         1988
Percent Similarity:       98.61%         Conservative:    0
Best Local Similarity:    98.61%         Mismatches:      21
Query Match:              47.14%         Indels:          28
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US-09-930-871-12 (1-2009) x AF225985 (1-8131)

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Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db    1159 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1218

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1219 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1278

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1279 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1338

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Db    1339 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1398

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Db    1399 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1458

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db    1459 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1518
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Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db   1519 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1578

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1638

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Db   1639 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1698

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1699 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGT 1758

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1818

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   1819 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1878

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
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Db   1879 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1938

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Db   1939 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1998

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Db   2027 GG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2085

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db   2086 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2145

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Qy    741 PheSerAsnIlePheLeu-IleTrpAspCysSerProTyrTrpLeuLysValLysHisVa 760
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Db   2206 TTTTCCAACATATT-CTCAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGT 2264

Qy    760 lValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLe 780
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Qy    780 uAsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLe 800
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Db   2325 AAATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCT 2384

Qy    800 uThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIl 820
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Qy    820 eAlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVa 840
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Qy    840 lThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSe 860
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Db   2505 GACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTC 2564

Qy    860 rPheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIl 880
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Db   2565 ATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAAT 2624

Qy    880 eLysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIl 900
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Qy    900 eValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVa 920
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Qy    920 lCysLysIleAlaSerAspCysGlnLeuPro---ArgTrpHisMetAsnAspPhePheHi 939
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Db   2745 CTGCAAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCA 2804

Qy    939 sSerPheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCy 959
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Db   2805 CTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTG 2864

Qy    959 sMetGluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGl 979
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Db   2865 TATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGG 2924

Qy    979 yAsnLeuValValLeuAsnLeuPheLeuAlaLeuLeu***-SerSerPheSerAlaAspA 999
          ||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db   2925 AAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCT-GAGCTCATTTAGTGCAGACA 2983

Qy    999 snLeuAlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgM 1019
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Qy   1019 etHisLysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheI 1039
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Db   3044 TGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCA 3103

Qy   1039 leArgLysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysA 1059
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Qy   1059 spSerCysMetSerAsnHisThr***-GluIleGlyLysAspLeuAspTyrLeuLysAsp 1078
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Qy   1079 ValAsnGlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAsp 1098
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Qy   1099 GluSerAspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAla 1118
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Qy   1139 GluGluSerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrVal-As 1158
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Qy   1158 pIleGlyAlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGl 1178
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Db   3463 CATCGGCGC-CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGA 3521

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Db   3642 CTGGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGA 3701

Qy   1238 uAspIleTyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysVa 1258

Db   3702 AGATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGT 3761

Qy   1258 lPheThrTyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnTh 1278

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Db   3882 TTTAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACT 3941

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Qy   1958 pMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSe 1978
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RESULT 12
AX391134
LOCUS       AX391134                4329 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 5 from Patent WO0214498.
ACCESSION   AX391134
VERSION     AX391134.1  GI:19584234
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 5 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
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                     /db_xref="taxon:9606"
BASE COUNT     1287 a    840 c    988 g   1211 t      3 others
ORIGIN

Alignment Scores:
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Score:                  763.00         Matches:        1429
Percent Similarity:     98.82%         Conservative:   0
Best Local Similarity:  98.82%         Mismatches:     17
Query Match:            37.98%         Indels:         17
DB:                     6              Gaps:           0

US-09-930-871-12 (1-2009) x AX391134 (1-4329)

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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
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Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
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Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
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Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
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Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy     721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Db    2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy     741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Qy     781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Qy     801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Db    2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy     821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Qy     841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Qy     861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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RESULT 13
AX391136
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DEFINITION  Sequence 7 from Patent WO0214498.
ACCESSION   AX391136
VERSION     AX391136.1  GI:19584235
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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  JOURNAL   Patent: WO 0214498-A 7 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
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                     /db_xref="taxon:9606"
BASE COUNT     1226 a    810 c    951 g   1156 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              0              Length:        4146
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Score:                  701.00        Matches:       1367
Percent Similarity:     98.77%        Conservative:  0
Best Local Similarity:  98.77%        Mismatches:    17
Query Match:            34.89%        Indels:        17
DB:                     6             Gaps:          0

US-09-930-871-12 (1-2009) x AX391136 (1-4146)

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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40

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Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

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Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

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Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100

Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120

Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

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Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

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Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

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Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

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Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

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RESULT 14
AX391138
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DEFINITION  Sequence 9 from Patent WO0214498.
ACCESSION   AX391138
VERSION     AX391138.1  GI:19584236
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 9 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1219 a     816 c     958 g    1168 t      3 others
ORIGIN

Alignment Scores:
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Score:                    670.00         Matches:         1317
Percent Similarity:       98.73%         Conservative:    0
Best Local Similarity:    98.73%         Mismatches:      17
Query Match:              33.35%         Indels:          17
DB:                       6              Gaps:            0

US-09-930-871-12 (1-2009) x AX391138 (1-4164)

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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
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Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
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Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
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Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
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Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

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Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

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Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

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Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

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Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

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RESULT 15
HSSCN1A

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DEFINITION  Homo sapiens mRNA for brain type I sodium channel alpha-subunit
            (SCN1A).
ACCESSION   X65362
VERSION     X65362.1  GI:36417
KEYWORDS    sodium channel.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Lu,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-1992) Chiung-Mei Lu, Sparks Ctr. Rm.1001,
            Psychiatry and Behavioral Neurobiology, University of Alabama at
            Birmingham, UAB Station, Birmingham, Alabama, 35294-0017, U.S.A
REFERENCE   2  (bases 1 to 1269)
  AUTHORS   Lu,C.M., Han,J., Rado,T.A. and Brown,G.B.
  TITLE     Differential expression of two sodium channel subtypes in human
            brain
  JOURNAL   FEBS Lett. 303 (1), 53-58 (1992)
  MEDLINE   92275082
   PUBMED   1317301
COMMENT     The authors changed locus name to SCN1A according to the consensus
            nomenclature. This gene is abbreviated as HBSC I for human brain
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                     FLAELIEKYFVSPTLFRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFNIGLLL
                     FLVMFIYAIFGMSNFAYVKREVGIDDMFNFETFGNSMICLFQITTSAGWDGLLAPILN
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                     MDLPMVSGDRIHCLDILFAFTKRVLGESGEMDALRIQMEERFMASNPSKVSYQPITTT
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BASE COUNT      325 a    284 c    275 g    385 t
ORIGIN
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Alignment Scores:

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Score:	403.00	Matches:	403
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	20.06%	Indels:	0
DB:	9	Gaps:	0

US-09-930-871-12 (1-2009) x HSSCN1A (1-1269)

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Qy   1538 ValThrArgGlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThr 1557
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Db     61 GTAACCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACA 120

Qy   1558 MetMetValGluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsn 1577
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Qy   1578 LeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHis 1597
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Qy   1938 AlaSerPhe 1940
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	185	9.2	579	14	BM718214	BM718214 UI-E-EJ1-
c	2	182	9.1	562	14	BM682680	BM682680 UI-E-EJ1-
	3	163	8.1	674	12	BG342331	BG342331 602374246
	4	161	8.0	547	12	BF470392	BF470392 UI-M-BH3-
	5	147	7.3	443	12	BE864903	BE864903 UI-M-BH1-
	6	142	7.1	683	13	BI667397	BI667397 603292178
	7	123	6.1	618	10	BB622500	BB622500 BB622500
	8	106	5.3	392	10	AW046964	AW046964 UI-M-BH1-
	9	104	5.2	951	9	AL533359	AL533359 AL533359
	10	103	5.1	1777	11	BC029489	BC029489 Homo sapi
	11	102	5.1	509	11	BC034643	BC034643 Mus muscu
	12	102	5.1	510	11	BC023034	BC023034 Mus muscu
	13	98	4.9	577	9	AU067361	AU067361 AU067361
c	14	97	4.8	495	12	BF563427	BF563427 UI-R-BT1-
	15	91	4.5	800	9	AU066802	AU066802 AU066802
c	16	90	4.5	540	10	BE121161	BE121161 UI-R-CA0-
	17	88	4.4	581	10	BB644560	BB644560 BB644560
	18	88	4.4	710	9	AL707423	AL707423 DKFZp686K
	19	87	4.3	928	14	BQ715936	BQ715936 AGENCOURT
	20	82	4.1	508	13	BI731882	BI731882 603353628
c	21	76	3.8	370	10	AW123974	AW123974 UI-M-BH2.
c	22	76	3.8	494	12	BE955837	BE955837 UI-M-BH4-
	23	75	3.7	735	13	BI488967	BI488967 603021693
	24	72	3.6	513	13	BI731739	BI731739 603353512
	25	70	3.5	455	9	AA912739	AA912739 ol41c12.s
c	26	70	3.5	717	12	BG724147	BG724147 602697466
	27	69	3.4	902	12	BG761119	BG761119 602717452
c	28	68	3.4	437	10	AW495598	AW495598 UI-M-BH3-
	29	68	3.4	778	9	AU035605	AU035605 AU035605
	30	66	3.3	662	12	BG253038	BG253038 602365660
	31	66	3.3	665	10	BB653350	BB653350 BB653350
	32	66	3.3	774	13	BI488799	BI488799 603021394
	33	65	3.2	480	13	BM494034	BM494034 IpCGBr1_1
	34	65	3.2	908	14	BQ946179	BQ946179 AGENCOURT
c	35	63	3.1	325	12	BF471558	BF471558 UI-M-BH3-
	36	63	3.1	379	12	BE947431	BE947431 UI-M-BH3-
	37	63	3.1	386	12	BE944106	BE944106 UI-M-BH3-
c	38	63	3.1	706	9	AA984063	AA984063 am76b09.s
	39	62	3.1	547	12	BE724185	BE724185 198931 MA
	40	62	3.1	561	12	BF076296	BF076296 225823 MA
	41	60	3.0	373	10	AW456773	AW456773 UI-M-BH3-
c	42	60	3.0	633	10	BB644172	BB644172 BB644172
	43	60	3.0	700	10	BB631922	BB631922 BB631922
c	44	60	3.0	1024	11	AK020721	AK020721 Mus muscu
	45	59	2.9	354	10	AW431606	AW431606 72271 MAR

ALIGNMENTS

RESULT 1
BM718214
LOCUS BM718214 579 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-EJ1-ajf-a-09-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajf-a-09-0-UI 5', mRNA sequence.
ACCESSION BM718214
VERSION BM718214.1 GI:19036382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene

```
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ1-ajf-a-09-0-UI"
                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      168 a    123 c    125 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                4.19e-188       Length:          579
Score:                    185.00          Matches:         185
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              9.21%           Indels:          0
DB:                       14              Gaps:            0

US-09-930-871-12 (1-2009) x BM718214 (1-579)

Qy    1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 AACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTG 62

Qy    1778 ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 GTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA 122

Qy    1798 GluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspPro 1817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 GAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCC 182

Qy    1818 AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluPro 1837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 GATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCG 242

Qy    1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 CCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTG 302

Qy    1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     303 AGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGA 362

Qy    1878 GluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     363 GAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAAT 422

Qy    1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluVal 1917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     423 CCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTA 482

Qy    1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     483 TCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAA 542

Qy    1938 AlaSerPheThrTyr 1942
           |||||||||||||||
Db     543 GCTTCCTTTACGTAC 557

RESULT 2
BM682680/c
LOCUS       BM682680                562 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  UI-E-EJ1-ajf-a-09-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajf-a-09-0-UI 3', mRNA sequence.
ACCESSION   BM682680
VERSION     BM682680.1  GI:18992576
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .562
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ1-ajf-a-09-0-UI"
                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
```

6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJ1
TAG_TISSUE=Foveal and Macular Retina
TAG_SEQ=GTCC"

BASE COUNT 161 a 121 c 118 g 162 t
ORIGIN

Alignment Scores:

Pred. No.:	6.97e-185	Length:	562
Score:	182.00	Matches:	182
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.06%	Indels:	0
DB:	14	Gaps:	0

US-09-930-871-12 (1-2009) x BM682680 (1-562)

```
Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 503

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 443

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 383

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 323

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 263

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 203

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 143

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 83

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 23

Qy   1941 ThrTyr 1942
          ||||||
Db     22 ACGTAC 17
```

RESULT 3
BG342331
LOCUS BG342331 674 bp mRNA linear EST 27-FEB-2001
DEFINITION 602374246F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5', mRNA sequence.
ACCESSION BG342331
VERSION BG342331.1 GI:13148769
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 674)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10317 row: l column: 12
High quality sequence stop: 672.
FEATURES Location/Qualifiers
source 1. .674
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4481819"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT 146 a 167 c 161 g 200 t
ORIGIN

Alignment Scores:

Pred. No.:	2.6e-164	Length:	674
Score:	163.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	8.11%	Indels:	0
DB:	12	Gaps:	0

US-09-930-871-12 (1-2009) x BG342331 (1-674)

```
Qy   1572 IleLeuSerArgIleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLys 1591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATTTTGTCACGCATCAACCTGGTGTTCATCGTCCTGTTCACCGGCGAGTGTGTGCTCAAG 180

Qy   1592 LeuIleSerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValVal 1611
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCATCTCGCTCCGCCATTATTATTTCACCATTGGATGGAACATTTTCGATTTTGTGGTG 240

Qy   1612 ValIleLeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSer 1631
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTCATCCTCTCCATTGTAGGGATGTTTCTTGCGGAGCTAATAGAAAAGTATTTTGTGTCT 300

Qy   1632 ProThrLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLys 1651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAA 360

Qy   1652 GlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPhe 1671
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGTGCCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTT 420

Qy   1672 AsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsn 1691
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACATCGGCCTCCTGCTTTTTCTCGTCATGTTCATCTACGCCATCTTTGGGATGTCCAAC 480
```

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Qy   1692 PheAlaTyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGly 1711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTGCCTATGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTCGGC 540

Qy   1712 AsnSerMetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAla 1731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTGCTGGCC 600

Qy   1732 ProIleLeu 1734
          |||||||||
Db    601 CCCATCCTC 609

RESULT 4
BF470392
LOCUS       BF470392                 547 bp    mRNA    linear   EST 04-DEC-2000
DEFINITION  UI-M-BH3-avc-c-07-0-UI.r1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-avc-c-07-0-UI 5', mRNA sequence.
ACCESSION   BF470392
VERSION     BF470392.1  GI:11539575
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
            should be noted that Bento Soares is generating a small number of
            additional specialized non-redundant arrays of BMAP cDNAs whose
            availability will be considered under appropriate and limited
            collaborative arrangements
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .547
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH3-avc-c-07-0-UI"
                     /clone_lib="NIH_BMAP_M_S4"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S4 library is a subtracted library of a series,
                     ultimately derived from a mixture of individually tagged
                     normalized libraries from ten regions of the mouse brain
                     (cerebellum, brain stems, olfactory bulbs, hypothalamus,
                     cortex, amygdala, basal ganglia, pineal gland, striatum,
                     hipoccampus) after a series of subtractions to reduce the
                     representation of cDNAs from which ESTs had already been
                     generated. The following serially subtracted libraries
                     were generated in this process: NIH_BMAP_M_S4,
                     NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
                     NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
                     (NIH_BMAP_M_S4) was constructed as follows: PCRamplified
                     cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
                     NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
                     was used as a driver in a hybridization with a pool of
                     the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
                     libraries in the form of single-stranded circles. The
                     remaining single-stranded circles (subtracted library)
                     was purified by hydroxyapatite column chromatography,
                     converted to double-stranded circles and electroporated
                     into DH10B bacteria (LifeTechnologies) to generate the
                     NIH_BMAP_M_S4 library. This procedure has been previously
                     described (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)"
BASE COUNT      110 a    143 c    128 g    166 t
ORIGIN

Alignment Scores:
Pred. No.:                2.98e-162      Length:          547
Score:                    161.00         Matches:         161
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              8.01%          Indels:          0
DB:                       12             Gaps:            0

US-09-930-871-12 (1-2009) x BF470392 (1-547)

Qy   1576 IleAsnLeuValPheIleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeu 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 ATCAACCTGGTGTTCATCGTCCTGTTCACCGGCGAGTGTGTGCTCAAGCTTATCTCACTC 81

Qy   1596 ArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSer 1615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 CGTCATTATTATTTCACCATTGGATGGAACATTTTTGATTTTGTGGTGGTCATCCTCTCC 141

Qy   1616 IleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPhe 1635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 ATTGTAGGGATGTTTCTCGCGGAGCTGATAGAGAAGTATTTCGTGTCCCCTACCCTGTTC 201

Qy   1636 ArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGly 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 CGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCCAAGGGG 261

Qy   1656 IleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeu 1675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 ATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTTAACATCGGCCTC 321

Qy   1676 LeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrVal 1695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTACGTT 381

Qy   1696 LysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIle 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 AAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATC 441

Qy   1716 CysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsn 1735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 TGCCTGTTCCAAATCACCACTTCTGCGGGCTGGGATGGACTGCTGGCCCCTATACTAAAT 501

Qy   1736 Ser 1736
          |||
Db    502 AGT 504

RESULT 5
BE864903
LOCUS       BE864903                 443 bp    mRNA    linear   EST 29-SEP-2000
DEFINITION  UI-M-BH1-alw-d-11-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone
            UI-M-BH1-alw-d-11-0-UI 5', mRNA sequence.
ACCESSION   BE864903
VERSION     BE864903.1  GI:10386411
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
```

```
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
            should be noted that Bento Soares is generating a small number of
            additional specialized non-redundant arrays of BMAP cDNAs whose
            availability will be considered under appropriate and limited
            collaborative arrangements
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH1-alw-d-11-0-UI"
                     /clone_lib="NIH_BMAP_M_S2"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S2 library is a subtracted library derived from
                     NIH_BMAP_M_S1, which in turn is a subtracted library
                     derived from a mixture of normalized libraries from ten
                     regions of the mouse brain (cerebellum, brain stems,
                     olfactory bulbs, hypothalamus, cortex, amygdala, basal
                     ganglia, pineal gland, striatum, hipoccampus). The driver
                     used for subtraction consisted of a pool of 5,000 clones
                     from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                     obtained from non-normalized and normalized mouse brain
                     spinal cord libraries."
BASE COUNT      117 a    110 c    106 g    110 t
ORIGIN

Alignment Scores:
Pred. No.:              2.96e-147       Length:         443
Score:                  147.00          Matches:        147
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            7.32%           Indels:         0
DB:                     12              Gaps:           0

US-09-930-871-12 (1-2009) x BE864903 (1-443)

Qy   1779 AsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGlu 1798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 AACATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACAGAAGAAAGTGCAGAG 62

Qy   1799 ProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAsp 1818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 CCTCTGAGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACCCTGAC 122

Qy   1819 AlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProPro 1838
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 GCCACCCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCTCTAGAACCCCCT 182

Qy   1839 LeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSer 1858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 CTCAATTTGCCACAACCAAACAAACTTCAGCTCATTGCCATGGACCTGCCCATGGTGAGT 242

Qy   1859 GlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGlu 1878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 GGAGACCGCATCCACTGCCTGGACATCTTATTTGCTTTTACAAAGCGGGTGTTGGGTGAG 302

Qy   1879 SerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnPro 1898
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 AGTGGAGAGATGGATGCTCTTCGAATCCAGATGGAAGAGCGGTTCATGGCTTCCAACCCC 362

Qy   1899 SerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSer 1918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    363 TCCAAGGTCTCTTATCAGCCCATCACTACTACATTAAAACGCAAACAAGAGGAGGTGTCA 422

Qy   1919 AlaValIleIleGlnArgAla 1925
           |||||||||||||||||||
Db    423 GCTGTTATCATTCAGCGAGCT 443

RESULT 6
BI667397
LOCUS       BI667397                683 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603292178F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5311627 5',
            mRNA sequence.
ACCESSION   BI667397
VERSION     BI667397.1  GI:15581630
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11789  row: k  column: 20
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5311627"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      236 a    136 c    139 g    172 t
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-141       Length:         683
Score:                  142.00          Matches:        142
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            7.07%           Indels:         0
DB:                     13              Gaps:           0

US-09-930-871-12 (1-2009) x BI667397 (1-683)

Qy   1863 HisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMet 1882
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 CACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATG 65

Qy   1883 AspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSer 1902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 GATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCC 125
```

```
Qy   1903 TyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaValIleIle 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 TATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATT 185

Qy   1923 GlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPheThrTyr 1942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTAC 245

Qy   1943 AsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIleIleAsp 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 AATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGAC 305

Qy   1963 ArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAlaAlaCys 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 AGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGT 365

Qy   1983 ProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGluGlyLys 2002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 CCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAA 425

Qy   2003 AspGlu 2004
          ||||||
Db    426 GATGAA 431
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RESULT 7
BB622500

```
LOCUS       BB622500                618 bp    mRNA    linear   EST 31-AUG-2001
DEFINITION  BB622500 RIKEN full-length enriched, adult male olfactory brain Mus
            musculus cDNA clone 6430408L10 5', mRNA sequence.
ACCESSION   BB622500
VERSION     BB622500.1  GI:15397780
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
            Ishii,Y. and Hayashizaki,Y.
             Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
            Func. Genomics 2 pre, L72-L86 (2001
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .618
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="6430408L10"
                     /clone_lib="RIKEN full-length enriched, adult male
                     olfactory brain"
                     /sex="male"
                     /tissue_type="olfactory brain"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with BamHI and XhoI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT      133 a    155 c    157 g    173 t
ORIGIN
```

```
Alignment Scores:
Pred. No.:                3.21e-121       Length:          618
Score:                    123.00          Matches:         123
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              6.12%           Indels:          0
DB:                       10              Gaps:            0

US-09-930-871-12 (1-2009) x BB622500 (1-618)

Qy   1614 LeuSerIleValGlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThr 1633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCTCCATTGTAGGGATGTTTCTCGCGGAGCTGATAGAGAAGTATTTCGTGTCCCCTACC 60

Qy   1634 LeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAla 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC 120

Qy   1654 LysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIle 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTTAACATC 180

Qy   1674 GlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAla 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGCCTCCTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 240

Qy   1694 TyrValLysArgGluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSer 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TACGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGC 300

Qy   1714 MetIleCysLeuPheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIle 1733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATGATCTGCCTGTTCCAAATCACCACTTCTGCGGGCTGGGATGGACTGCTGGCCCCTATA 360

Qy   1734 LeuAsnSer 1736
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          |||||||||
Db    361 CTAAATAGT 369

RESULT 8
AW046964
LOCUS       AW046964                392 bp    mRNA    linear   EST 18-SEP-1999
DEFINITION  UI-M-BH1-alp-c-08-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
            UI-M-BH1-alp-c-08-0-UI 3', mRNA sequence.
ACCESSION   AW046964
VERSION     AW046964.1  GI:5907493
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized corpus striatum library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means is determined.
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH1-alp-c-08-0-UI"
                     /clone_lib="NIH_BMAP_M_S2"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S2 library is a subtracted library derived from
                     NIH_BMAP_M_S1, which in turn is a subtracted library
                     derived from a mixture of normalized libraries from ten
                     regions of the mouse brain (cerebellum, brain stems,
                     olfactory bulbs, hypothalamus, cortex, amygdala, basal
                     ganglia, pineal gland, striatum, hipoccampus). The driver
                     used for subtraction consisted of a pool of 5,000 clones
                     from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                     obtained from non-normalized and normalized mouse brain
                     spinal cord libraries.
                     TAG_LIB=NIH_BMAP_M_S2
                     TAG_TISSUE=corpus-striatum
                     TAG_SEQ=ACGGC"
BASE COUNT       95 a     92 c     93 g    112 t
ORIGIN

Alignment Scores:
Pred. No.:              4.2e-103       Length:         392
Score:                  106.00         Matches:        119
Percent Similarity:     99.17%         Conservative:   0
Best Local Similarity:  99.17%         Mismatches:     0
Query Match:            5.28%          Indels:         1

DB:                     10             Gaps:           0

US-09-930-871-12 (1-2009) x AW046964 (1-392)

Qy   1764 PhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMetTyrIleAla 1783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 TTTTTTTTTGTCTCCTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATTGCT 66

Qy   1784 ValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeuSerGluAsp 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 GTCATCCTGGAGAACTTCAGCGTTGCCACAGAAGAAAGTGCAGAGCCTCTGAGTGAGGAC 126

Qy   1804 AspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMet 1823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 GACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACCCTGACGCCACCCAGTTCATG 186

Qy   1824 GluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGlu-ProProLeuAsnLeuProGl 1843
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    187 GAATTTGAAAAATTATCTCAGTTTGCAGCTGCTCTAGAACCCCCCTCTCAATTTGCCACA 246

Qy   1843 nProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHi 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 ACCAAACAAACTTCAGCTCATTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATCCA 306

Qy   1863 sCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMet 1882
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 CTGCCTGGACATCCTATTTGCTTTTACAAAGCGGGTGTTGGGTGAGAGTGGAGAGATG 364

RESULT 9
AL533359
LOCUS       AL533359                951 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL533359 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN004YF22 5
            prime, mRNA sequence.
ACCESSION   AL533359
VERSION     AL533359.1  GI:12796852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DN004YF22"
                     /clone_lib="LTI_FL015_Brn1"
                     /sex="male"
                     /tissue_type="Adult brain"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was constructed by Life Technologies.
                     Contact : Feng Liang Life Technologies, a division of
                     Invitrogen 9800 Medical Center Drive Rockville, Maryland
                     20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      303 a    189 c    203 g    247 t      9 others
ORIGIN

Alignment Scores:
Pred. No.:              1.57e-100      Length:         951
Score:                  104.00         Matches:        104
Percent Similarity:     100.00%        Conservative:   0
```

```
Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            5.18%         Indels:        0
DB:                     9             Gaps:          0

US-09-930-871-12 (1-2009) x AL533359 (1-951)

Qy   1807 MetPheTyrGluValTrpGluLysPheAspProAspAlaThrGlnPheMetGluPheGlu 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 ATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAA 125

Qy   1827 LysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsnLeuProGlnProAsnLys 1846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAA 185

Qy   1847 LeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAspArgIleHisCysLeuAsp 1866
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGAT 245

Qy   1867 IleLeuPheAlaPheThrLysArgValLeuGlyGluSerGlyGluMetAspAlaLeuArg 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 ATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGA 305

Qy   1887 IleGlnMetGluGluArgPheMetAlaSerAsnProSerLysValSerTyrGlnProIle 1906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATC 365

Qy   1907 ThrThrThrLeu 1910
          ||||||||||||
Db    366 ACTACTACTTTA 377

RESULT 10
BC029489
LOCUS       BC029489               1777 bp    mRNA    linear   HTC 16-MAY-2002
DEFINITION  Homo sapiens, clone IMAGE:5278436, mRNA.
ACCESSION   BC029489
VERSION     BC029489.1  GI:20809571
KEYWORDS    HTC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1777)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 48 Row: h Column: 9
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 10337596
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .1777
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5278436"
                     /tissue_type="Brain, hypothalamus"
                     /clone_lib="NIH_MGC_96"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
BASE COUNT      526 a    333 c    395 g    523 t
ORIGIN

Alignment Scores:
Pred. No.:              3.7e-99       Length:        1777
Score:                  103.00        Matches:       145
Percent Similarity:     98.64%        Conservative:  0
Best Local Similarity:  98.64%        Mismatches:    1
Query Match:            5.13%         Indels:        2
DB:                     11            Gaps:          0

US-09-930-871-12 (1-2009) x BC029489 (1-1777)

Qy    132 MetLeuIleMetCysThrIleLeuThrAsnCysValPheMetThrMetSerAsnProPro 151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 ATGCTCATTATGTGCACGATTCTTACCAACTGTGTATTTATGACCATGAGTAACCCTCCA 703

Qy    152 AspTrpThrLysAsnValGluTyrThrPheThrGlyIleTyrThrPheGluSerLeuIle 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 GACTGGACAAAGAATGTGGAGTATACCTTTACAGGAATTTATACTTTTGAATCACTTATT 763

Qy    172 LysIleIle-AlaArgGlyPheCysLeuGluAspPheThrPheLeuArgAspProTrpAs 191
          ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    764 AAAATACT-TGCAAGGGGCTTTTGTTTAGAAGATTTCACATTTTTACGGGATCCATGGAA 822

Qy    191 nTrpLeuAspPheThrValIleThrPheAlaTyrValThrGluPheValAspLeuGlyAs 211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 TTGGTTGGATTTCACAGTCATTACTTTTGCATATGTGACAGAGTTTGTGGACCTGGGCAA 882

Qy    211 nValSerAlaLeuArgThrPheArgValLeuArgAlaLeuLysThrIleSerValIlePr 231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TGTCTCAGCGTTGAGAACATTCAGAGTTCTCCGAGCATTGAAAACAATTTCAGTCATTCC 942

Qy    231 oGlyLeuLysThrIleValGlyAlaLeuIleGlnSerValLysLysLeuSerAspValMe 251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 AGGCCTGAAGACCATTGTGGGGGCCCTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCAT 1002

Qy    251 tIleLeuThrValPheCysLeuSerValPheAlaLeuIleGlyLeuGlnLeuPheMetGl 271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 GATCTTGACTGTGTTCTGTCTAAGCGTGTTCGCGCTAATAGGATTGCAGTTGTTCATGGG 1062

Qy    271 yAsnLeuArgAsnLysCys 277
          |||||||||||||||||||
Db   1063 CAACCTACGAAATAAATGT 1081

RESULT 11
BC034643
LOCUS       BC034643               509 bp    mRNA    linear   HTC 07-AUG-2002
DEFINITION  Mus musculus, Similar to sodium channel, voltage-gated, type I,
            alpha polypeptide, clone IMAGE:5361050, mRNA.
ACCESSION   BC034643
VERSION     BC034643.1  GI:21961658
KEYWORDS    HTC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 54 Row: o Column: 1
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .509
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5361050"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
BASE COUNT      155 a    105 c    128 g    121 t
ORIGIN

Alignment Scores:
Pred. No.:              1.15e-98        Length:         509
Score:                  102.00          Matches:        102
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            5.08%           Indels:         0
DB:                     11              Gaps:           0

US-09-930-871-12 (1-2009) x BC034643 (1-509)

Qy     346 ProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGlyTyrThrSerPhe 365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 CCAGAAGGATATATGTGTGTAAAAGCTGGTAGAAACCCTAATTATGGTTACACAAGCTTT 85

Qy     366 AspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGlnAspPheTrpGlu 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 GATACCTTCAGTTGGGCATTTTTGTCCCTGTTTCGACTGATGACTCAGGACTTCTGGGAA 145

Qy     386 AsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIlePhePheValLeu 405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 AATCTATACCAACTGACATTGCGTGCTGCTGGCAAAACCTACATGATATTTTTTGTGCTG 205

Qy     406 ValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaValValAlaMetAla 425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206 GTCATTTTCTTGGGCTCATTCTACCTGATAAACTTGATCCTGGCTGTGGTGGCCATGGCC 265

Qy     426 TyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGluAlaGluPheGln 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266 TATGAGGAGCAGAATCAGGCCACACTGGAGGAGGCTGAACAGAAAGAGGCAGAATTTCAG 325

Qy     446 GlnMet 447
           ||||||
Db     326 CAGATG 331

RESULT 12
BC023034
LOCUS       BC023034                 510 bp    mRNA    linear   HTC 07-AUG-2002
DEFINITION  Mus musculus, clone IMAGE:5361055, mRNA.
ACCESSION   BC023034
VERSION     BC023034.1  GI:18606017
KEYWORDS    HTC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 54 Row: o Column: 3
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5361055"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
BASE COUNT      156 a    105 c    128 g    121 t
ORIGIN

Alignment Scores:
Pred. No.:              1.15e-98        Length:         510
Score:                  102.00          Matches:        102
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            5.08%           Indels:         0
DB:                     11              Gaps:           0

US-09-930-871-12 (1-2009) x BC023034 (1-510)

Qy     346 ProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyrGlyTyrThrSerPhe 365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 CCAGAAGGATATATGTGTGTAAAAGCTGGTAGAAACCCTAATTATGGTTACACAAGCTTT 85

Qy     366 AspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThrGlnAspPheTrpGlu 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 GATACCTTCAGTTGGGCATTTTTGTCCCTGTTTCGACTGATGACTCAGGACTTCTGGGAA 145

Qy     386 AsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMetIlePhePheValLeu 405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 AATCTATACCAACTGACATTGCGTGCTGCTGGCAAAACCTACATGATATTTTTTGTGCTG 205

Qy     406 ValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAlaValValAlaMetAla 425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206 GTCATTTTCTTGGGCTCATTCTACCTGATAAACTTGATCCTGGCTGTGGTGGCCATGGCC 265

Qy     426 TyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLysGluAlaGluPheGln 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266 TATGAGGAGCAGAATCAGGCCACACTGGAGGAGGCTGAACAGAAAGAGGCAGAATTTCAG 325

Qy     446 GlnMet 447
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          ||||||
Db    326 CAGATG 331

RESULT 13
AU067361
LOCUS       AU067361                577 bp    mRNA    linear   EST 12-JUL-2000
DEFINITION  AU067361 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-3353
            5', mRNA sequence.
ACCESSION   AU067361
VERSION     AU067361.1  GI:4968098
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   Hashimoto,K., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Toyoda,A.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
FEATURES             Location/Qualifiers
     source          1. .577
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-3353"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
                     cloned into distinct DraIII sites of the pME18S-FL3. XhoI
                     sites just outside the DraIII sites can be used to isolate
                     the cDNA insert. Size selection was performed to exclude
                     fragments <1.5 kb. Library was constructed by Sugano et
                     al.(University of Tokyo, Institute of Medical Science).
                     Custom primer used for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG], 3' end primer
                     [CGACCTGCAGCTCGAGCACA]"
BASE COUNT      178 a    118 c    130 g    148 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              2.7e-94       Length:         577
Score:                  98.00         Matches:        98
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            4.88%         Indels:         0
DB:                     9             Gaps:           0

US-09-930-871-12 (1-2009) x AU067361 (1-577)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 250

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 TCCCTTGCAGCTATTGAAAGGCGCATTGCAGAAGAGAAGGCTAAGAATCCCAAGCCAGAC 310

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 AAAAAAGATGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCTGGGAAGAAC 370

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CTTCCATTTATCTATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTG 430

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAla 98
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GACCCCTACTATATCAATAAGAAGACTTTTATAGTATTGAATAAAGGGAAGGCA 484

RESULT 14
BF563427/c
LOCUS       BF563427                495 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-BT1-akh-f-12-0-UI.r1 UI-R-BT1 Rattus norvegicus cDNA clone
            UI-R-BT1-akh-f-12-0-UI 5', mRNA sequence.
ACCESSION   BF563427
VERSION     BF563427.1  GI:11673157
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1799538 The following
            repetitive elements were found in this cDNA sequence: 31-100, >(CAG
            )n#Simple_repeat
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                     /clone="UI-R-BT1-akh-f-12-0-UI"
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                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The library
                     UI-R-BT1 is a subtracted library derived from a mixture of
                     the following tissues: hippocampus, thalamus, mid-brain,
                     medulla, corpus striatum, cerebral cortex and testis. For
                     a detailed description of the library from  which this
                     clone was derived, please visit our web site at
                     ratest.eng.uiowa.edu. The subtraction has been previously
                     described in (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)"
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US-09-930-871-12 (1-2009) x BF563427 (1-495)
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DEFINITION  AU066802 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2584
            5', mRNA sequence.
ACCESSION   AU066802
VERSION     AU066802.1  GI:4967539
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 800)
  AUTHORS   Hashimoto,K., Kusuda,J., Tanuma,R., Ito,A., Hirata,M., Toyoda,A.,
            Suzuki,Y., Sasaki,M. and Sugano,S.
  TITLE     Isolation of full-length cDNA clones from a mouse brain cDNA
            library made by oligo-capping method
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            URL: http://www.nih.go.jp/yoken/genbank/.
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                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
                     cloned into distinct DraIII sites of the pME18S-FL3. XhoI
                     sites just outside the DraIII sites can be used to isolate
                     the cDNA insert. Size selection was performed to exclude
                     fragments <1.5 kb. Library was constructed by Sugano et
                     al.(University of Tokyo, Institute of Medical Science).
                     Custom primer used for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG], 3' end primer
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US-09-930-871-12 (1-2009) x AU066802 (1-800)

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Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

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Word size: 1

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5	77	3.8	6556	3	US-09-024-020B-7	Sequence 7, Appli
6	77	3.8	6556	4	US-09-425-043-7	Sequence 7, Appli
7	77	3.8	6586	3	US-09-024-020B-43	Sequence 43, Appl
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10	72	3.6	930	3	US-08-605-284B-2	Sequence 2, Appli
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23	33	1.6	5874	4	US-08-843-417-9	Sequence 9, Appli
24	33	1.6	6344	4	US-08-843-417-1	Sequence 1, Appli
25	33	1.6	6524	4	US-08-669-656A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
US-09-024-020B-1
; Sequence 1, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,020B
; FILING DATE: 16-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-1

Alignment Scores:
Pred. No.:              2.78e-63      Length:         5977
Score:                  77.00         Matches:        77
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.83%         Indels:         0
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-024-020B-1 (1-5977)

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RESULT 2
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; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-1

Alignment Scores:
Pred. No.:              2.78e-63      Length:         5977
Score:                  77.00         Matches:        77
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.83%         Indels:         0
DB:                     4             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-425-043-1 (1-5977)

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RESULT 3
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;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-2

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DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-024-020B-2 (1-6007)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 693

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 753

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 813

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 864

RESULT 4
US-09-425-043-2
; Sequence 2, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-2

Alignment Scores:
Pred. No.:              2.8e-63       Length:         6007
Score:                  77.00         Matches:        77
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.83%         Indels:         0
DB:                     4             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-425-043-2 (1-6007)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 693

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 753

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 813

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 864

RESULT 5
US-09-024-020B-7
; Sequence 7, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
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;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-7

Alignment Scores:
Pred. No.:              3.04e-63      Length:         6556
Score:                  77.00         Matches:        77
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.83%         Indels:         0
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-024-020B-7 (1-6556)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 840

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 900

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 960

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 1011

RESULT 6
US-09-425-043-7
; Sequence 7, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-7

Alignment Scores:
Pred. No.:              3.04e-63      Length:         6556
Score:                  77.00         Matches:        77
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.83%         Indels:         0
DB:                     4             Gaps:           0

US-09-930-871-12 (1-2009) x US-09-425-043-7 (1-6556)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 840

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 900

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 960

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 1011

RESULT 7
US-09-024-020B-43
; Sequence 43, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/024,020B
;       FILING DATE:  16-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/039,447
;       FILING DATE:  26-FEB-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CLARK, JANET P.
;       REGISTRATION NUMBER:  34,799
;       REFERENCE/DOCKET NUMBER:  R0020B-REG
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 852-3097
;       TELEFAX:  (650) 855-5322
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6586 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-43

Alignment Scores:
Pred. No.:                3.06e-63        Length:         6586
Score:                    77.00           Matches:        77
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              3.83%           Indels:         0
DB:                       3               Gaps:           0

US-09-930-871-12 (1-2009) x US-09-024-020B-43 (1-6586)

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 840

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 900

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 960

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 1011

RESULT 8
US-09-425-043-43
; Sequence 43, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;     APPLICANT:  DELGADO, STEPHEN G.
;     APPLICANT:  DIETRICH, PAUL S.
;     APPLICANT:  FISH, LINDA M.
;     APPLICANT:  HERMAN, RONALD C.
;     APPLICANT:  SANGAMESWARAN, LAKSHMI
;     TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;     TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;     NUMBER OF SEQUENCES:  43
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  JANET PAULINE CLARK
;       STREET:  3401 HILLVIEW AVENUE, MS A2-250
;       CITY:  PALO ALTO
;       STATE:  CA
;       COUNTRY:  U.S.A.
;       ZIP:  94304-1397
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/425,043
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 09/024,020
;       FILING DATE:  16-FEB-1998
;       APPLICATION NUMBER:  US 60/039,447
;       FILING DATE:  26-FEB-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CLARK, JANET P.
;       REGISTRATION NUMBER:  34,799
;       REFERENCE/DOCKET NUMBER:  R0020B-REG
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 852-3097
;       TELEFAX:  (650) 855-5322
;   INFORMATION FOR SEQ ID NO:  43:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6586 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-425-043-43

Alignment Scores:
Pred. No.:                3.06e-63        Length:         6586
Score:                    77.00           Matches:        77
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              3.83%           Indels:         0
DB:                       4               Gaps:           0

US-09-930-871-12 (1-2009) x US-09-425-043-43 (1-6586)

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 840

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 900

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 960

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCys 277
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TTCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGT 1011

RESULT 9
US-08-605-284B-1
; Sequence 1, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;     APPLICANT:  WALEWSKI, JOSE L.
;     APPLICANT:  RECIO-PINTO, ESPERANZA
;     TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;     TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;       STREET:  CLINTON SQUARE, P.O. BOX 1051
;       CITY:  ROCHESTER
;       STATE:  NEW YORK
;       COUNTRY:  USA
;       ZIP:  14603
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
```

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-605-284B-1

Alignment Scores:
Pred. No.:              2.71e-59      Length:         930
Score:                  72.00         Matches:        72
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.58%         Indels:         0
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-08-605-284B-1 (1-930)

Qy   1625 IleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 ATAGAAAAGTATTTTGTGTCCCCTACCTTGTTCCGAGTGATCCGTCTTGCCAGGATTGGC 495

Qy   1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 CGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATG 555

Qy   1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyr 1684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 ATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTCCTGGTCATGTTTATCTAT 615

Qy   1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696
          ||||||||||||||||||||||||||||||||||
Db    616 GCCATCTTTGGGATGTCCAACTTTGCCTATGTAAAA 651

RESULT 10
US-08-605-284B-2
; Sequence 2, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-605-284B-2

Alignment Scores:
Pred. No.:              2.71e-59      Length:         930
Score:                  72.00         Matches:        102
Percent Similarity:     98.08%        Conservative:   0
Best Local Similarity:  98.08%        Mismatches:     1
Query Match:            3.58%         Indels:         2
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-08-605-284B-2 (1-930)

Qy   1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIle 1613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 TCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGACTTTGTGGTGGTGATT 402

Qy   1614 LeuSerIleValGlyMetPheLeuAlaGluLeu-IleGluLysTyrPheValSerProTh 1633
          |||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db    403 CTCTCCATTGTAGGTATGTTTCTGGCTGAGAT-GATAGAAAAGTATTTTGTGTCCCCTAC 461

Qy   1633 rLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAl 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 CTTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGC 521

Qy   1653 aLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIl 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 AAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACAT 581

Qy   1673 eGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAl 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    582 CGGCCTCCTGCTCTTCCTGGTCATGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGC 641

Qy   1693 aTyrValLys 1696
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Db    642 CTATGTTAAA 651

RESULT 11
US-08-605-284B-21
; Sequence 21, Application US/08605284B
; Patent No. 6060271
;  GENERAL INFORMATION:
;    APPLICANT:  WALEWSKI, JOSE L.
;    APPLICANT:  RECIO-PINTO, ESPERANZA
;    TITLE OF INVENTION:  VOLTAGE GATED SODIUM CHANNELS FROM
;    TITLE OF INVENTION:  HUMAN PERIPHERAL NERVE
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  CLINTON SQUARE, P.O. BOX 1051
;      CITY:  ROCHESTER
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/605,284B
;      FILING DATE:  09-FEB-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/800 (CRF D-1705)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  930 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-605-284B-21

Alignment Scores:
Pred. No.:              2.71e-59      Length:         930
Score:                  72.00         Matches:        102
Percent Similarity:     98.08%        Conservative:   0
Best Local Similarity:  98.08%        Mismatches:     1
Query Match:            3.58%         Indels:         2
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-08-605-284B-21 (1-930)

Qy   1594 SerLeuArgHisTyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIle 1613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 TCCCTCAGACACTACTACTTCACTATAGGCTGGAACATCTTTGACTTTGTGGTGGTGATT 402

Qy   1614 LeuSerIleValGlyMetPheLeuAlaGluLeu-IleGluLysTyrPheValSerProTh 1633
          ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||
Db    403 CTCTCCATTGTAGGTATGTTTCTGGCTGAGAT-GATAGAAAAGTATTTTGTGTCCCCTAC 461

Qy   1633 rLeuPheArgValIleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAl 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    462 CTTGTTCCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGC 521

Qy   1653 aLysGlyIleArgThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIl 1673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    522 AAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACAT 581

Qy   1673 eGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAl 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    582 CGGCCTCCTGCTCTTCCTGGTCATGTTTATCTATGCCATCTTTGGGATGTCCAACTTTGC 641

Qy   1693 aTyrValLys 1696
          |||||||||
Db    642 CTATGTTAAA 651

RESULT 12
US-08-836-325-1
; Sequence 1, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3033 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..3033
US-08-836-325-1

Alignment Scores:
Pred. No.:              8.56e-59      Length:         3033
Score:                  72.00         Matches:        72
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            3.58%         Indels:         0
DB:                     3             Gaps:           0

US-09-930-871-12 (1-2009) x US-08-836-325-1 (1-3033)

Qy   1625 IleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644
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Db   1930 ATAGAGAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGA 1989

Qy   1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1990 CGAATCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGCACTCTGCTCTTTGCTTTGATG 2049

Qy   1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyr 1684
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2050 ATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCTGGTCATGTTCATCTAC 2109

Qy   1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696
          ||||||||||||||||||||||||||||||||||
Db   2110 GCCATCTTTGGGATGTCCAACTTTGCCTACGTTAAA 2145

RESULT 13
US-08-836-325-9
; Sequence 9, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
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;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6452 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  326..6277
US-08-836-325-9

Alignment Scores:
Pred. No.:                1.78e-58      Length:          6452
Score:                    72.00         Matches:         72
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              3.58%         Indels:          0
DB:                       3             Gaps:            0

US-09-930-871-12 (1-2009) x US-08-836-325-9 (1-6452)

Qy   1625 IleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeuAlaArgIleGly 1644
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5114 ATAGAGAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGA 5173

Qy   1645 ArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeuPheAlaLeuMet 1664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5174 CGAATCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGCACTCTGCTCTTTGCTTTGATG 5233

Qy   1665 MetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuValMetPheIleTyr 1684
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5234 ATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTTTTCCTGGTCATGTTCATCTAC 5293

Qy   1685 AlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696
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Db   5294 GCCATCTTTGGGATGTCCAACTTTGCCTACGTTAAA 5329

RESULT 14
US-09-024-020B-8
; Sequence 8, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6826 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-8

Alignment Scores:
Pred. No.:                1.38e-55      Length:          6826
Score:                    69.00         Matches:         69
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              3.43%         Indels:          0
DB:                       3             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-024-020B-8 (1-6826)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 798
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Qy    261 PheAlaLeuIleGlyLeuGlnLeuPhe 269
          ||||||||||||||||||||||||||
Db    799 TTCGCCCTGATTGGCCTGCAGCTCTTT 825

RESULT 15
US-09-425-043-8
; Sequence 8, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6826 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-8

Alignment Scores:
Pred. No.:              1.38e-55      Length:          6826
Score:                  69.00         Matches:         69
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            3.43%         Indels:          0
DB:                     4             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-425-043-8 (1-6826)

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 GCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTT 678

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    679 CTCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTA 738

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    739 ATCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTT 798

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPhe 269
          ||||||||||||||||||||||||||
Db    799 TTCGCCCTGATTGGCCTGCAGCTCTTT 825


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Job time : 197 secs
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GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 23, 2003, 07:14:12 ; Search time 449 Seconds
(without alignments)
4868.710 Million cell updates/sec

Title: US-09-930-871-12
Perfect score: 2009
Sequence: 1 MEQTVLVPPGPDSFNFFTRE.....TKPIVEKHEQEGKDEKAKGK 2009

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 709820 seqs, 544064369 residues

Word size: 1

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09930871/runat_16042003_114927_9102/app_query.fasta_1.2183
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=oligop2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09930871_@CGN_1_1_182_@runat_16042003_114927_9102
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2007	99.9	6030	10	US-09-930-871-11	Sequence 11, Appl
2	1970	98.1	5922	10	US-09-930-871-13	Sequence 13, Appl
3	1444	71.9	4362	10	US-09-930-871-15	Sequence 15, Appl
4	1382	68.8	4179	10	US-09-930-871-17	Sequence 17, Appl
5	1332	66.3	4197	10	US-09-930-871-19	Sequence 19, Appl
6	1326	66.0	5997	10	US-09-930-871-1	Sequence 1, Appli
7	1289	64.2	5889	10	US-09-930-871-3	Sequence 3, Appli
8	763	38.0	4329	10	US-09-930-871-5	Sequence 5, Appli
9	701	34.9	4146	10	US-09-930-871-7	Sequence 7, Appli
10	670	33.3	4164	10	US-09-930-871-9	Sequence 9, Appli
c 11	392	19.5	1992	10	US-09-864-761-10189	Sequence 10189, A
c 12	385	19.2	1194	10	US-09-864-761-18334	Sequence 18334, A
c 13	379	18.9	1178	10	US-09-864-761-26829	Sequence 26829, A
c 14	322	16.0	969	10	US-09-864-761-1576	Sequence 1576, Ap
15	99	4.9	6822	10	US-09-917-800A-1604	Sequence 1604, Ap
16	88	4.4	490	10	US-09-864-761-10615	Sequence 10615, A
17	87	4.3	487	10	US-09-864-761-15573	Sequence 15573, A
18	83	4.1	249	10	US-09-864-761-32083	Sequence 32083, A
19	83	4.1	264	10	US-09-864-761-27235	Sequence 27235, A
20	80	4.0	249	10	US-09-864-761-27066	Sequence 27066, A
21	77	3.8	465	10	US-09-864-761-10437	Sequence 10437, A
22	74	3.7	347	10	US-09-864-761-31970	Sequence 31970, A
23	74	3.7	467	10	US-09-864-761-15456	Sequence 15456, A
24	49	2.4	343	10	US-09-030-482B-17	Sequence 17, Appl
25	46	2.3	473	10	US-09-864-761-3944	Sequence 3944, Ap
26	46	2.3	473	10	US-09-864-761-13959	Sequence 13959, A
c 27	40	2.0	297	10	US-09-864-761-22921	Sequence 22921, A
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29	36	1.8	6048	9	US-09-896-994-1	Sequence 1, Appli
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c 33	29	1.4	472	10	US-09-864-761-6181	Sequence 6181, Ap
34	23	1.1	123	10	US-09-030-482B-16	Sequence 16, Appl
35	10	0.5	31	10	US-09-801-274-97	Sequence 97, Appl
36	10	0.5	31	10	US-09-801-274-98	Sequence 98, Appl
37	10	0.5	31	10	US-09-801-274-99	Sequence 99, Appl
38	10	0.5	31	10	US-09-801-274-100	Sequence 100, App
39	10	0.5	31	10	US-09-801-274-101	Sequence 101, App
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41	10	0.5	31	10	US-09-801-274-103	Sequence 103, App
42	10	0.5	31	10	US-09-801-274-106	Sequence 106, App
43	10	0.5	31	10	US-09-801-274-107	Sequence 107, App
44	10	0.5	31	10	US-09-801-274-108	Sequence 108, App
45	10	0.5	31	10	US-09-801-274-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-930-871-11
; Sequence 11, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-11

Alignment Scores:

Pred. No.:	0	Length:	6030
Score:	2007.00	Matches:	2009
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 99.90% Indels: 0
DB: 10 Gaps: 0

US-09-930-871-12 (1-2009) x US-09-930-871-11 (1-6030)

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Db  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

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Qy  1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300

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Qy  1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320

Db  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy  1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340

Db  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy  1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360

Db  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy  1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380

Db  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy  1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400

Db  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy  1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420

Db  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy  1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440

Db  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
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Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
          |||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
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RESULT 2
US-09-930-871-13
; Sequence 13, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5922
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-13

Alignment Scores:

Pred. No.:	0	Length:	5922
Score:	1970.00	Matches:	1972
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.06%	Indels:	0

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DB:                 10          Gaps:          0

US-09-930-871-12 (1-2009) x US-09-930-871-13 (1-5922)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
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Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
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Db  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
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Db  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy  1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy  1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy  1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy  1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy  1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy  1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy  1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy  1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy  1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy  1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy  1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy  1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy  1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy  1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy  1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy  1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy  1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy  1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
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Db  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy  1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy  1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy  1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy  1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
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Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
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Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5916

RESULT 3
US-09-930-871-15
; Sequence 15, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 4362
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-15

Alignment Scores:
Pred. No.:                0              Length:          4362
Score:                    1444.00        Matches:         1446
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              71.88%         Indels:          0
DB:                       10             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-15 (1-4362)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100

Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120

Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160

Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180

Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200

Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220

Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240

Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy     601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy     621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy     641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy     661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy     681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy     701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy     721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db    2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy     741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db    2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
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Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
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Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
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Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
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Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
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Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
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Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   1441 AlaValAspSerArgAsn 1446
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Db   4321 GCAGTTGATTCCAGAAAT 4338
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RESULT 4
US-09-930-871-17
; Sequence 17, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:

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;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 4179
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-17

Alignment Scores:
Pred. No.:              0           Length:         4179
Score:                  1382.00     Matches:        1384
Percent Similarity:     100.00%     Conservative:   0
Best Local Similarity:  100.00%     Mismatches:     0
Query Match:            68.79%      Indels:         0
DB:                     10          Gaps:           0

US-09-930-871-12 (1-2009) x US-09-930-871-17 (1-4179)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
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Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
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Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
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Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy     501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy     521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy     541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy     561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy     581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   1381 ThrGlyAspArg 1384
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Db   4141 ACTGGTGACAGG 4152

RESULT 5
US-09-930-871-19
; Sequence 19, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 4197
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-19

Alignment Scores:
Pred. No.:              0              Length:          4197
Score:                  1332.00        Matches:         1334
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            66.30%         Indels:          0
DB:                     10             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-19 (1-4197)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

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Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200

Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220

Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg 1334
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGG 4002

RESULT 6
US-09-930-871-1
; Sequence 1, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5997
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-1

Alignment Scores:
Pred. No.:              0              Length:          5997
Score:                  1326.00        Matches:         1992
Percent Similarity:     99.15%         Conservative:    0
Best Local Similarity:  99.15%         Mismatches:      17
Query Match:            66.00%         Indels:          17
DB:                     10             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-1 (1-5997)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
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Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProAlaAsnGlyLys 640
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Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
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Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
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Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
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Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
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Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
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Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
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Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
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Db  3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy  1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
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Db  3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy  1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy  1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy  1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy  1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy  1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
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Db  3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy  1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
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Db  3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy  1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
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Db  3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy  1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy  1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db  4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy  1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
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Db  4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy  1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
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Db  4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy  1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
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Db  4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy  1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy  1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
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Db  4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy  1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
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Db  4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy  1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
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Db  4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy  1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
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Db  4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy  1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
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Db  4588 CAAGTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy  1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
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Db  4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy  1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy  1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
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Db  4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy  1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy  1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy  1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
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Db  4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy  1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
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Db  5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy  1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
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Db  5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy  1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
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Db  5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy  1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
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Db  5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy  1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
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Db  5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy  1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
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Db  5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy  1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
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Db  5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy  1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy  1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
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Db  5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy  1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
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Db  5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy  1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667
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Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   1961 IleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMetSerThrAla 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy   1981 AlaCysProProSerTyrAspArgValThrLysProIleValGluLysHisGluGlnGlu 2000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy   2001 GlyLysAspGluLysAlaLysGlyLys 2009
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Db   5968 GGCAAAGATGAAAAAGCCAAAGGGAAA 5994

RESULT 7
US-09-930-871-3
; Sequence 3, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 5889
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-3

Alignment Scores:
Pred. No.:              0           Length:          5889
Score:                  1289.00     Matches:         1955
Percent Similarity:     99.14%      Conservative:    0
Best Local Similarity:  99.14%      Mismatches:      17
Query Match:            64.16%      Indels:          17
DB:                     10          Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-3 (1-5889)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
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Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
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Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsnValGluLeuGlnProLysTyrGluGluSerLeuTyrMetTyr 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   1461 LeuTyrPheValIlePheIleIlePheGlySerPhePheThrLeuAsnLeuPheIleGly 1480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   1481 ValIleIleAspAsnPheAsnGlnGlnLysLysLysPheGlyGlyGlnAspIlePheMet 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   1501 ThrGluGluGlnLysLysTyrTyrAsnAlaMetLysLysLeuGlySerLysLysProGln 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   1521 LysProIleProArgProGlyAsnLysPheGlnGlyMetValPheAspPheValThrArg 1540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587
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Qy   1541 GlnValPheAspIleSerIleMetIleLeuIleCysLeuAsnMetValThrMetMetVal 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   1561 GluThrAspAspGlnSerGluTyrValThrThrIleLeuSerArgIleAsnLeuValPhe 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   1581 IleValLeuPheThrGlyGluCysValLeuLysLeuIleSerLeuArgHisTyrTyrPhe 1600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   1601 ThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleValGlyMetPhe 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   1621 LeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgValIleArgLeu 1640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   1641 AlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArgThrLeuLeu 1660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   1661 PheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeuPheLeuVal 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   1681 MetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArgGluValGly 1700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   1701 IleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeuPheGlnIle 1720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   1721 ThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLysProProAsp 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   1741 CysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGlyAsnProSer 1760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   1761 ValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValValValAsnMet 1780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   1781 TyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAlaGluProLeu 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   1801 SerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspProAspAlaThr 1820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   1821 GlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluProProLeuAsn 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   1841 LeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetValSerGlyAsp 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   1861 ArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGlyGluSerGly 1880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   1881 GluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsnProSerLys 1900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   1901 ValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluValSerAlaVal 1920
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500

Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680

Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700

Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720

Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740

Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760

Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780

Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800

Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820

Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840

Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860

Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880

Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900

Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920

Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940

Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960

Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980

Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000

Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020

Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040

Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060

Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080

Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100

Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120

Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140

Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160

Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180

Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
           ||||||||||||
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547
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Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627
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Db    5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy    1921 IleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGlnAlaSerPhe 1940

Db    5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy    1941 ThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGluAspMetIle 1960

Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy    1961 IleAspArgIleAsnGluAsnSerIleThrGluLys 1972

Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAA 5883

RESULT 8
US-09-930-871-5
; Sequence 5, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4329
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-5

Alignment Scores:
Pred. No.:                0              Length:          4329
Score:                    763.00         Matches:         1429
Percent Similarity:       98.82%         Conservative:    0
Best Local Similarity:    98.82%         Mismatches:      17
Query Match:              37.98%         Indels:          17
DB:                       10             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-5 (1-4329)

Qy       1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20

Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40

Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy      41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60

Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy      61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80

Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy      81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100

Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120

Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140

Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160

Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180

Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200

Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220

Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240

Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260

Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280

Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300

Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320

Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340

Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy     341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360

Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy     361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380

Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy     381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400

Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy     401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420

Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy     421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440

Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy     441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460

Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy     461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480

Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy     481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
Db   1201 ATATTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValProProAlaAsnGlyLys 640
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
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Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPhePheHisSer 940
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147
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Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArgPheAspIleGluAspValAsnAsnHisThrAspCysLeuLysLeuIle 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   1401 GluArgAsnGluThrAlaArgTrpLysAsnValLysValAsnPheAspAsnValGlyPhe 1420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   1421 GlyTyrLeuSerLeuLeuGlnValAlaThrPheLysGlyTrpMetAspIleMetTyrAla 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   1441 AlaValAspSerArgAsn 1446
          |||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAAT 4305

RESULT 9
US-09-930-871-7
; Sequence 7, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 4146
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-7

Alignment Scores:
Pred. No.:              0              Length:        4146
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Score:                  701.00        Matches:       1367
Percent Similarity:     98.77%        Conservative:  0
Best Local Similarity:  98.77%        Mismatches:    17
Query Match:            34.89%        Indels:        17
DB:                     10            Gaps:          0

US-09-930-871-12 (1-2009) x US-09-930-871-7 (1-4146)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
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Qy    221 LeuArgAlaLeuLysThrIleSerValIleProGlyLeuLysThrIleValGlyAlaLeu 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    241 IleGlnSerValLysLysLeuSerAspValMetIleLeuThrValPheCysLeuSerVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    261 PheAlaLeuIleGlyLeuGlnLeuPheMetGlyAsnLeuArgAsnLysCysIleGlnTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    281 ProProThrAsnAlaSerLeuGluGluHisSerIleGluLysAsnIleThrValAsnTyr 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    301 AsnGlyThrLeuIleAsnGluThrValPheGluPheAspTrpLysSerTyrIleGlnAsp 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    321 SerArgTyrHisTyrPheLeuGluGlyPheLeuAspAlaLeuLeuCysGlyAsnSerSer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    341 AspAlaGlyGlnCysProGluGlyTyrMetCysValLysAlaGlyArgAsnProAsnTyr 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    361 GlyTyrThrSerPheAspThrPheSerTrpAlaPheLeuSerLeuPheArgLeuMetThr 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    381 GlnAspPheTrpGluAsnLeuTyrGlnLeuThrLeuArgAlaAlaGlyLysThrTyrMet 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    401 IlePhePheValLeuValIlePheLeuGlySerPheTyrLeuIleAsnLeuIleLeuAla 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    421 ValValAlaMetAlaTyrGluGluGlnAsnGlnAlaThrLeuGluGluAlaGluGlnLys 440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    441 GluAlaGluPheGlnGlnMetIleGluGlnLeuLysLysGlnGlnGluAlaAlaGlnGln 460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    461 AlaAlaThrAlaThrAlaSerGluHisSerArgGluProSerAlaAlaGlyArgLeuSer 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    481 AspSerSerSerGluAlaSerLysLeuSerSerLysSerAlaLysGluArgArgAsnArg 500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    501 ArgLysLysArgLysGlnLysGluGlnSerGlyGlyGluGluLysAspGluAspGluPhe 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    521 GlnLysSerGluSerGluAspSerIleArgArgLysGlyPheArgPheSerIleGluGly 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    541 AsnArgLeuThrTyrGluLysArgTyrSerSerProHisGlnSerLeuLeuSerIleArg 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    561 GlySerLeuPheSerProArgArgAsnSerArgThrSerLeuPheSerPheArgGlyArg 580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    581 AlaLysAspValGlySerGluAsnAspPheAlaAspAspGluHisSerThrPheGluAsp 600
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    601 AsnGluSerArgArgAspSerLeuPheValProArgArgHisGlyGluArgArgAsnSer 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    621 AsnLeuSerGlnThrSerArgSerSerArgMetLeuAlaValPheProAlaAsnGlyLys 640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    641 MetHisSerThrValAspCysAsnGlyValValSerLeuValGlyGlyProSerValPro 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    661 ThrSerProValGlyGlnLeuLeuProGluValIleIleAspLysProAlaThrAspAsp 680
          ||||||||||||
Db   1981 ACATCGCCTGTTG--G--A--C--A--G--C--T--T--C--T--G--C--C--A--G-- 2008

Qy    681 AsnGlyThrThrThrGluThrGluMetArgLysArgArgSerSerSerPheHisValSer 700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2009 AG-GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    701 MetAspPheLeuGluAspProSerGlnArgGlnArgAlaMetSerIleAlaSerIleLeu 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    721 ThrAsnThrValGluGluLeuGluGluSerArgGlnLysCysProProCysTrpTyrLys 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy    741 PheSerAsnIlePheLeuIleTrpAspCysSerProTyrTrpLeuLysValLysHisVal 760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy    761 ValAsnLeuValValMetAspProPheValAspLeuAlaIleThrIleCysIleValLeu 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTGYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy    781 AsnThrLeuPheMetAlaMetGluHisTyrProMetThrAspHisPheAsnAsnValLeu 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy    801 ThrValGlyAsnLeuValPheThrGlyIlePheThrAlaGluMetPheLeuLysIleIle 820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy    821 AlaMetAspProTyrTyrTyrPheGlnGluGlyTrpAsnIlePheAspGlyPheIleVal 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy    841 ThrLeuSerLeuValGluLeuGlyLeuAlaAsnValGluGlyLeuSerValLeuArgSer 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy    861 PheArgLeuLeuArgValPheLysLeuAlaLysSerTrpProThrLeuAsnMetLeuIle 880
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Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    881 LysIleIleGlyAsnSerValGlyAlaLeuGlyAsnLeuThrLeuValLeuAlaIleIle 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    901 ValPheIlePheAlaValValGlyMetGlnLeuPheGlyLysSerTyrLysAspCysVal 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    921 CysLysIleAlaSerAspCysGlnLeuProArgTrpHisMetAsnAspPheHisSer 940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    941 PheLeuIleValPheArgValLeuCysGlyGluTrpIleGluThrMetTrpAspCysMet 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
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Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArgValValValAsnAlaLeu 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   1341 LeuGlyAlaIleProSerIleMetAsnValLeuLeuValCysLeuIlePheTrpLeuIle 1360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   1361 PheSerIleMetGlyValAsnLeuPheAlaGlyLysPheTyrHisCysIleAsnThrThr 1380
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Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   1381 ThrGlyAspArg 1384
          ||||||||||||
Db   4108 ACTGGTGACAGG 4119

RESULT 10
US-09-930-871-9
; Sequence 9, Application US/09930871
; Patent No. US20020076780A1
;
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynucl
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 4164
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-9

Alignment Scores:
Pred. No.:              0           Length:          4164
Score:                  670.00      Matches:         1317
Percent Similarity:     98.73%      Conservative:    0
Best Local Similarity:  98.73%      Mismatches:      17
Query Match:            33.35%      Indels:          17
DB:                     10          Gaps:            0

US-09-930-871-12 (1-2009) x US-09-930-871-9 (1-4164)

Qy      1 MetGluGlnThrValLeuValProProGlyProAspSerPheAsnPhePheThrArgGlu 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     21 SerLeuAlaAlaIleGluArgArgIleAlaGluGluLysAlaLysAsnProLysProAsp 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     41 LysLysAspAspAspGluAsnGlyProLysProAsnSerAspLeuGluAlaGlyLysAsn 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     61 LeuProPheIleTyrGlyAspIleProProGluMetValSerGluProLeuGluAspLeu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     81 AspProTyrTyrIleAsnLysLysThrPheIleValLeuAsnLysGlyLysAlaIlePhe 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    101 ArgPheSerAlaThrSerAlaLeuTyrIleLeuThrProPheAsnProLeuArgLysIle 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    121 AlaIleLysIleLeuValHisSerLeuPheSerMetLeuIleMetCysThrIleLeuThr 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    141 AsnCysValPheMetThrMetSerAsnProProAspTrpThrLysAsnValGluTyrThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    161 PheThrGlyIleTyrThrPheGluSerLeuIleLysIleIleAlaArgGlyPheCysLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    181 GluAspPheThrPheLeuArgAspProTrpAsnTrpLeuAspPheThrValIleThrPhe 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    201 AlaTyrValThrGluPheValAspLeuGlyAsnValSerAlaLeuArgThrPheArgVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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DB:                 10          Gaps:        0

US-09-930-871-12 (1-2009) x US-09-864-761-10189 (1-1992)

Qy   1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgVal 1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1445 GGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTG 1386

Qy   1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1385 ATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGC 1326

Qy   1658 ThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeu 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1325 ACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTC 1266

Qy   1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArg 1697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGG 1206

Qy   1698 GluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeu 1717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTA 1146

Qy   1718 PheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLys 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAG 1086

Qy   1738 ProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGly 1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 CCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGG 1026

Qy   1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 AACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTG 966

Qy   1778 ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 GTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA 906

Qy   1798 GluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspPro 1817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 GAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCC 846

Qy   1818 AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluPro 1837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 GATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCG 786

Qy   1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 CCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTG 726

Qy   1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 AGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGA 666

Qy   1878 GluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 GAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAAT 606

Qy   1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluVal 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 CCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTA 546

Qy   1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 TCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAA 486

Qy   1938 AlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGlu 1957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 GCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAA 426

Qy   1958 AspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMet 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 GACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATG 366

Qy   1978 SerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHis 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 TCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACAT 306

Qy   1998 GluGlnGluGlyLysAspGluLysAlaLysGlyLys 2009
          ||||||||||||||||||||||||||||||||||
Db    305 GAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAA 270

RESULT 12
US-09-864-761-18334/c
; Sequence 18334, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18334
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
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Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    961 GluValAlaGlyGlnAlaMetCysLeuThrValPheMetMetValMetValIleGlyAsn 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    981 LeuValValLeuAsnLeuPheLeuAlaLeuLeu***SerSerPheSerAlaAspAsnLeu 1000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   1001 AlaAlaThrAspAspAspAsnGluMetAsnAsnLeuGlnIleAlaValAspArgMetHis 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   1021 LysGlyValAlaTyrValLysArgLysIleTyrGluPheIleGlnGlnSerPheIleArg 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   1041 LysGlnLysIleLeuAspGluIleLysProLeuAspAspLeuAsnAsnLysLysAspSer 1060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   1061 CysMetSerAsnHisThr***GluIleGlyLysAspLeuAspTyrLeuLysAspValAsn 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   1081 GlyThrThrSerGlyIleGlyThrGlySerSerValGluLysTyrIleIleAspGluSer 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   1101 AspTyrMetSerPheIleAsnAsnProSerLeuThrValThrValProIleAlaValGly 1120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   1121 GluSerAspPheGluAsnLeuAsnThrGluAspPheSerSerGluSerAspLeuGluGlu 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   1141 SerLysGluLysLeuAsnGluSerSerSerSerSerGluGlySerThrValAspIleGly 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   1161 AlaProValGluGluGlnProValValGluProGluGluThrLeuGluProGluAlaCys 1180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   1181 PheThrGluGlyCysValGlnArgPheLysCysCysGlnIleAsnValGluGluGlyArg 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   1201 GlyLysGlnTrpTrpAsnLeuArgArgThrCysPheArgIleValGluHisAsnTrpPhe 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   1221 GluThrPheIleValPheMetIleLeuLeuSerSerGlyAlaLeuAlaPheGluAspIle 1240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   1241 TyrIleAspGlnArgLysThrIleLysThrMetLeuGluTyrAlaAspLysValPheThr 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   1261 TyrIlePheIleLeuGluMetLeuLeuLysTrpValAlaTyrGlyTyrGlnThrTyrPhe 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   1281 ThrAsnAlaTrpCysTrpLeuAspPheLeuIleValAspValSerLeuValSerLeuThr 1300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   1301 AlaAsnAlaLeuGlyTyrSerGluLeuGlyAlaIleLysSerLeuArgThrLeuArgAla 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   1321 LeuArgProLeuArgAlaLeuSerArgPheGluGlyMetArg 1334
          ||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGG 3969

RESULT 11
US-09-864-761-10189/c
; Sequence 10189, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL I
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10189
;   LENGTH: 1992
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-10189

Alignment Scores:
Pred. No.:              0              Length:          1992
Score:                  392.00         Matches:         392
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            19.51%         Indels:          0
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;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26829
;   LENGTH: 1178
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
;   OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
;   OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
US-09-864-761-26829

Alignment Scores:
Pred. No.:                0          Length:          1178
Score:                    379.00     Matches:         379
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              18.87%     Indels:          0
DB:                       10         Gaps:            0

US-09-930-871-12 (1-2009) x US-09-864-761-26829 (1-1178)

Qy   1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgVal 1637
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 GGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTG 1080

Qy   1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 ATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGC 1020

Qy   1658 ThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeu 1677
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 ACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTC 960

Qy   1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArg 1697
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 TTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGG 900

Qy   1698 GluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeu 1717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 GAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTA 840

Qy   1718 PheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLys 1737
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Db    839 TTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAG 780

Qy   1738 ProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGly 1757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 CCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGG 720

Qy   1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 AACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTG 660

Qy   1778 ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA 600

Qy   1798 GluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspPro 1817
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 GAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCC 540

Qy   1818 AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluPro 1837
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCG 480

Qy   1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 CCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTG 420

Qy   1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 AGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGA 360

Qy   1878 GluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAAT 300

Qy   1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluVal 1917
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 CCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTA 240

Qy   1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 TCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAA 180

Qy   1938 AlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGlu 1957
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179 GCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAA 120

Qy   1958 AspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMet 1977
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 GACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATG 60

Qy   1978 SerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLys 1996
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     59 TCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAA 3

RESULT 14
US-09-864-761-1576/c
; Sequence 1576, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
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;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
;   OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
US-09-864-761-18334

Alignment Scores:
Pred. No.:                0          Length:          1194
Score:                    385.00     Matches:         385
Percent Similarity:       100.00%    Conservative:    0
Best Local Similarity:    100.00%    Mismatches:      0
Query Match:              19.16%     Indels:          0
DB:                       10         Gaps:            0

US-09-930-871-12 (1-2009) x US-09-864-761-18334 (1-1194)

Qy   1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgVal 1637
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Db   1155 GGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTG 1096

Qy   1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657
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Db   1095 ATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGC 1036

Qy   1658 ThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeu 1677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1035 ACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTC 976

Qy   1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLysArg 1697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    975 TTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGG 916

Qy   1698 GluValGlyIleAspAspMetPheAsnPheGluThrPheGlyAsnSerMetIleCysLeu 1717
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Db    915 GAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTA 856

Qy   1718 PheGlnIleThrThrSerAlaGlyTrpAspGlyLeuLeuAlaProIleLeuAsnSerLys 1737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 TTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAG 796

Qy   1738 ProProAspCysAspProAsnLysValAsnProGlySerSerValLysGlyAspCysGly 1757
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Db    795 CCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGG 736

Qy   1758 AsnProSerValGlyIlePhePhePheValSerTyrIleIleIleSerPheLeuValVal 1777
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Db    735 AACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTG 676

Qy   1778 ValAsnMetTyrIleAlaValIleLeuGluAsnPheSerValAlaThrGluGluSerAla 1797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 GTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCA 616

Qy   1798 GluProLeuSerGluAspAspPheGluMetPheTyrGluValTrpGluLysPheAspPro 1817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCC 556

Qy   1818 AspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAlaAlaAlaLeuGluPro 1837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 GATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCG 496

Qy   1838 ProLeuAsnLeuProGlnProAsnLysLeuGlnLeuIleAlaMetAspLeuProMetVal 1857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 CCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTG 436

Qy   1858 SerGlyAspArgIleHisCysLeuAspIleLeuPheAlaPheThrLysArgValLeuGly 1877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 AGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGA 376

Qy   1878 GluSerGlyGluMetAspAlaLeuArgIleGlnMetGluGluArgPheMetAlaSerAsn 1897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 GAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAAT 316

Qy   1898 ProSerLysValSerTyrGlnProIleThrThrThrLeuLysArgLysGlnGluGluVal 1917
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Db    315 CCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTA 256

Qy   1918 SerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLysArgThrValLysGln 1937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 TCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAA 196

Qy   1938 AlaSerPheThrTyrAsnLysAsnLysIleLysGlyGlyAlaAsnLeuLeuIleLysGlu 1957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 GCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAA 136

Qy   1958 AspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLysThrAspLeuThrMet 1977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 GACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATG 76

Qy   1978 SerThrAlaAlaCysProProSerTyrAspArgValThrLysProIleValGluLysHis 1997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 TCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACAT 16

Qy   1998 GluGlnGluGlyLys 2002
           ||||||||||||||||
Db     15 GAGCAAGAAGGCAAA 1

RESULT 13
US-09-864-761-26829/c
; Sequence 26829, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
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; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013119
US-09-917-800A-1604

Alignment Scores:

Pred. No.:	1.55e-90	Length:	6822
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Query Match:	4.93%	Indels:	0
DB:	10	Gaps:	0

US-09-930-871-12 (1-2009) x US-09-917-800A-1604 (1-6822)

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Qy   1598 TyrTyrPheThrIleGlyTrpAsnIlePheAspPheValValValIleLeuSerIleVal 1617
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Db   5013 TACTACTTCACGATAGGGTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCGATTGTA 5072

Qy   1618 GlyMetPheLeuAlaGluLeuIleGluLysTyrPheValSerProThrLeuPheArgVal 1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5073 GGAATGTTTCTCGCAGAGCTGATAGAGAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTC 5132

Qy   1638 IleArgLeuAlaArgIleGlyArgIleLeuArgLeuIleLysGlyAlaLysGlyIleArg 1657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5133 ATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCCAAGGGGATCCGC 5192

Qy   1658 ThrLeuLeuPheAlaLeuMetMetSerLeuProAlaLeuPheAsnIleGlyLeuLeuLeu 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5193 ACTCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGCTGTTCAACATCGGCCTCCTGCTT 5252

Qy   1678 PheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPheAlaTyrValLys 1696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5253 TTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAA 5309
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Job time : 713 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 06:22:18 ; Search time 10003 Seconds
(without alignments)
17543.729 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	5963.2	98.9	8378	6	AX164172	AX164172 Sequence
4	5952.8	98.7	5997	6	AX391130	AX391130 Sequence
5	5941.2	98.5	6046	9	AY043484	AY043484 Homo sapi
6	5917.4	98.1	8131	9	AF225985	AF225985 Homo sapi
7	5915.8	98.1	5922	6	AX391142	AX391142 Sequence
8	5839.8	96.8	5889	6	AX391132	AX391132 Sequence
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10	5062.4	84.0	8399	10	RATNACHI	M22253 Rattus norv
11	4336.8	71.9	4362	6	AX391144	AX391144 Sequence
12	4260.8	70.7	4329	6	AX391134	AX391134 Sequence
13	4219	70.0	8349	6	AX164203	AX164203 Sequence
14	4219	70.0	8349	6	AX164204	AX164204 Sequence
15	4217.4	69.9	6328	9	HUMHBAX	M94055 Human volta
16	4150.8	68.8	4179	6	AX391146	AX391146 Sequence
17	4074.8	67.6	4146	6	AX391136	AX391136 Sequence
18	4057.8	67.3	4197	6	AX391148	AX391148 Sequence
19	4045	67.1	9123	9	AF225987	AF225987 Homo sapi
20	3981.8	66.0	4164	6	AX391138	AX391138 Sequence
21	3959.8	65.7	8553	10	RNSCPIIR	X03639 Rat brain m
22	3949.4	65.5	8552	10	RATNACHII	M22254 Rattus norv
23	3787.8	62.8	8976	9	AF225986	AF225986 Homo sapi
24	3785.4	62.8	9112	6	AX164235	AX164235 Sequence
25	3771.8	62.6	6599	9	HSA251507	AJ251507 Homo sapi
26	3758.2	62.3	9112	6	AX164236	AX164236 Sequence
27	3563.8	59.1	6822	6	AX401928	AX401928 Sequence
28	3563.8	59.1	6822	10	RNSCIII	Y00766 Rat mRNA fo
29	3544.8	58.8	6404	6	AR107906	AR107906 Sequence
30	3543	58.8	8378	5	AF123593	AF123593 Cynops py
31	3477.2	57.7	5955	4	OCU35238	U35238 Oryctolagus
32	3476.8	57.7	6371	6	AR107905	AR107905 Sequence
33	3476.8	57.7	6371	9	HSVASCAS	X82835 H.sapiens m
34	3412	56.6	9316	10	AF000368	AF000368 Rattus no
35	3410.4	56.6	5952	10	RNU79568	U79568 Rattus norv
36	3410.4	56.6	6452	6	AR107904	AR107904 Sequence
37	2821.2	46.8	7008	9	AB027567	AB027567 Homo sapi
38	2807	46.6	7053	6	BD012084	BD012084 Human sod
39	2807	46.6	7053	6	E37451	E37451 Sodium chan
40	2807	46.6	7053	9	AF225988	AF225988 Homo sapi
41	2807	46.6	7053	23	BD004564	Bd004564 Human sod
42	2787.6	46.2	6007	6	AR181336	AR181336 Sequence
43	2787.6	46.2	6586	10	AF049240	AF049240 Rattus no
44	2758.2	45.7	6586	6	AR181360	AR181360 Sequence
45	2754.2	45.7	5937	10	AF049617	AF049617 Mus muscu

ALIGNMENTS

RESULT 1
AX391140
LOCUS AX391140 6030 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 11 from Patent WO0214498.
ACCESSION AX391140
VERSION AX391140.1 GI:19584237
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same

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;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1576
;   LENGTH: 969
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.2
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
US-09-864-761-1576

Alignment Scores:
Pred. No.:                0              Length:          969
Score:                    322.00         Matches:         322
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              16.03%         Indels:          0
DB:                       10             Gaps:            0

US-09-930-871-12 (1-2009) x US-09-864-761-1576 (1-969)

Qy   1673 IleGlyLeuLeuLeuPheLeuValMetPheIleTyrAlaIlePheGlyMetSerAsnPhe 1692
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Db    968 ATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTT 909

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Db    908 GCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAAC 849

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Db    608 ACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGG 549

Qy   1813 GluLysPheAspProAspAlaThrGlnPheMetGluPheGluLysLeuSerGlnPheAla 1832
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Qy   1913 LysGlnGluGluValSerAlaValIleIleGlnArgAlaTyrArgArgHisLeuLeuLys 1932
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Qy   1953 LeuLeuIleLysGluAspMetIleIleAspArgIleAsnGluAsnSerIleThrGluLys 1972
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Qy   1993 IleVal 1994
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RESULT 15
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; Sequence 1604, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5038-US
;  CURRENT APPLICATION NUMBER: US/09/917,800A
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 1740
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1604
;   LENGTH: 6822
;   TYPE: DNA
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1786 a   1190 c   1345 g   1706 t      3 others
ORIGIN

  Query Match           100.0%;  Score 6028.8;  DB 6;  Length 6030;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 6030;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

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Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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RESULT 2
AX164171
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DEFINITION  Sequence 1 from Patent WO0138564.
ACCESSION   AX164171
VERSION     AX164171.1  GI:14545110
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 1 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8378
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                 /db_xref="taxon:9606"
BASE COUNT     2496 a   1575 c   1782 g   2525 t
ORIGIN

  Query Match           99.8%;  Score 6015.2;  DB 6;  Length 8378;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches 6025;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

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Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db     326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785
Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845
Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905
Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Db   3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085
Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145
Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205
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Db   3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3265
Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db   3326 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3385
Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3446 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3505
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Db   3506 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3565
Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3566 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3625
Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db   3626 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3685
Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3686 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3745
Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044
Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db   4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164
Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Db   4165 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4224
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Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db   4285 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4344
Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Db   4525 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4584

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Db   4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Db   4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764

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Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4945 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5004

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Db   5245 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5304

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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RESULT 3
AX164172
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DEFINITION  Sequence 2 from Patent WO0138564.
ACCESSION   AX164172
VERSION     AX164172.1  GI:14545111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 2 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2498 a   1571 c   1775 g   2534 t
ORIGIN
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Query Match 98.9%; Score 5963.2; DB 6; Length 8378;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 5999; Conservative 3; Mismatches 26; Indels 2; Gaps 2;

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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
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Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db    2065 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2124

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db    2125 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2184

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db    2185 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2244

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Db   2485 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2544

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Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Db   2605 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2664

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Db   2665 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2724

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Db   2725 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2784

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Db   2785 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2844

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Db   2845 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2904

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Db   2905 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2964

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Db   2965 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3024

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Db   3025 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3084

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Db   3085 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3144

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Db   3145 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3204

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Db   3205 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3264

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Db   3265 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3324

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Db   3325 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3384

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Db   3445 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3504

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Db   3505 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3564

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Db   3565 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3624

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Db   3865 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3924

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

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Db   4344 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4403

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Db   4404 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4463

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Db   4524 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4583
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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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RESULT 4
AX391130
LOCUS AX391130 5997 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 1 from Patent WO0214498.
ACCESSION AX391130
VERSION AX391130.1 GI:19584232
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0214498-A 1 21-FEB-2002;
Lexicon Genetics Incorporated (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1773 a 1185 c 1338 g 1698 t 3 others
ORIGIN

Query Match 98.7%; Score 5952.8; DB 6; Length 5997;
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Matches 5997; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
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RESULT 5
AY043484

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LOCUS       AY043484               6046 bp    mRNA    linear   PRI 24-APR-2002
DEFINITION  Homo sapiens voltage-gated sodium channel type I mRNA, complete
            cds.
ACCESSION   AY043484
VERSION     AY043484.1  GI:15421161
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimomura,J.,
            Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa,K.
  TITLE     Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy
  JOURNAL   Neurology 58 (7), 1122-1124 (2002)
  MEDLINE   21938587
   PUBMED   11940708
REFERENCE   2  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
            mRNA
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,
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FEATURES             Location/Qualifiers
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BASE COUNT     1808 a   1188 c   1345 g   1704 t      1 others
ORIGIN

  Query Match           98.5%;  Score 5941.2;  DB 9;  Length 6046;
  Best Local Similarity  99.3%;  Pred. No. 0;
  Matches 5986;  Conservative    4;  Mismatches    7;  Indels   33;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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```

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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747
Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807
Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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RESULT 6
AF225985
LOCUS       AF225985               8131 bp    mRNA    linear   PRI 01-FEB-2001
DEFINITION  Homo sapiens voltage-gated sodium channel alpha subunit SCN1A
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ACCESSION   AF225985
VERSION     AF225985.1  GI:12642269
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Cloning of cDNA for human voltage-gated sodium channel alpha
            subunit, SCN1A
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Department of Neurology, University of
            Tokyo, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo
            113-8655, Japan
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                     FTGIYTFESLIKIIARGFCLEDFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTF
                     RVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNK
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ORIGIN
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  Best Local Similarity   99.1%;  Pred. No. 0;
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Db   2266 GTCAACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2325

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Db   2386 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2445

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCC---ACGCTGGCACATGAATGACTTCTTCCAC 2817
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VERSION     AX391142.1  GI:19584238
KEYWORDS    .
SOURCE      human.
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REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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            Lexicon Genetics Incorporated (US)
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BASE COUNT     1746 a   1166 c   1320 g   1687 t      3 others
ORIGIN
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Query Match 98.1%; Score 5915.8; DB 6; Length 5922;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5917; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

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Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
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FEATURES             Location/Qualifiers
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BASE COUNT     1733 a    1161 c    1313 g    1679 t      3 others
ORIGIN

  Query Match           96.8%;  Score 5839.8;  DB 6;  Length 5889;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches 5884;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db    2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy    2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy    2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy    2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
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Qy    2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Qy    2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy    2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Qy    2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Qy    2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Qy    2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy    2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Qy    2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy    3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

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Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

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Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Qy    5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Qy    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db    5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Qy    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db    5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

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Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5884


RESULT 9
RNSCPIR
LOCUS       RNSCPIR                 8398 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat brain mRNA for sodium channel protein I.
ACCESSION   X03638
VERSION     X03638.1  GI:57216
KEYWORDS    glycoprotein; sodium channel.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8398)
  AUTHORS   Noda,M., Ikeda,T., Kayano,T., Suzuki,H., Takeshima,H., Kurasaki,M.,
            Takahashi,H. and Numa,S.
  TITLE     Existence of distinct sodium channel messenger RNAs in rat brain
  JOURNAL   Nature 320 (6058), 188-192 (1986)
  MEDLINE   86146901
   PUBMED   3754035
FEATURES             Location/Qualifiers
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     variation       2031. .2033
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     variation       2262. .2294
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     variation       2718. .2720
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     misc_feature    4383. .4391
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     misc_feature    4425. .4433
                     /note="pot. glycosylation site"
     misc_feature    8376. .8381
                     /note="put. polyA signal"
     polyA_site      8398
                     /note="polyA site"
BASE COUNT     2370 a   1798 c   1918 g   2312 t
ORIGIN

  Query Match             84.0%;  Score 5062.4;  DB 10;  Length 8398;
  Best Local Similarity   89.9%;  Pred. No. 0;
  Matches 5423;  Conservative    3;  Mismatches  604;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 311

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          |||||||| |||||||||| |||||||||||||||| || |||||||||| ||||||
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Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Db    372 AAAAAAGATGATGATGAAAATGGCCCAAAGCCGAACAGTGACTTGGAAGCTGGGAAGAAC 431

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Db    432 CTTCCATTTATCTATGGAGACATTCCTCCAGAGATGGTGTCGGAGCCTCTGGAGGACCTG 491

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Db    492 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 551

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Db    552 CGGTTCAGTGCCACTTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 611

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Db    612 GCTATTAAGATTTTGGTACACTCATTATTCAGCATGTTAATTATGTGCACTATTTTGACG 671

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Db    672 AACTGTGTATTTATGACAATGAGTAACCCTCCTGACTGGACAAAGAATGTAGAGTACACC 731

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Db    732 TTCACAGGAATATATACCTTTGAATCACTAATAAAAATTATTGCAAGGGGCTTCTGTTTA 791

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Db    792 GAAGATTTTACTTTCCTTCGTGACCCATGGAACTGGCTGGACTTCACTGTCATTACATTC 851

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Db    852 GCATATGTGACGGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTT 911

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Db    912 CTTCGAGCATTGAAAACAATATCAGTCATTCCAGGCCTGAAGACCATCGTGGGGGCCCTG 971

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Db    972 ATCCAGTCTGTGAAGAAGCTCTCTGACGTCATGATCCTCACCGTGTTCTGTCTCAGTGTG 1031

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Db   1032 TTTGCTCTAATCGGGTTGCAGCTTTTCATGGGCAACCTGAGGAATAAGTGTGTACAGTGG 1091

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Db   1092 CCCCCCACCAACGCTTCCCTTGAGGAACATAGCATAGAGAAGAATGTAACTACGGATTAC 1151

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Db   1152 AACGGCACACTTGTAAATGAAACCGTGTTTGAATTTGACTGGAAATCATACATTCAAGAC 1211

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Db   1212 TCAAGATATCATTATTTCCTGGAGGGTGTTTTAGATGCACTACTGTGTGGAAATAGCTCT 1271

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Db   1272 GATGCAGGCCAATGTCCAGAAGGTTACATGTGTGTAAAAGCTGGCAGAAACCCTAACTAT 1331

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Db   1332 GGTTACACAAGCTTTGACACCTTCAGCTGGGCATTTCTGTCCCTGTTTCGACTGATGACT 1391

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Db   1392 CAGGACTTCTGGGAAAATCTTTACCAACTGACATTGCGTGCTGCCGGGAAAACATACATG 1451

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Db   1452 ATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTACCTGATAAACTTGATCCTGGCT 1511

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Db   1512 GTGGTGGCCATGGCCTATGAGGAACAGAACCAGGCCACATTGGAGGAGGCTGAACAGAAG 1571

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Db   1572 GAGGCAGAGTTTCAGCAGATGCTGGAGCAACTGAAGAAGCAGCAGGAAGCCGCACAGCAG 1631

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Db   1632 GCGGCGGCAGCAACAGCATCAGAACATTCCAGGGAGCCCAGTGCAGCGGGCAGGCTCTCA 1691

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Db   1692 GATAGCTCTTCAGAAGCCTCCAAGTTGAGTTCAAAGAGCGCTAAAGAAAGGCGGAATCGG 1751

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Db   1752 AGGAAAAAAAGAAAACAGAAAGAGCAGTCTGGAGGGGAAGAGAAAGATGATGATGAATTC 1811

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Db   1812 CACAAATCCGAGTCCGAAGATAGCATCAGGAGGAAGGGCTTCCGCTTCTCCATAGAAGGG 1871

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Db   1872 AACAGACTGACCTATGAAAAGAGGTACTCTTCCCCACATCAGTCTCTGTTGAGCATTCGC 1931

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Db   1932 GGCTCACTGTTTTCCCCGAGACGCAATAGCAGAACAAGTCTTTTCAGCTTCAGAGGGCGA 1991

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Db   1992 GCGAAGGACGTGGGGTCTGAGAATGATTTTGCGGACGATGAGCACAGCACCTTCGAGGAC 2051

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Db   2052 AATGAGAGCAGGAGAGACTCTCTGTTTGTTCCCCGAAGACATGGAGAGCGACGCAACAGT 2111

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Db   2112 AACCTCAGCCAAACCAGCAGATCCTCCCGAATGCTGGCGGGGGCTTCCAGCAAACGGGAAG 2171

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Db   2172 ATGCACAGCACAGTGGATTGCAATGGTGTGGTTTCCTTGGTGGGCGGACCCTCGGTTCCG 2231

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Db   2292 AATGGAACAACTACTGAAACTGAGATGAGAAAGAGGAGGTCAAGTTCTTTCCATGTTTCC 2351

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Db   2352 ATGGACTTTCTTGAGGATCCTTCCCAGAGGCAAAGGGCAATGAGCATTGCCAGCATCTTA 2411

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Db   2412 ACAAATACAGTAGAAGAACTAGAAGAATCCAGACAGAAATGTCCACCCTGTTGGTATAAA 2471

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Db   2472 TTTTCCAACATATTTTTAATTTGGGACTGTTCTCCATATTGGCTAAAAGTTAAACATATT 2531

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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Db   4992 ATTGTGCTGTTCACCGGCGAGTGCGTGCTGAAGCTCATCTCCCTCCGCCATTATTATTTC 5051

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Db   5052 ACCATTGGCTGGAATATTTTCGATTTTGTGGTGGTCATCCTCTCCATTGTAGGAATGTTT 5111

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
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Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Db   5352 ATTGATGACATGTTCAACTTTGAGACTTTTGGCAACAGCATGATCTGCCTGTTCCAAATC 5411

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db   5472 TGTGACCCTAATAAAGTTAACCCCGGAAGCTCGGTGAAGGGGGACTGTGGGAACCCATCC 5531

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Db   5532 GTGGGGATTTTCTTTTTTGTCAGCTACATCATCATATCCTTCCTGGTGGTGGTGAACATG 5591

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
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Db   5652 AGTGAGGACGACTTTGAGATGTTCTACGAGGTCTGGGAGAAGTTCGACCCTGACGCCACT 5711

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5712 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCTCTCGAACCCCCTCTCAAC 5771

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Db   5832 CGCATCCACTGCCTGGACATCTTGTTTGCTTTTACAAAGCGGGTCTTGGGCGAGAGTGGA 5891
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Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5952 GTCTCCTATCAGCCAATCACTACAACGTTAAAACGAAAGCAAGAGGAGGTGTCAGCCGTT 6011

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Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Db   6132 ATTGACAGGATAAATGAAAACTCTATTACAGAGAAAACTGACCTGACGATGTCCACTGCA 6191

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Db   6192 GCTTGTCCGCCCTCCTACGACCGGGTGACAAAGCCAATCGTGGAGAAACACGAGCAGGAA 6251

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Db   6252 GGAAAAGATGAGAAAGCCAAAGGGAAATGA 6281
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RESULT 10
RATNACHI
LOCUS       RATNACHI                8399 bp    mRNA    linear   ROD 26-OCT-1995
DEFINITION  Rattus norvegicus sodium channel I mRNA, complete cds.
ACCESSION   M22253
VERSION     M22253.1  GI:1041088
KEYWORDS    Na+ channel; sodium channel.
SOURCE      Rattus norvegicus cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 8399)
  AUTHORS   Noda,M. and Numa,S.
  TITLE     Structure and function of sodium channel
  JOURNAL   J. Recept. Res. 7 (1-4), 467-497 (1987)
  MEDLINE   87311395
   PUBMED   2442385
COMMENT     On Oct 27, 1995 this sequence version replaced gi:340711.
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                     RVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNK
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BASE COUNT     2371 a   1798 c   1918 g   2312 t
ORIGIN

  Query Match           84.0%;  Score 5062.4;  DB 10;  Length 8399;
  Best Local Similarity  89.9%;  Pred. No. 0;
  Matches 5423;  Conservative    3;  Mismatches  604;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db     552 CGGTTCAGTGCCACTTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 611

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Db     672 AACTGTGTATTTATGACAATGAGTAACCCTCCTGACTGGACAAAGAATGTAGAGTACACC 731

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db     732 TTCACAGGAATATATACCTTTGAATCACTAATAAAAATTATTGCAAGGGGCTTCTGTTTA 791

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db    1152 AACGGCACACTTGTAAATGAAACCGTGTTTGAATTTGACTGGAAATCATACATTCAAGAC 1211

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
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Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db    1932 GGCTCACTGTTTTCCCCGAGACGCAATAGCAGAACAAGTCTTTTCAGCTTCAGAGGGCGA 1991

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Db  1992 GCGAAGGACGTGGGGTCTGAGAATGATTTTGCGGACGATGAGCACAGCACCTTCGAGGAC 2051

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Qy  1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
         |||||||||| || |||||||||| |||||| | |||||||| || |||||||  ||
Db  2352 ATGGACTTTCTTGAGGATCCTTCCCAGAGGCAAAGGGCAATGAGCATTGCCAGCATCTTA 2411

Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Db  2532 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCAATTACTATCTGTATTGTGTTA 2591

Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Db  2592 AATACCCTTTTCATGGCCATGGAGCACTACCCCATGACTGAACATTTCAATCATGTACTT 2651

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Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Db  2952 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTGTTCGGCAAAAGTTACAAAGATTGTGTC 3011

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Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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DEFINITION Sequence 15 from Patent WO0214498.
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  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 0;
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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy   4321 GCAGTTGATTCCAGAAAT 4338
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RESULT 12
AX391134
LOCUS       AX391134               4329 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 5 from Patent WO0214498.
ACCESSION   AX391134
VERSION     AX391134.1  GI:19584234
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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  JOURNAL   Patent: WO 0214498-A 5 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1287 a    840 c    988 g   1211 t      3 others
ORIGIN

  Query Match           70.7%;  Score 4260.8;  DB 6;  Length 4329;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 4305;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

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Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

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Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

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Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db  2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Db  2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db  3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db  3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   4321 GCAGTTGATTCCAGAAAT 4338
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Db   4288 GCAGTTGATTCCAGAAAT 4305
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RESULT 13
AX164203
LOCUS       AX164203               8349 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 33 from Patent WO0138564.
ACCESSION   AX164203
VERSION     AX164203.1  GI:14545141
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8349)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 33 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8349
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2496 a   1591 c   1775 g   2487 t
ORIGIN
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  Query Match             70.0%;  Score 4219;  DB 6;  Length 8349;
  Best Local Similarity   82.5%;  Pred. No. 0;
  Matches 4989;  Conservative    2;  Mismatches  987;  Indels   69;  Gaps   11;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||  ||  |||||||  |||||  ||||||||||||||||||  ||||||  |||||  |||
Db    106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
          ||  |||||  |||||||||  ||||||||||||||| || ||  ||||  |||||||  ||
Db    166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

Qy    120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
            |||  | || || || ||||||||||||||||||||| ||||||||||||||| |||||
Db    226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy    178 AACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGAC 237
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy    238 CTGGACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATC 297
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Db    346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy    298 TTCCGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAA 357
          |  || |||||||||||| ||||||| |||||||||||||||||||| ||| |||| |||
Db    406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy    358 ATAGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTG 417
          ||||||||||||||||||||||||||||| ||||||  ||||| |||||||||||| || |
Db    466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525

Qy    418 ACAAACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATAC 477
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Qy    478 ACCTTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGT 537
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Db    586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy    538 TTAGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACA 597
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Qy    598 TTTGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGA 657
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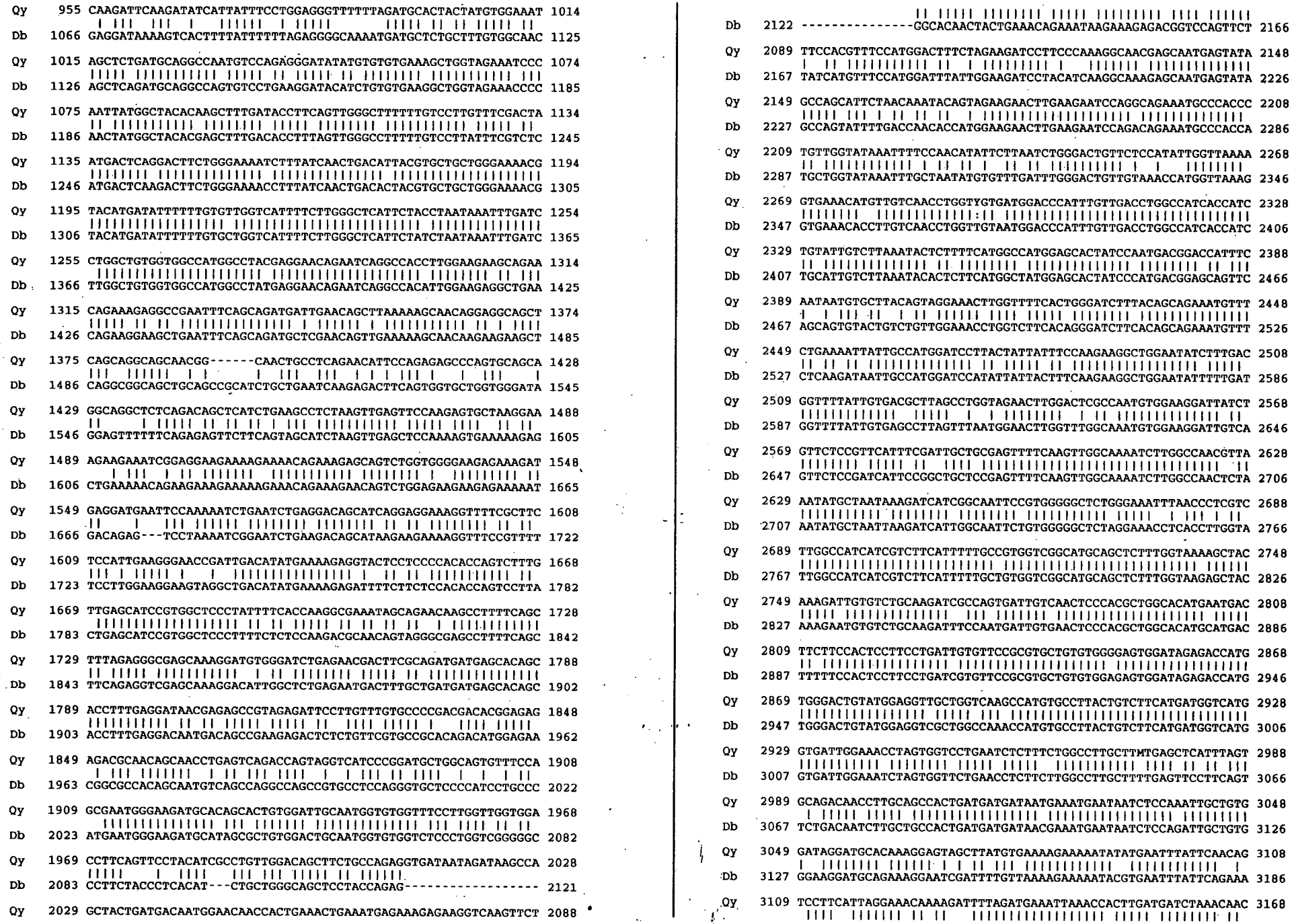
Qy    658 GTTCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCC 717
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Db    766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825

Qy    718 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 777
          |||||||||| |||||||||| || ||||| |||||| |||||||||||||||| |||
Db    826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885

Qy    778 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 837
          || ||||| ||||| ||  ||||| ||||||||||||||||  | |||||||| | |||
Db    886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945

Qy    838 TGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGTG 894
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Db    946 TGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATTG 1005

Qy    895 AATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATT 954
          ||   ||||||||   | | |||   || ||       ||| ||||| |   |||||||
Db   1006 GATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATATT 1065
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Db   3187 GCCTTTGTTAGGAAGCAGAAAGCTTTAGATGAAATTAAACCGCTTGAAGATCTAAATAAT 3246

Qy   3169 AAGAAAGACAGTTGTATGTCCAATCATACARC---AGAAATTGGGAAAGATCTTGACTAT 3225
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Db   3247 AAAAAAGACAGCTGTATTTCCAACCATACCACCATAGAAATAGGCAAAGACCTCAATTAT 3306

Qy   3226 CTTAAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATAC 3285
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Db   3307 CTCAAAGACGGAAATGGAACTACTAGTGGCATA------GGCAGCAGTGTAGAAAAATAT 3360

Qy   3286 ATTATTGATGAAAGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTA 3345
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Db   3361 GTCGTGGATGAAAGTGATTACATGTCATTTATAAACAACCCTAGCCTCACTGTGACAGTA 3420

Qy   3346 CCAATTGCTGTAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAA 3405
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Db   3421 CCAATTGCTGTTGGAGAATCTGACTTTGAAAATTTAAATACTGAAGAATTCAGCAGCGAG 3480

Qy   3406 TCGGATCTGGAAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGC 3465
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Db   3481 TCAGATATGGAGGAAAGCAAAGAGAAGCTAAATGCA---ACTAGTTCATCTGAAGGCAGC 3537

Qy   3466 ACTGTGGACATCGGCGCACCTGTAGA---AGAACAGCCCGTAGTGGAACCTGAAGAAACT 3522
          || || || || || || || |  ||   ||||||||| |  || |||||||| ||| |
Db   3538 ACGGTTGATATTGGAGCTCCCGCCGAGGGAGAACAGCCTGAGGTTGAACCTGAGGAATCC 3597

Qy   3523 CTTGAACCAGAAGCTTGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATC 3582
          |||||||| ||||| ||||| || |||| |||||||| |  ||||||||||||||| ||
Db   3598 CTTGAACCTGAAGCCTGTTTTACAGAAGACTGTGTACGGAAGTTCAAGTGTTGTCAGATA 3657

Qy   3583 AATGTGGAAGAAGGCAGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATA 3642
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Db   3658 AGCATAGAAGAAGGCAAAGGGAAACTCTGGTGGAATTTGAGGAAAACATGCTATAAGATA 3717

Qy   3643 GTTGAACATAACTGGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCT 3702
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Db   3718 GTGGAGCACAATTGGTTCGAAACCTTCATTGTCTTCATGATTCTGCTGAGCAGTGGGGCT 3777

Qy   3703 CTGGCATTTGAAGATATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATAT 3762
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Db   3778 CTGGCCTTTGAAGATATATACATTGAGCAGCGAAAAACCATTAAGACCATGTTAGAATAT 3837

Qy   3763 GCTGACAAGGTTTTCACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATAT 3822
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Db   3838 GCTGACAAGGTTTTCACTTACATATTCATTCTGGAAATGCTGCTAAAGTGGGTTGCATAT 3897

Qy   3823 GGCTATCAAACATATTTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTT 3882
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Qy   3883 TCATTGGTCAGTTTAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCT 3942
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Db   3958 TCACTGGTTAGCTTAACTGCAAATGCCTTGGGTTACTCAGAACTTGGTGCCATCAAATCC 4017

Qy   3943 CTCAGGACACTAAGAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGG 4002
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Qy   4003 GTGGTTGTGAATGCCCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGT 4062
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Db   4078 GCTGTTGTAAATGCTCTTTTAGGAGCCATTCCATCTATCATGAATGTACTTCTGGTTTGT 4137

Qy   4063 CTTATATTCTGGCTAATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTAC 4122
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Db   4138 CTGATCTTTTGGCTAATATTCAGTATCATGGGAGTGAATCTCTTTGCTGGCAAGTTTTAC 4197

Qy   4123 CACTGTATTAACACCACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACT 4182
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Db   4198 CATTGTATTAATTACACCACTGGAGAGATGTTTGATGTAAGCGTGGTCAACAACTACAGT 4257

Qy   4183 GATTGCCTAAAACTAATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAAC 4242
          || |||  |  || || || || ||| | |||||  | ||||||||||||||||||||
Db   4258 GAGTGCAAAGCTCTCATTGAGAGCAATCAAACTGCCAGGTGGAAAAATGTGAAAGTAAAC 4317
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Qy   4243 TTTGATAATGTAGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGG 4302
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Db   4318 TTTGATAACGTAGGACTTGGATATCTGTCTCTACTTCAAGTAGCCACGTTTAAGGGATGG 4377

Qy   4303 ATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAA 4362
          |||||||| |||||||||| ||||||||  ||||||| ||| | || || |||||||||
Db   4378 ATGGATATTATGTATGCAGCTGTTGATTCACGAAATGTAGAATTACAACCCAAGTATGAA 4437

Qy   4363 GAAAGTCTGTACATGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACC 4422
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Db   4438 GACAACCTGTACATGTATCTTTATTTTGTCATCTTTATTATTTTTGGTTCATTCTTTACC 4497

Qy   4423 TTGAACCTGTTTATTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGA 4482
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Db   4498 TTGAATCTTTTCATTGGTGTCATCATAGATAACTTCAACCAACAGAAAAAGAAGTTTGGA 4557

Qy   4483 GGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTA 4542
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Db   4558 GGTCAAGACATTTTTATGACAGAAGAACAGAAGAAATACTACAATGCAATGAAAAAACTG 4617

Qy   4543 GGATCGAAAAAACCGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTC 4602
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Db   4738 ATGGTCACCATGATGGTGGAAACCGATGACCAGAGTCAAGAAATGACAAACATTCTGTAC 4797

Qy   4723 CGCATCAATCTGGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCT 4782
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Db   4798 TGGATTAATCTGGTGTTTATTGTTCTGTTCACTGGAGAATGTGTGCTGAAACTGATCTCT 4857

Qy   4783 CTACGCCATTATTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTC 4842
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Qy   5263 GACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTTGTCAGTTACATCATCATATCCTTC 5322
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Qy   5323 CTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAA 5382
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ACCESSION   AX164204
VERSION     AX164204.1  GI:14545142
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SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8349)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 34 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
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ORIGIN
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Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
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Qy    120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
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Qy    178 AACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGAC 237
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy    238 CTGGACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATC 297
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||| || |||
Db    346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy    298 TTCCGGTTCAGTGCCACCCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAA 357
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Db    406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy    358 ATAGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTG 417
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Qy    658 GTTCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCC 717
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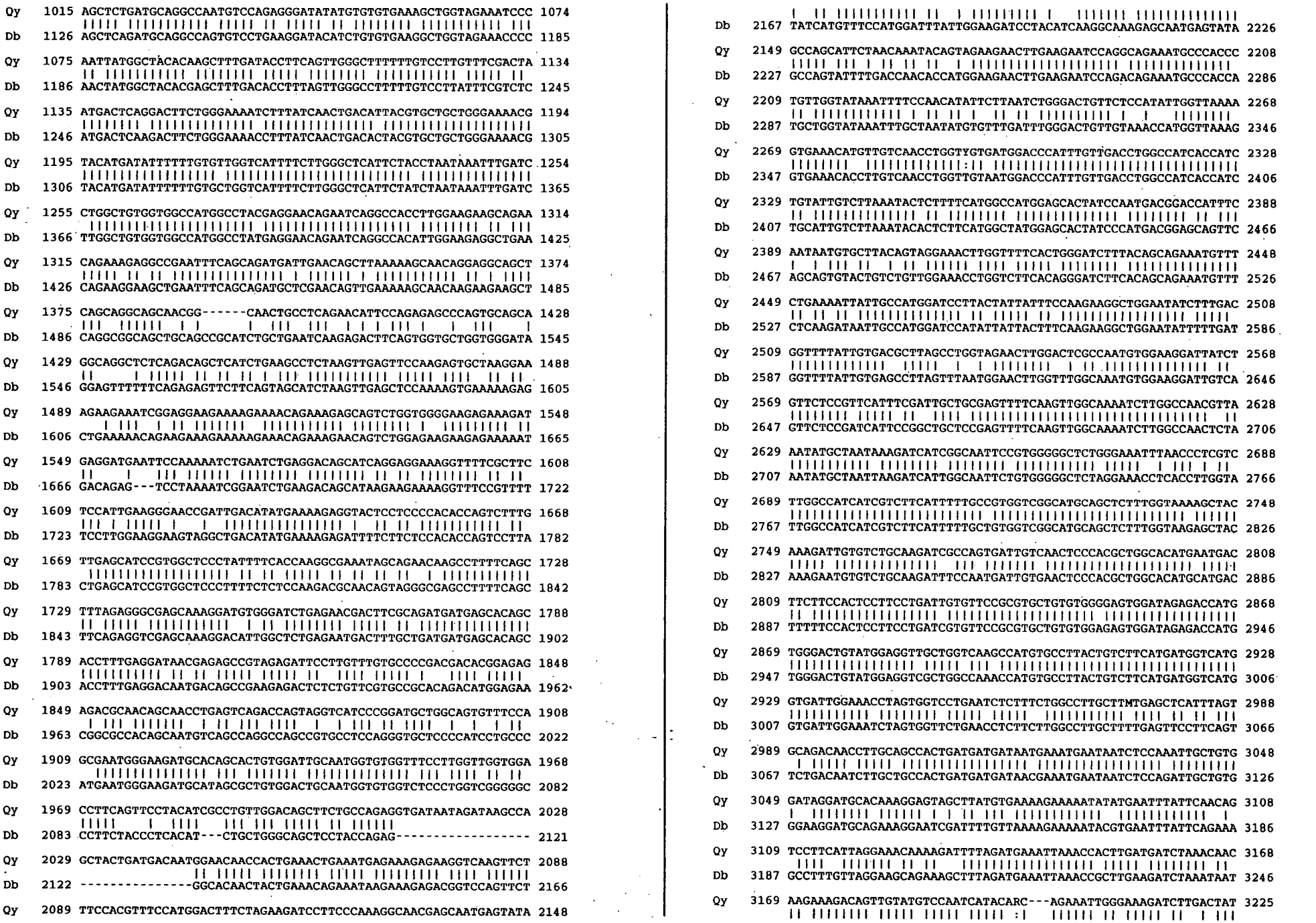
Qy    718 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 777
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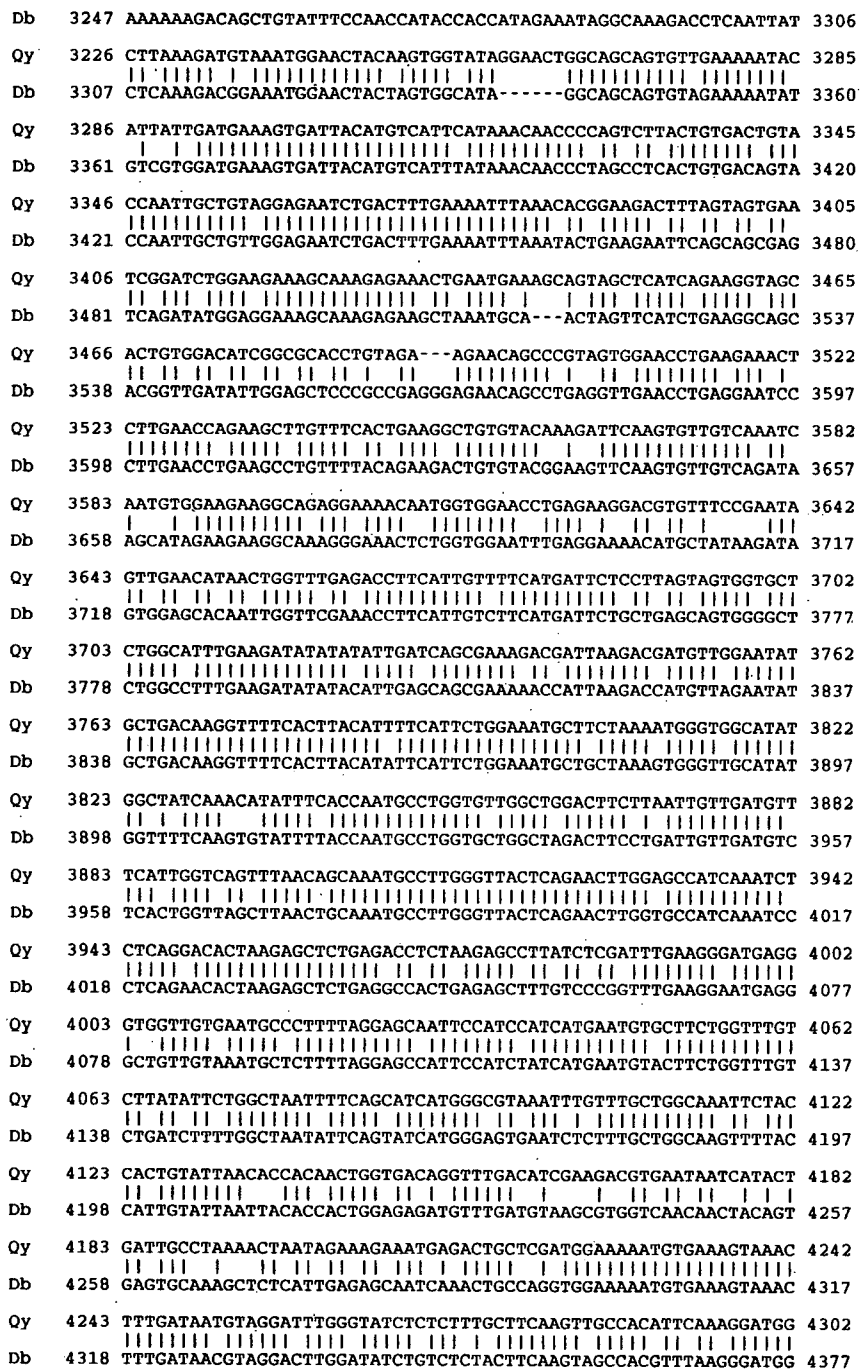
Qy    778 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 837
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Db    886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945

Qy    838 TGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGTG 894
          ||||||||    ||| |||||| ||   | ||   | |          || |   | ||
Db    946 TGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATTG 1005

Qy    895 AATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATT 954
          ||   ||||||||   | | |||   || ||       ||| ||||| |   |||||||
Db   1006 GATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATATT 1065

Qy    955 CAAGATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAAT 1014
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Db   1066 GAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCTCTGCTTTGTGGCAAC 1125
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           || ||| | |  ||   ||  ||||| ||| |||||  |||||   | | |       |
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RESULT 15
HUMHBAX

LOCUS	HUMHBAX	6328 bp mRNA linear PRI 09-JUN-1994
DEFINITION	Human voltage-gated sodium channel mRNA, complete cds.	
ACCESSION	M94055	
VERSION	M94055.1 GI:456678	
KEYWORDS	sodium channel alpha subunit; voltage-sensitive sodium channel.	
SOURCE	Homo sapiens cDNA to mRNA.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 6328)	
AUTHORS	Ahmed,C.M., Ware,D.H., Lee,S.C., Patten,C.D., Ferrer-Montiel,A.V., Schinder,A.F., McPherson,J.D., Wagner-McPherson,C.B., Wasmuth,J.J., Evans,G.A. and Montal,M.	
TITLE	Primary structure, chromosomal localization, and functional expression of a voltage-gated sodium channel from human brain	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (17), 8220-8224 (1992)	
MEDLINE	92390418	
PUBMED	1325650	
REFERENCE	2 (bases 1 to 6328)	
AUTHORS	Sun,W.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-OCT-1992) William Sun, Biology Department, 9500 Gilman Drive, University of California, San Diego, La Jolla, CA 92093-0357, USA	
COMMENT	On Feb 25, 1994 this sequence version replaced gi:183806.	
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	FSATPALYILTPFNPIRKLAIKILVHSLFNMLIMCTILTNCVFMTMSNPPDWTKNVEY	
	TFTGIYTFESLIKILARGFCLEDFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRT	
	FRVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRN	
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	VSQASRASRVLPILPMNGKMHSAVDCNGVVSLVGGPSTLTSAGQLLPEGTTTETEIRK	
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	TGIFTAEMFLKIIAMDPYYYFQEGWNIFDGFIVSLSLMELGLANVEGLSVLRSFRLLR	
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BASE COUNT 1847 a 1257 c 1433 g 1791 t
ORIGIN

Query Match 69.9%; Score 4217.4; DB 9; Length 6328;
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Matches 4988; Conservative 2; Mismatches 988; Indels 69; Gaps 11;

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Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
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Qy    120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
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Db   4798 TGGATTAATCTGGTGTTTATTGTTCTGTTCACTGGAGAATGTGTGCTGAAACTGATCTCT 4857

Qy   4783 CTACGCCATTATTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTC 4842
          || ||  | || ||||| || |||||||||||||||||||||||||||||||| |||||||||
Db   4858 CTTCGTTACTACTATTTCACTATTGGATGGAATATTTTTGATTTTGTGGTGGTCATTCTC 4917

Qy   4843 TCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTG 4902
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Qy   4903 TTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAG 4962
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Qy   4963 GGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGC 5022
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Qy   5023 CTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTAT 5082
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Qy   5083 GTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATG 5142
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Qy   5143 ATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTC 5202
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Qy   5203 AACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGA 5262
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Qy   5263 GACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTC 5322
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Qy   5323 CTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAA 5382
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Qy   5443 TTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCG 5502
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Qy   5623 GTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATG 5682
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Qy   5683 GCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAA 5742
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Qy   5983 GAAAAACATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATA 6029
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Search completed: April 22, 2003, 09:58:47
Job time : 10048 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 05:50:48 ; Search time 767 Seconds
(without alignments)
17704.759 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6028.8	100.0	6030	24	AAD32844	Human ion channel
2	6015.2	99.8	8378	22	AAH55763	Human adult form o
3	6006.6	99.6	6027	24	AAD27266	Human transporter
4	5963.2	98.9	8378	22	AAH55764	Human neonatal for
5	5952.8	98.7	5997	24	AAD32839	Human ion channel
6	5917.4	98.1	8131	24	ABL39689	Human sodium chann
7	5915.8	98.1	5922	24	AAD32845	Human ion channel
8	5839.8	96.8	5889	24	AAD32840	Human ion channel
9	4336.8	71.9	4362	24	AAD32846	Human ion channel
10	4260.8	70.7	4329	24	AAD32841	Human ion channel
11	4219	70.0	8349	22	AAH55793	Human adult form o
12	4219	70.0	8349	22	AAH55794	Human neonatal for
13	4150.8	68.8	4179	24	AAD32847	Human ion channel
14	4074.8	67.6	4146	24	AAD32842	Human ion channel
15	4057.8	67.3	4197	24	AAD32848	Human ion channel
16	4045	67.1	9123	24	ABL39690	Human sodium chann
17	3981.8	66.0	4164	24	AAD32843	Human ion channel
18	3785.4	62.8	9112	22	AAH55823	Human adult form o
19	3758.2	62.3	9112	22	AAH55824	Human neonatal for
20	3563.8	59.1	6822	24	ABK63697	Rat sequence diffe
21	3541.6	58.7	6404	17	AAT30195	Peripheral nervous
22	3476.8	57.7	6371	17	AAT30194	Peripheral nervous
23	3397.6	56.3	6452	17	AAT30193	Peripheral nervous
24	2807	46.6	7053	21	AAA93791	Human cDNA encodin
25	2807	46.6	7053	24	AAL42751	Human sodium chann
26	2787.6	46.2	6007	19	AAV58421	Tetrodotoxin-sensi
27	2758.2	45.7	6586	19	AAV58423	PN4 sodium channel
28	2738.8	45.4	5977	19	AAV58420	Tetrodotoxin-sensi
29	2738.8	45.4	6556	19	AAV58419	PN4 sodium channel
30	1962.4	32.5	6021	24	ABL42420	Rat voltage gated
31	1907.2	31.6	6048	19	AAV09029	Human hH1 sodium c
32	1907.2	31.6	6048	22	AAF30825	Human SCN5A gene.
33	1890.6	31.4	7555	16	AAQ81328	Cardiac sodium cha
34	1865	30.9	7555	11	AAQ05831	Cardiac sodium cha
35	1828.6	30.3	8530	22	AAS31089	Human diagnostic a
36	1789.8	29.7	3033	17	AAT30192	Peripheral nervous
37	1590	26.4	6606	20	AAX60872	NaNG polypeptide e
38	1544.4	25.6	5874	22	AAI66961	Human SNS1 ion cha
39	1542.8	25.6	5874	22	AAF57016	Human hPN3 cDNA se
40	1494.6	24.8	6373	22	AAI66960	Mouse SNS1 ion cha
41	1474.8	24.5	6527	18	AAT77806	cDNA encoding vari
42	1469	24.4	6524	18	AAT77803	cDNA encoding wild
43	1468.4	24.4	6344	22	AAI66959	Rat SNS1 ion chann
44	1468.4	24.4	6344	22	AAF57009	Rat PN3 cDNA seque
45	1361.4	22.6	7052	18	AAT77805	cDNA encoding vari

ALIGNMENTS

RESULT 1
AAD32844
ID AAD32844 standard; cDNA; 6030 BP.
XX
AC AAD32844;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #6.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..6030
FT /*tag= a
FT /product= "Human ion channel protein #6"
FT /transl_except= (pos:2974..2976, aa:Xaa)
FT /transl_except= (pos:3199..3201, aa:Xaa)
FT /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX

PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20515.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 2; Page 55-57; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other;

Query Match 100.0%; Score 6028.8; DB 24; Length 6030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy     5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy     6001 GGCAAAGATGAAAAAGCCAAAGGAAATAA 6030
              ||||||||||||||||||||||||||||||
Db     6001 GGCAAAGATGAAAAAGCCAAAGGAAATAA 6030


RESULT 2
AAH55763
ID   AAH55763 standard; cDNA; 8378 BP.
XX
AC   AAH55763;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99674.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 90-93; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

  Query Match             99.8%;  Score 6015.2;  DB 22;  Length 8378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6025;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy       61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy      121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy      181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy      241 GACCCCTACTATATCAATAAGAAAACTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      506 GACCCCTACTATATCAATAAGAAAACTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy      301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy      361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy      421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy      481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy      541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy      601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      866 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 925

Qy      661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      926 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy      721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy      781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy      841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy      901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy      961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy     1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy     1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy  1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy  1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
         ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy  1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy  1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy  1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy  1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy  1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy  1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy  1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy  1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy  1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065

Qy  1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy  1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2186 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2245

Qy  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2246 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2305

Qy  2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2306 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2365

Qy  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2366 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2425

Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2426 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2485

Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

Qy  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
         ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db  2546 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2605

Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2606 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2665

Qy  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2666 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2725

Qy  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785

Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845

Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2966 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3025

Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085

Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145

Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205

Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
         ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db  3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3265

Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3266 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3325

Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3326 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3385

Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3386 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3445

Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
         ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db  3446 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3505

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAAATACATTATTGATGAAAGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3506 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3565
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Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3566 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3625

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3626 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3685

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3686 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3745

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3746 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3805

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3806 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3865

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3866 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3925

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   3926 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTC-GGCATTTGAAGATATA 3984

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 4104

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4165 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4224

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4225 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4284

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4285 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4344

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4345 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4404

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4405 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4464

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4465 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4524

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4525 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4584

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4585 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4644

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4765 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4824

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4825 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4884

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4885 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4944

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4945 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5004

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5005 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 5064

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5065 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 5124

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5125 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 5184

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5185 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 5244

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5245 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5304

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5305 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5364

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5365 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5424

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5425 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5484

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5485 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5544

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5545 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5604

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5605 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5664

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5665 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5724

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    5725 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5784

Qy    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5785 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5844

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5845 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5904

Qy    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5905 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5964

Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5965 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 6024

Qy    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6025 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 6084

Qy    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6085 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 6144

Qy    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6145 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6204

Qy    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6205 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6264

Qy    6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
           ||||||||||||||||||||||||||||||
Db    6265 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6294


RESULT 3
AAD27266
ID   AAD27266 standard; cDNA; 6027 BP.
XX
AC   AAD27266;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human transporter and ion channel-13 (TRICH-13) cDNA.
XX
KW   Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW   nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW   antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW   Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW   amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW   Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW   cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW   bradyarrythmia; gene expression; drug screening; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..6027
FT                   /*tag= a
FT                   /product= "Human TRICH-13 protein"
FT                   /note= "CDS does not include stop codon"
FT                   /partial
XX
PN   WO200192304-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US17065.
XX
PR   26-MAY-2000; 2000US-208424P.
PR   01-JUN-2000; 2000US-209001P.
PR   08-JUN-2000; 2000US-210588P.
PR   16-JUN-2000; 2000US-212335P.
PR   22-JUN-2000; 2000US-213747P.
PR   29-JUN-2000; 2000US-215391P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Thornton M,  Walia NK,  Yue H,  Nguyen DB,  Lai P,  Gandhi AR;
PI   Tribouley CM,  Yao MG,  Ramkumar J,  Au-Young J,  Lu Y,  Tang YT;
PI   Azimzai Y,  Bruns CM,  Griffin JA,  Yang J,  Sanjanwala MS;
PI   Raumann BE,  Lee EA,  Hafalia A,  Baughn MR,  Green BD,  Khan FA;
PI   Kearney L,  Elliot VS,  Seilhamer JJ,  Policky JL,  Borowsky ML;
PI   Burford N,  Ding L,  Lu DAM,  Hillman JL;
XX
DR   WPI; 2002-122055/16.
DR   P-PSDB; AAE16776.
XX
PT   New human transporters and ion channels (TRICH) polypeptides useful for
PT   diagnosing, treating or preventing disorders associated with aberrant
PT   expression of TRICH  -
XX
PS   Claim 11; Page 196-197; 210pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH)
CC   polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC   sequences are useful in the diagnosis, treatment, and prevention of
CC   disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC   palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC   amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC   muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC   asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC   cardiac disease (angina, hypertension, or bradyarrythmia) and in the
CC   assessment of the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of transporters and ion channels.
CC   The polynucleotides may be used to detect and quantify gene expression
CC   in biopsied tissues in which TRICH expression may be correlated with a
CC   disease, to generate hybridization probes for mapping naturally occurring
CC   genomic sequence, and in drug screening. The present sequence is human
CC   TRICH-13 cDNA.
XX
SQ   Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;

  Query Match             99.6%;  Score 6006.6;  DB 24;  Length 6027;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 6012;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
           |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGCAGACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAGTACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Db    961 TCAGGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Db   1021 GATGCAGGGCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Db   1201 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Db   2281 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Db   2401 ACAGTAGGAAACTTGGTATTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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```
Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGGGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db   2941 CTAGTGGTACTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db   3541 TTCACTGAAGGTTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTAGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Db   4321 GCAGTTGATTCCAGAAATGTAGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
          ||||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
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RESULT 4
AAH55764
ID AAH55764 standard; cDNA; 8378 BP.
XX
AC AAH55764;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99675.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 93-96; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Query Match 98.9%; Score 5963.2; DB 22; Length 8378;
Best Local Similarity 99.5%; Pred. No. 0;

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Matches 5999;  Conservative    3;  Mismatches   26;  Indels    2;  Gaps    2;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db     326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
Db     506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
Db     566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db     626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db     686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db     746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Db     806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db     866 GCGTTTGTAACAGAATTTGTAAACCTAGGCAATTTTTCAGCTCTTCGCACTTTCAGAGTC 925

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db     926 TTGAGAGCTTTGAAAACTATTTCGGTAATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db     986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db    1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db    1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db    1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db    1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db    1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db    1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db    1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db    1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db    1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db    1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db    1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db    1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db    1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db    1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db    2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGC-CAGCACCTTTGAGGAT 2064

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db    2065 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2124

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db    2125 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2184

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db    2185 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2244

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db    2245 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2304

Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db    2305 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2364

Qy    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db    2365 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2424
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Qy 2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db 2425 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2484
Qy 2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db 2485 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2544
Qy 2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db 2545 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2604
Qy 2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db 2605 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2664
Qy 2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db 2665 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2724
Qy 2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db 2725 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2784
Qy 2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db 2785 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2844
Qy 2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db 2845 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2904
Qy 2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db 2905 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2964
Qy 2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db 2965 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3024
Qy 2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db 3025 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3084
Qy 2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db 3085 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3144
Qy 2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db 3145 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3204
Qy 2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db 3205 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3264
Qy 3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db 3265 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3324
Qy 3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db 3325 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3384
Qy 3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db 3385 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3444
Qy 3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db 3445 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3504
Qy 3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db 3505 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3564
Qy 3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db 3565 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3624
Qy 3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db 3625 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3684
Qy 3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db 3685 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3744
Qy 3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db 3745 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3804
Qy 3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db 3805 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3864
Qy 3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db 3865 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3924
Qy 3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db 3925 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3984
Qy 3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db 3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044
Qy 3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db 4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAA-ATATTTC 4103
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Db 4344 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4403
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Db 4524 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4583
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RESULT 5
AAD32839
ID AAD32839 standard; cDNA; 5997 BP.
XX
AC AAD32839;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #1.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..5997
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FT		/product= "Human ion channel protein #1"
FT		/transl_except= (pos:2941..2943, aa:Xaa)
FT		/transl_except= (pos:3166..3168, aa:Xaa)
FT		/note= "Xaa = any amino acid"

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PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.

XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20510.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 28-30; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 5997 BP; 1773 A; 1185 C; 1338 G; 1698 T; 3 other;

Query Match 98.7%; Score 5952.8; DB 24; Length 5997;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 5997; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767
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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847
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Qy    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy    6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
           ||||||||||||||||||||||||||||||
Db    5968 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 5997


RESULT 6
ABL39689
ID   ABL39689 standard; cDNA; 8131 BP.
XX
AC   ABL39689;
XX
DT   10-MAY-2002  (first entry)
XX
DE   Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.
XX
KW   Human; sodium channel; SCN1A; chromosome 2q24; gene; ss;
KW   familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             15..6018
FT                   /*tag= a
FT                   /product= "sodium channel SCN1A"
XX
PN   WO200196552-A1.
XX
PD   20-DEC-2001.
XX
PF   12-JUN-2001; 2001WO-JP04956.
XX
PR   13-JUN-2000; 2000JP-0177540.
PR   13-JUN-2000; 2000JP-0177544.
XX
PA   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI   Kanazawa I,  Goto J,  Jeong S;
XX
DR   WPI; 2002-098066/13.
DR   P-PSDB; ABB06026.
XX
PT   Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT   studying physiological mechanism in which excitant cells participate
PT   and causes of diseases and developing drugs for motor endplate disease
PT   -
XX
PS   Claim 5; Page 20-40; 88pp; Japanese.
XX
CC   The present invention describes human sodium channels SCN1A and SCN3A.
CC   The present sequence encodes the human sodium channel SCN1A. SCN1A and
CC   SCN3A have been located to the human chromosome 2 long arm, positions
CC   2q24 and 2q24-31 respectively. The sodium channel proteins are useful
CC   in studying the physiological mechanism in which excitant cells
CC   participate and cause human diseases, and in developing remedies for
CC   e.g. familial hypercalcaemic periodic paralysis of extremities and
CC   motor endplate disease.
XX
SQ   Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other;

  Query Match             98.1%;  Score 5917.4;  DB 24;  Length 8131;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 5980;  Conservative    3;  Mismatches   14;  Indels   36;  Gaps    2;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      19 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 78

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 138

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 198

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 258

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 318

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 378

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 438

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     439 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 498

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     499 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 558

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     559 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 618

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     619 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 678

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     679 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 738

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     739 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 798

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     799 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 858

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     859 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 918

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     919 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 978

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     979 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1038

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1039 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1098

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1099 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTCTGTCCTTGTTTCGACTAATGACT 1158
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Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1159 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1218

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1219 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1278

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1279 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1338

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1339 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1398

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1399 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1458

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1459 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1518

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1519 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1578

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1579 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1638

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1639 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1698

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1699 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGT 1758

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1759 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1818

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1819 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1878

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1879 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1938

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1998

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          |||||||||||||||||||||||| |
Db   1999 ACATCGCCTGTTGGACAGCTTCTGCCAGGG---------------------------- 2028

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2085

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2086 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2145

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2146 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2205
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   2206 TTTTCCAACATATTCTCAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2265

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2266 GTCAACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2325

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2326 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2385

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2386 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2445

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2446 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2505

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2506 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2565

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2566 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2625

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2626 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2685

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2686 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2745

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCC---ACGCTGGCACATGAATGACTTCTTCCAC 2817
          |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db   2746 TGCAAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCAC 2805

Qy   2818 TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGT 2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2806 TCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGT 2865

Qy   2878 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2866 ATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGA 2925

Qy   2938 AACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAAC 2997
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db   2926 AACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAAC 2985

Qy   2998 CTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATG 3057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2986 CTTGCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATG 3045

Qy   3058 CACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATT 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3046 CACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATT 3105

Qy   3118 AGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGAC 3177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3106 AGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGAC 3165

Qy   3178 AGTTGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTA 3237
          ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db   3166 AGTTGTATGTCCAATCATACAACAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTA 3225

Qy   3238 AATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAA 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3226 AATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAA 3285

Qy   3298 AGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTA 3357
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Db   3286 AGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTA 3345

Qy   3358 GGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAA 3417

Db   3346 GGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAA 3405

Qy   3418 GAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATC 3477

Db   3406 GAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGGACAT 3465

Qy   3478 GGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCT 3537

Db   3466 CGGCGCCCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCT 3525

Qy   3538 TGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGC 3597

Db   3526 TGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGC 3585

Qy   3598 AGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGG 3657

Db   3586 AGAGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGG 3645

Qy   3658 TTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGAT 3717

Db   3646 TTTGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGAT 3705

Qy   3718 ATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTC 3777

Db   3706 ATATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTC 3765

Qy   3778 ACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATAT 3837

Db   3766 ACTTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATAT 3825

Qy   3838 TTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTA 3897

Db   3826 TTCACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTA 3885

Qy   3898 ACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGA 3957

Db   3886 ACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGA 3945

Qy   3958 GCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCC 4017

Db   3946 GCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCC 4005

Qy   4018 CTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTA 4077

Db   4006 CTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTA 4065

Qy   4078 ATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACC 4137

Db   4066 ATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACC 4125

Qy   4138 ACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTA 4197

Db   4126 ACAACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTA 4185

Qy   4198 ATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGA 4257

Db   4186 ATAGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGA 4245

Qy   4258 TTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTAT 4317

Db   4246 TTTGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTAT 4305

Qy   4318 GCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATG 4377

Db   4306 GCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATG 4365

Qy   4378 TATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATT 4437

Db   4366 TATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATT 4425

Qy   4438 GGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTT 4497

Db   4426 GGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTT 4485

Qy   4498 ATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCG 4557

Db   4486 ATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCG 4545

Qy   4558 CAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACC 4617

Db   4546 CAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACC 4605

Qy   4618 AGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATG 4677

Db   4606 AGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATG 4665

Qy   4678 GTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTG 4737

Db   4666 GTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTG 4725

Qy   4738 TTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTAT 4797

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Qy   4798 TTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATG 4857

Db   4786 TTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATG 4845

Qy   4858 TTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGT 4917

Db   4846 TTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGT 4905

Qy   4918 CTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTG 4977

Db   4906 CTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTG 4965

Qy   4978 CTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTA 5037

Db   4966 CTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTA 5025

Qy   5038 GTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTT 5097

Db   5026 GTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTT 5085

Qy   5098 GGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAA 5157

Db   5086 GGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAA 5145

Qy   5158 ATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCC 5217

Db   5146 ATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCC 5205

Qy   5218 GACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCA 5277

Db   5206 GACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCA 5265

Qy   5278 TCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAAC 5337

Db   5266 TCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAAC 5325

Qy   5338 ATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCT 5397

Db   5326 ATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCT 5385

Qy   5398 CTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCA 5457

Db   5386 CTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCA 5445

Qy   5458 ACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTC 5517

Db   5446 ACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTC 5505
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Qy   5518 AATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGT 5577
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Db   5506 AATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGT 5565

Qy   5578 GACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGT 5637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5566 GACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGT 5625

Qy   5638 GGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCC 5697
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Db   5626 GGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCC 5685

Qy   5698 AAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCT 5757
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Db   5686 AAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCT 5745

Qy   5758 GTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCC 5817
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Db   5746 GTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCC 5805

Qy   5818 TTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATG 5877
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Db   5806 TTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATG 5865

Qy   5878 ATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACT 5937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5938 GCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAA 5997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5926 GCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAA 5985

Qy   5998 GAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
          ||||||||||||||||||||||||||||||||
Db   5986 GAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6018


RESULT 7
AAD32845
ID   AAD32845 standard; cDNA; 5922 BP.
XX
AC   AAD32845;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #7.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5922
FT                   /*tag= a
FT                   /product= "Human ion channel protein #7"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20516.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 62-64; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;

  Query Match             98.1%;  Score 5915.8;  DB 24;  Length 5922;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
          |||||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
```

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RESULT 8
AAD32840
ID   AAD32840 standard; cDNA; 5889 BP.
XX
AC   AAD32840;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5889
FT                   /*tag= a
FT                   /product= "Human ion channel protein #2"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20511.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 35-36; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;
```

Query Match 96.8%; Score 5839.8; DB 24; Length 5889;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 5884; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db    2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db  2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Db  2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db  2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db  3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db  3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Db  3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Qy  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Qy  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Qy  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
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RESULT 9
AAD32846
ID AAD32846 standard; cDNA; 4362 BP.
XX
AC AAD32846;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #8.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..4362
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FT		/product= "Human ion channel protein #8"
FT		/transl_except= (pos:2974..2976, aa:Xaa)
FT		/transl_except= (pos:3199..3201, aa:Xaa)
FT		/note= "Xaa = any amino acid"

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PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX

DR WPI; 2002-280757/32.
DR P-PSDB; AAE20517.
XX
PT Novel polynucleotides encoding human sodium channel proteins, particularly voltage-gated sodium channel proteins useful for drug screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 69-70; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion channel protein. NHP share structural similarity with mammalian sodium channel proteins particularly voltage-gated sodium channel proteins. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are useful to genetically engineer host cells to express NHP products in vivo. These genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products in vivo. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases.
XX
SQ Sequence 4362 BP; 1300 A; 845 C; 995 G; 1219 T; 3 other;

Query Match 71.9%; Score 4336.8; DB 24; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAAT 4338
          |||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAAT 4338
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RESULT 10
AAD32841
ID   AAD32841 standard; cDNA; 4329 BP.
XX
AC   AAD32841;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #3.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4329
FT                   /*tag= a
FT                   /product= "Human ion channel protein #3"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;.
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20512.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 41-42; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4329 BP; 1287 A; 840 C; 988 G; 1211 T; 3 other;
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  Query Match             70.7%;  Score 4260.8;  DB 24;  Length 4329;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 4305;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db  2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Db  2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Db  2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Db  2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Db  2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Db  2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Db  2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Db  3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Db  3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Db  3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Db  3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Db  3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Db  3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Db  3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Db  3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Db  3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Db  3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Db  3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Db  3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Db  3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Db  3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Db  3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Db  4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Db  4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Db  4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Db  4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy  4321 GCAGTTGATTCCAGAAAT 4338

Db  4288 GCAGTTGATTCCAGAAAT 4305
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RESULT 11
AAH55793
ID AAH55793 standard; cDNA; 8349 BP.
XX
AC AAH55793;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human adult form of SCN2A nucleotide sequence SEQ ID NO:33.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX
PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX

PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99676.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 116-119; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 8349 BP; 2496 A; 1591 C; 1775 G; 2487 T; 0 other;

Query Match 70.0%; Score 4219; DB 22; Length 8349;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 4989; Conservative 2; Mismatches 987; Indels 69; Gaps 11;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db     106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
Db     166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

Qy     120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
Db     226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy     178 AACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGAC 237
Db     286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy     238 CTGGACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATC 297
Db     346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy     298 TTCCGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAA 357
Db     406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy     358 ATAGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTG 417
Db     466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525

Qy     418 ACAAACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATAC 477
Db     526 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 585

Qy     478 ACCTTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGT 537
Db     586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy     538 TTAGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACA 597
Db     646 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 705

Qy     598 TTTGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGA 657
Db     706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765

Qy     658 GTTCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCC 717
Db     766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825

Qy     718 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 777
Db     826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885

Qy     778 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 837
Db     886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945

Qy     838 TGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGTG 894
Db     946 TGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATTG 1005

Qy     895 AATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATT 954
Db    1006 GATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATATT 1065

Qy     955 CAAGATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAAT 1014
Db    1066 GAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCTCTGCTTTGTGGCAAC 1125

Qy    1015 AGCTCTGATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCC 1074
Db    1126 AGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAGGCTGGTAGAAACCCC 1185

Qy    1075 AATTATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTA 1134
Db    1186 AACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTGTCCTTATTTCGTCTC 1245

Qy    1135 ATGACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACG 1194
Db    1246 ATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGTGCTGCTGGGAAAACG 1305

Qy    1195 TACATGATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATC 1254
Db    1306 TACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTATCTAATAAATTTGATC 1365

Qy    1255 CTGGCTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAA 1314
Db    1366 TTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACATTGGAAGAGGCTGAA 1425

Qy    1315 CAGAAAGAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCT 1374
Db    1426 CAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAGCAACAAGAAGAAGCT 1485

Qy    1375 CAGCAGGCAGCAACGG------CAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCA 1428
Db    1486 CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTCAGTGGTGCTGGTGGGATA 1545

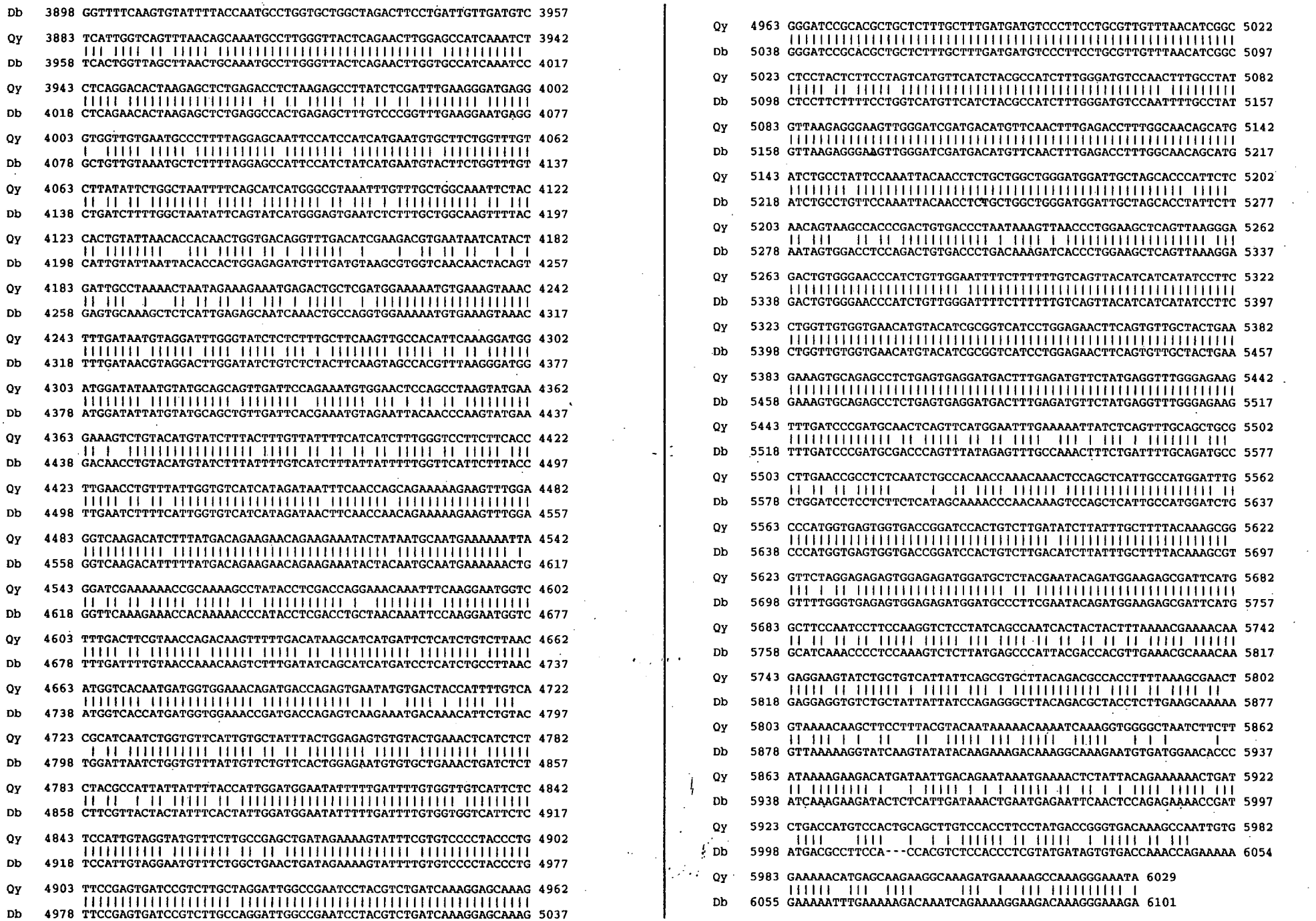
Qy    1429 GGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAA 1488
Db    1546 GGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGCTCCAAAAGTGAAAAAGAG 1605

Qy    1489 AGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGAT 1548
Db    1606 CTGAAAAACAGAAGAAAGAAAAAGAAACAGAAAGAACAGTCTGGAGAAGAAGAGAAAAAT 1665

Qy    1549 GAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTC 1608
Db    1666 GACAGAG---TCCTAAAATCGGAATCTGAAGACAGCATAAGAAGAAAAGGTTTCCGTTTT 1722

Qy    1609 TCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTG 1668
Db    1723 TCCTTGGAAGGAAGTAGGCTGACATATGAAAAGAGATTTTCTTCTCCACACCAGTCCTTA 1782
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RESULT 12
AAH55794
ID   AAH55794 standard; cDNA; 8349 BP.
XX
AC   AAH55794;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human neonatal form of SCN2A nucleotide sequence SEQ ID NO:34.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99677.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 119-122; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8349 BP; 2496 A; 1591 C; 1775 G; 2487 T; 0 other;

  Query Match             70.0%;  Score 4219;  DB 22;  Length 8349;
  Best Local Similarity   82.5%;  Pred. No. 0;
  Matches 4989;  Conservative    2;  Mismatches  987;  Indels   69;  Gaps   11;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db     106 ATGGCACAGTCAGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 165

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
Db     166 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 225

Qy     120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
Db     226 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 285

Qy     178 AACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGAC 237
Db     286 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 345

Qy     238 CTGGACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATC 297
Db     346 CTGGACCCCTACTATATCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 405

Qy     298 TTCCGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAA 357
Db     406 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 465

Qy     358 ATAGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTG 417
Db     466 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 525

Qy     418 ACAAACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATAC 477
Db     526 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 585

Qy     478 ACCTTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGT 537
Db     586 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 645

Qy     538 TTAGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACA 597
Db     646 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 705

Qy     598 TTTGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGA 657
Db     706 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 765

Qy     658 GTTCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCC 717
Db     766 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 825

Qy     718 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 777
Db     826 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 885

Qy     778 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 837
Db     886 GTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 945

Qy     838 TGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGTG 894
Db     946 TGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATTG 1005

Qy     895 AATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATT 954
Db    1006 GATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATATT 1065

Qy     955 CAAGATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAAT 1014
Db    1066 GAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCTCTGCTTTGTGGCAAC 1125

Qy    1015 AGCTCTGATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCC 1074
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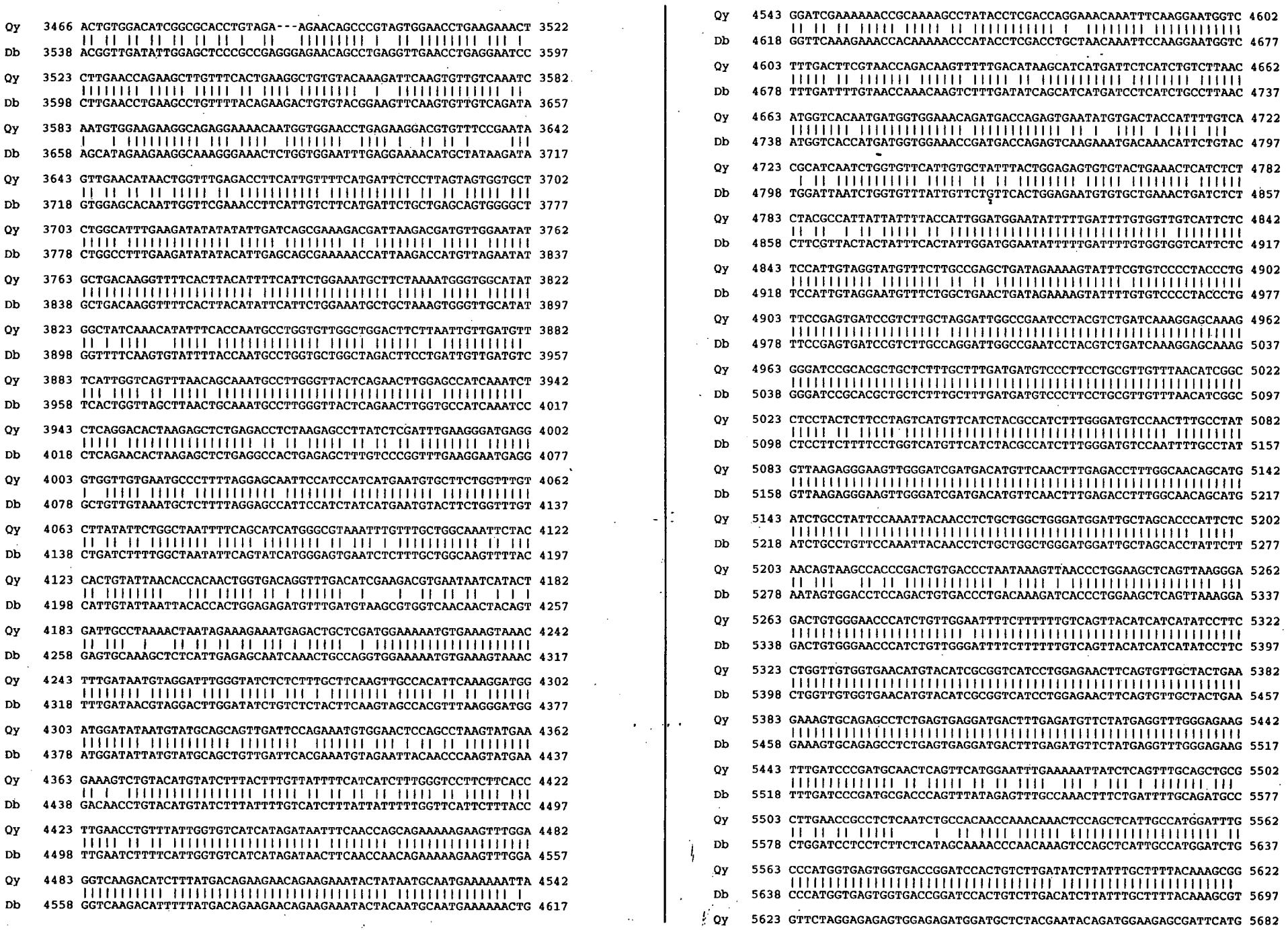
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Db    1186 AACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTGTCCTTATTTCGTCTC 1245

Qy    1135 ATGACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACG 1194
Db    1246 ATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGTGCTGCTGGGAAAACG 1305

Qy    1195 TACATGATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATC 1254
Db    1306 TACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTATCTAATAAATTTGATC 1365

Qy    1255 CTGGCTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAA 1314
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Db 1366 TTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACATTGGAAGAGGCTGAA 1425
Qy 1315 CAGAAAGAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCT 1374
Db 1426 CAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAGCAACAAGAAGAAGCT 1485
Qy 1375 CAGCAGGCAGCAACGG------CAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCA 1428
Db 1486 CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTCAGTGGTGCTGGTGGGATA 1545
Qy 1429 GGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAA 1488
Db 1546 GGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGCTCCAAAAGTGAAAAAGAG 1605
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Qy 1549 GAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTC 1608
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Qy 1669 TTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGC 1728
Db 1783 CTGAGCATCCGTGGCTCCCTTTTCTCTCCAAGACGCAACAGTAGGGCGAGCCTTTTCAGC 1842
Qy 1729 TTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGC 1788
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Db 2083 CCTTCTACCCTCACAT---CTGCTGGGCAGCTCCTACCAGAG---------- 2121
Qy 2029 GCTACTGATGACAATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCT 2088
Db 2122 ----------GGCACAACTACTGAAACAGAAATAAGAAAGAGACGGTCCAGTTCT 2166
Qy 2089 TTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATA 2148
Db 2167 TATCATGTTTCCATGGATTTATTGGAAGATCCTACATCAAGGCAAAGAGCAATGAGTATA 2226
Qy 2149 GCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCC 2208
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Qy 2209 TGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAA 2268
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Qy 2449 CTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGAC 2508
Db 2527 CTCAAGATAATTGCCATGGATCCATATTATTACTTTCAAGAAGGCTGGAATATTTTTGAT 2586
Qy 2509 GGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCT 2568
Db 2587 GGTTTTATTGTGAGCCTTAGTTTAATGGAACTTGGTTTGGCAAATGTGGAAGGATTGTCA 2646
Qy 2569 GTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTA 2628
Db 2647 GTTCTCCGATCATTCCGGCTGCTCCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACTCTA 2706
Qy 2629 AATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTC 2688
Db 2707 AATATGCTAATTAAGATCATTGGCAATTCTGTGGGGGCTCTAGGAAACCTCACCTTGGTA 2766
Qy 2689 TTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTAC 2748
Db 2767 TTGGCCATCATCGTCTTCATTTTTGCTGTGGTCGGCATGCAGCTCTTTGGTAAGAGCTAC 2826
Qy 2749 AAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGAC 2808
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Qy 2809 TTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATG 2868
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Qy 2869 TGGGACTGTATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATG 2928
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Qy 2929 GTGATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGT 2988
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Qy 3109 TCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAAC 3168
Db 3187 GCCTTTGTTAGGAAGCAGAAAGCTTTAGATGAAATTAAACCGCTTGAAGATCTAAATAAT 3246
Qy 3169 AAGAAAGACACGTTGTATGTCCAATCATACARC---AGAAATTGGGAAAGATCTTGACTAT 3225
Db 3247 AAAAAAGACAGCTGTATTTCCAACCATACCACCATAGAAATAGGCAAAGACCTCAATTAT 3306
Qy 3226 CTTAAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATAC 3285
Db 3307 CTCAAAGACGGAAATGGAACTACTAGTGGCATA------GGCAGCAGTGTAGAAAAATAT 3360
Qy 3286 ATTATTGATGAAAGTGATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTA 3345
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Qy 3346 CCAATTGCTGTAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAA 3405
Db 3421 CCAATTGCTGTTGGAGAATCTGACTTTGAAAATTTAAATACTGAAGAATTCAGCAGCGAG 3480
Qy 3406 TCGGATCTGGAAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGC 3465
Db 3481 TCAGATATGGAGGAAAGCAAAGAGAAGCTAAATGCA---ACTAGTTCATCTGAAGGCAGC 3537



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Qy   5683 GCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAA 5742

Db   5758 GCATCAAACCCCTCCAAAGTCTCTTATGAGCCCATTACGACCACGTTGAAACGCAAACAA 5817

Qy   5743 GAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACT 5802

Db   5818 GAGGAGGTGTCTGCTATTATTATCCAGAGGGCTTACAGACGCTACCTCTTGAAGCAAAAA 5877

Qy   5803 GTAAAACAAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTT 5862

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Qy   5863 ATAAAAGAAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGAT 5922

Db   5938 ATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAATTCAACTCCAGAGAAAACCGAT 5997

Qy   5923 CTGACCATGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTG 5982

Db   5998 ATGACGCCTTCCA---CCACGTCTCCACCCTCGTATGATAGTGTGACCAAACCAGAAAAA 6054

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Db   6055 GAAAAATTTGAAAAAGACAAATCAGAAAAGGAAGACAAAGGGAAAGA 6101


RESULT 13
AAD32847
ID   AAD32847 standard; cDNA; 4179 BP.
XX
AC   AAD32847;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #9.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Human ion channel protein #9"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20518.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 73-75; 83pp; English.
XX
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CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4179 BP; 1239 A; 815 C; 958 G; 1164 T; 3 other;

  Query Match          68.8%;  Score 4150.8;  DB 24;  Length 4179;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4152;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCCTGGAGGACCTG 240

Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGG 4152
          ||||||||||||
Db   4141 ACTGGTGACAGG 4152
```

RESULT 14
AAD32842
ID AAD32842 standard; cDNA; 4146 BP.
XX
AC AAD32842;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #4.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..4146
FT   /*tag= a
FT   /product= "Human ion channel protein #4"
FT   /transl_except= (pos:2941..2943, aa:Xaa)
FT   /transl_except= (pos:3166..3168, aa:Xaa)
FT   /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20513.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders
XX
PS Claim 1; Page 46-47; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect

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CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;

  Query Match           67.6%;  Score 4074.8;  DB 24;  Length 4146;
  Best Local Similarity  99.2%;  Pred. No. 0;
  Matches 4119;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Db  1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy  1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Db  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
         ||||||||||||||||||||||||||||||
Db  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy  2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db  2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
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Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Db  2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Db  2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Db  2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db  2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db  2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Db  3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db  3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db  3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db  3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   4141 ACTGGTGACAGG 4152
          ||||||||||||
Db   4108 ACTGGTGACAGG 4119
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RESULT 15
AAD32848
ID AAD32848 standard; cDNA; 4197 BP.
XX
AC AAD32848;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #10.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4197
FT /*tag= a
FT /product= "Human ion channel protein #10"
FT /transl_except= (pos:2974..2976, aa:Xaa)
FT /transl_except= (pos:3199..3201, aa:Xaa)
FT /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20519.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 78-79; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;

Query Match 67.3%; Score 4057.8; DB 24; Length 4197;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 4133; Conservative 0; Mismatches 0; Indels 64; Gaps 1;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGA---------- 4000

Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGATAATCTTGCTCCAACT 4020

Qy   4001 ----------GGGTGGTTGTGAATGC 4016

Db   4021 TGGATGGGGTGGAGCGCTGGTTCCTCCCCTGAGCCCTTTATTATGGGTGGTTGTGAATGC 4080

Qy   4017 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4076

Db   4081 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4140

Qy   4077 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAA 4133

Db   4141 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAA 4197
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Search completed: April 22, 2003, 07:08:22
Job time : 804 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 06:56:18 ; Search time 5065 Seconds
(without alignments)
19281.103 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1039.8	17.2	1777	11	BC029489	BC029489 Homo sapi
	2	670	11.1	951	9	AL533359	AL533359 AL533359
	3	668.2	11.1	928	14	BQ715936	BQ715936 AGENCOURT
	4	634.2	10.5	735	13	BI488967	BI488967 603021693
	5	570.6	9.5	579	14	BM718214	BM718214 UI-E-EJ1-
	6	557.4	9.2	674	12	BG342331	BG342331 602374246
c	7	555.8	9.2	562	14	BM682680	BM682680 UI-E-EJ1-
	8	548	9.1	774	13	BI488799	BI488799 603021394
	9	518.8	8.6	618	10	BB622500	BB622500 BB622500
	10	511.6	8.5	602	9	AL706368	AL706368 DKFZp686H
	11	495.8	8.2	778	9	AU035605	AU035605 AU035605
c	12	468.4	7.8	731	9	AI796228	AI796228 wh44d06.x
	13	454.8	7.5	816	14	BQ444145	BQ444145 UI-M-EX0-
c	14	447.8	7.4	706	9	AA984063	AA984063 am76b09.s
	15	438.8	7.3	547	12	BF470392	BF470392 UI-M-BH3-
	16	435.4	7.2	598	14	BM726341	BM726341 UI-E-EJ0-
	17	431.8	7.2	665	10	BB653350	BB653350 BB653350
	18	431.4	7.2	683	13	BI667397	BI667397 603292178
	19	421.4	7.0	689	12	BF347024	BF347024 602021819
	20	414	6.9	510	11	BC023034	BC023034 Mus muscu
	21	413.8	6.9	561	12	BF076296	BF076296 225823 MA
	22	413	6.8	509	11	BC034643	BC034643 Mus muscu
	23	407	6.7	908	14	BQ946179	BQ946179 AGENCOURT
	24	402.4	6.7	700	10	BB631922	BB631922 BB631922
	25	399.2	6.6	873	12	BF527027	BF527027 602039918
	26	398	6.6	662	12	BG253038	BG253038 602365660
	27	397.6	6.6	952	13	BI458325	BI458325 603199282
	28	395.4	6.6	809	12	BG541438	BG541438 602570863
	29	390.6	6.5	508	13	BI731882	BI731882 603353628
	30	389.8	6.5	934	9	AL517958	AL517958 AL517958
	31	388	6.4	513	13	BI731739	BI731739 603353512
	32	384.2	6.4	902	12	BG761119	BG761119 602717452
	33	374.2	6.2	608	10	AW140953	AW140953 EST290960
	34	371	6.2	443	12	BE864903	BE864903 UI-M-BH1-
	35	366.8	6.1	450	9	AL120392	AL120392 DKFZp761E
	36	363.6	6.0	812	12	BG666779	BG666779 DRABWE08
	37	359.2	6.0	939	13	BI600029	BI600029 603251413
c	38	353	5.9	437	10	AW495598	AW495598 UI-M-BH3-
c	39	351.2	5.8	656	10	AV721039	AV721039 AV721039
	40	350.8	5.8	402	13	BM484672	BM484672 538604 MA
	41	350.6	5.8	547	12	BE724185	BE724185 198931 MA
c	42	345.6	5.7	540	10	BE121161	BE121161 UI-R-CA0-
c	43	345.6	5.7	700	17	AQ631408	AQ631408 RPCI-11-4
	44	345.4	5.7	610	9	AL588672	AL588672 AL588672
	45	338	5.6	854	13	BI599275	BI599275 603246719

ALIGNMENTS

RESULT 1
BC029489
LOCUS BC029489 1777 bp mRNA linear HTC 16-MAY-2002
DEFINITION Homo sapiens, clone IMAGE:5278436, mRNA.
ACCESSION BC029489
VERSION BC029489.1 GI:20809571
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1777)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 48 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10337596
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers
source 1. .1777
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5278436"
/tissue_type="Brain, hypothalamus"
/clone_lib="NIH_MGC_96"
/lab_host="DH10B"
/note="Vector: pBluescript"

BASE COUNT 526 a 333 c 395 g 523 t
ORIGIN

Query Match 17.2%; Score 1039.8; DB 11; Length 1777;
Best Local Similarity 81.4%; Pred. No. 1.3e-235;
Matches 1245; Conservative 0; Mismatches 272; Indels 12; Gaps 3;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||  ||  | ||||| ||||| |||||||||||||||||  |||||| ||||| |||
Db    248 ATGGCACAGTCGGTGCTGGTACCGCCAGGACCTGACAGCTTCCGCTTCTTTACCAGGGAA 307

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGA- 119
          || ||||| |||||||||  |||||||||||||||| || || ||||  |||||||  ||
Db    308 TCCCTTGCTGCTATTGAACAACGCATTGCAGAAGAGAAAGCTAAGAGACCCAAACAGGAA 367

Qy    120 --CAAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAG 177
            |||  | || || || ||||||||||||||||||||||| |||||||||||||| |||||
Db    368 CGCAAGGATGAGGATGATGAAAATGGCCCAAAGCCAAACAGTGACTTGGAAGCAGGAAAA 427

Qy    178 AACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGAC 237
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    428 TCTCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGTGCCCCTGGAGGAT 487

Qy    238 CTGGACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATC 297
          |||||||||||||||| |||||||||||| ||||||||||||||||||||||| || |||
Db    488 CTGGACCCCTACTATGTCAATAAGAAAACGTTTATAGTATTGAATAAAGGGAAAGCAATC 547

Qy    298 TTCCGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAA 357
          |  || |||||||||||| ||||||| |||||||||||||||||||| ||| |||| |||
Db    548 TCTCGATTCAGTGCCACCCCTGCCCTTTACATTTTAACTCCCTTCAACCCTATTAGAAAA 607

Qy    358 ATAGCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTG 417
          ||||||||||||||||||||||||||||||| |||||||  ||||| |||||||||| ||| |
Db    608 TTAGCTATTAAGATTTTGGTACATTCTTTATTCAATATGCTCATTATGTGCACGATTCTT 667

Qy    418 ACAAACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATAC 477
          || |||||||| |||||||| |||||||||||||| || ||||||||||||||| || ||
Db    668 ACCAACTGTGTATTTATGACCATGAGTAACCCTCCAGACTGGACAAAGAATGTGGAGTAT 727

Qy    478 ACCTTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGT 537
          ||||| |||||||| |||||||||||||||||||||| |||||  |||||||||| || |||
Db    728 ACCTTTACAGGAATTTATACTTTTGAATCACTTATTAAAATACTTGCAAGGGGCTTTTGT 787

Qy    538 TTAGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACA 597
          |||||||||| || ||  | |||||||||||||| ||| | |||||||| ||||||||
Db    788 TTAGAAGATTTCACATTTTTACGGGATCCATGGAATTGGTTGGATTTCACAGTCATTACT 847

Qy    598 TTTGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGA 657
          ||||| || || |||||||||||||||||||||||||||||| || ||||||||||||||
Db    848 TTTGCATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGA 907

Qy    658 GTTCTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCC 717
          |||||||||||||||| || |||||||||||||||||||||| |||||||||| |||
Db    908 GTTCTCCGAGCATTGAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGTGGGGGCC 967

Qy    718 CTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGC 777
          |||||||||||| |||||||||||| || ||||| |||||| |||||||||||||||| |||
Db    968 CTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAGC 1027

Qy    778 GTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAA 837
          || || || ||||| ||  ||||| |||||||||||||||||  | ||||||||| | |||
Db   1028 GTGTTCGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCAA 1087

Qy    838 TGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGTG 894
          ||||||||    ||| ||||||| ||  | ||   | |        || |   |  ||
Db   1088 TGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATTG 1147

Qy    895 AATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATT 954
          ||   ||||||||   | | |||   || ||       ||| ||||| |   |||||||
Db   1148 GATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATATT 1207

Qy    955 CAAGATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAAT 1014
          | |||  ||| |   ||||||  | |||||       ||||| || || ||||| ||
Db   1208 GAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCTCTGCTTTGTGGCAAC 1267

Qy    1015 AGCTCTGATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCC 1074
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Db   1268 AGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAGGCTGGTAGAAACCCC 1327

Qy    1075 AATTATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTA 1134
          || |||||||||||| |||||||| ||||| |||||||| |||||||||| ||||| ||
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Qy    1135 ATGACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACG 1194
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Db   1388 ATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGTGCTGCTGGGAAAACG 1447

Qy    1195 TACATGATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATC 1254
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Db   1448 TACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTATCTAATAAATTTGATC 1507

Qy    1255 CTGGCTGTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAA 1314
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Db   1508 TTGGCTGTGGTGGCCATGGCCTATGAGGAACAGAATCAGGCCACATTGGAAGAGGCTGAA 1567

Qy    1315 CAGAAAGAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCT 1374
          ||||| || || |||||||||||||| | |||||| | |||||||||||| || | ||||
Db   1568 CAGAAGGAAGCTGAATTTCAGCAGATGCTCGAACAGTTGAAAAAGCAACAAGAAGAAGCT 1627

Qy    1375 CAGCAGGCAGCAACGG------CAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCA 1428
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Db   1628 CAGGCGGCAGCTGCAGCCGCATCTGCTGAATCAAGAGACTTCAGTGGTGCTGGTGGGATA 1687

Qy    1429 GGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAA 1488
          ||      | ||||| || || || | ||| |||||||||| |||||  |||| || ||
Db   1688 GGAGTTTTTTCAGAGAGTTCTTCAGTAGCATCTAAGTTGAGCTCCAAAAGTGAAAAAGAG 1747

Qy    1489 AGAAGAAATCGGAGGAAGAAAAGAAAACA 1517
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Db   1748 CTGAAAAACAGAAGAAAAAAAAAAAAAAA 1776
```

RESULT 2
AL533359
LOCUS AL533359 951 bp mRNA linear EST 13-FEB-2001
DEFINITION AL533359 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN004YF22 5 prime, mRNA sequence.
ACCESSION AL533359
VERSION AL533359.1 GI:12796852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 951)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

```
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DN004YF22"
                     /clone_lib="LTI_FL015_Brn1"
                     /sex="male"
                     /tissue_type="Adult brain"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was constructed by Life Technologies.
                     Contact : Feng Liang Life Technologies, a division of
                     Invitrogen 9800 Medical Center Drive Rockville, Maryland
                     20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      303 a    189 c    203 g    247 t      9 others
ORIGIN

  Query Match             11.1%;  Score 670;  DB 9;  Length 951;
  Best Local Similarity   98.5%;  Pred. No. 7e-148;
  Matches  667;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    5354 TCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACT 5413
           ||||||||||||||::||||||||||||||||||||||||||||||:||||||||||
Db       1 TCCTGGAGAACTTCWKTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAKTGAGGATGACT 60

Qy    5414 TTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAAT 5473
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TTTAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAAT 120

Qy    5474 TTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAA 5533
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Db     121 TTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAA 180

Qy    5534 ACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTC 5593
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Db     181 ACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTC 240

Qy    5594 TTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTC 5653
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Db     241 TTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTC 300

Qy    5654 TACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGC 5713
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Db     301 TACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGC 360

Qy    5714 CAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTG 5773
           ||||||||||||||||||:||||||||:||||||||||||||||||||||||||||||||
Db     361 CAATCACTACTACTTTAAWACGAAAACWAGAGGAAGTATCTGCTGTCATTATTCAGCGTG 420

Qy    5774 CTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAA 5833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAA 480

Qy    5834 ACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGACAGAATAA 5893
           ||||||||||||||||||||||||||||||||:|:|||||||||||||||||||||||||
Db     481 ACAAAATCAAAGGTGGGGCTAATCTTCTTATAAWAKAAGACATGATAATTGACAGAATAA 540

Qy    5894 ATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGTCCACCTT 5953
           |||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     541 ATGATAACTCTATTACAGNAAAAACTGATCTGACCATGTCCACTGCAGCTTGTCCACCTT 600

Qy    5954 CCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAAGATGAAA 6013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAAGATGAAA 660

Qy    6014 AAGCCAAAGGGAAATAA 6030
           |||||||||||||||||
Db     661 AAGCCAAAGGGAAATAA 677


RESULT 3
BQ715936
LOCUS       BQ715936                928 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8294886 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6309535
            5', mRNA sequence.
ACCESSION   BQ715936
VERSION     BQ715936.1  GI:21854835
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13730  row: g  column: 08
            High quality sequence stop: 715.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6309535"
                     /clone_lib="NIH_MGC_129"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: olfactory epithelium; Vector:
                     pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
                     unidirectionally. Primer: Oligo dT. Average insert size
                     2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                     is a NIH_MGC Library."
BASE COUNT      204 a    247 c    227 g    249 t      1 others
ORIGIN

  Query Match             11.1%;  Score 668.2;  DB 14;  Length 928;
  Best Local Similarity   84.0%;  Pred. No. 1.9e-147;
  Matches  778;  Conservative    0;  Mismatches  144;  Indels    4;  Gaps    2;

Qy    4828 GTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTC 4887
           ||||| || |||||||| |||||||| ||||| ||||| |||||||||||| ||||||||
Db       1 GTGGTGGTGATTCTCTCAATTGTAGGAATGTTCCTTGCTGAGCTGATAGAGAAGTATTTT 60

Qy    4888 GTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTG 4947
           ||||| |||||||||||||||| ||||| || || |||||||| |||||||||| |||
Db      61 GTGTCTCCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTG 120

Qy    4948 ATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCG 5007
           |||||||| || |||||||||||||||||||||||||| ||||||||||||||||||||
Db     121 ATCAAAGGCGCCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCG 180

Qy    5008 TTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATG 5067
           |||| |||||||||||||| || ||||| ||||||||||||||||||||||||||||||
Db     181 CTGTTCAACATCGGCCTCCTGCTTTTCCTCGTCATGTTCATCTACGCCATCTTTGGGATG 240

Qy    5068 TCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACC 5127
           |||||||||||||||||||| |  || | ||| || ||||||||||||||||||||||||
Db     241 TCCAACTTTGCCTATGTTAAAAAAGAGGCTGGAATTGATGACATGTTCAACTTTGAGACT 300

Qy    5128 TTTGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTG 5187
           |||||||||||||||||||||||| |||||||| || |||||||| |||||||||||| ||
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Db     301 TTTGGCAACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTG 360

Qy    5188 CTAGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGA 5247
           | || ||||| |||||||||    || || ||||||||||| ||  | || ||||||||
Db     361 TTGGCCCCCATCCTCAACAGTGCACCTCCTGACTGTGACCCTGATGCAATTCACCCTGGA 420

Qy    5248 AGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTAC 5307
           |||||||| |||||||||||||||||||||||| || ||||||||||||||||| |||
Db     421 AGCTCAGTGAAGGGAGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGCTAC 480

Qy    5308 ATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTC 5367
           |||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Db     481 ATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATTGCTGTCATCCTGGAGAACTTC 540

Qy    5368 AGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTAT 5427
           || ||||| || |||||||||||||||| |||||||||| ||||||||||||||||||
Db     541 AGCGTTGCCACAGAAGAAAGTGCAGAGCCCCTGAGTGAGGACGACTTTGAGATGTTCTAC 600

Qy    5428 GAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCT 5487
           ||||| |||||||||| || || || || || |||||||| || ||    ||  | |||
Db     601 GAGGTCTGGGAGAAGTTCGACCCTGACGCCACCCAGTTCATAGAGTTCTGCAAGCTCTCT 660

Qy    5488 CAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTC 5547
           | |||||||||| || || || || |||    |  || | |||||||| ||||||||
Db     661 GACTTTGCAGCTGCCCTGGATCCTCCCCTCCTCATCGCAAAGCCAAACAAAGTCCAGCTC 720

Qy    5548 ATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTT 5607
           |||||||||||  |||||||||||||||| ||||| |||||||| || || |||||||||
Db     721 ATTGCCATGGACCTGCCCATGGTGAGTGGAGACCGCATCCACTGCCTGGACATCTTATTT 780

Qy    5608 GCTTTTACAAAGCGGGTTCTAGG--AGAGAGTGGAGAGATGGATGCTCTACGAATACAGA 5665
           |||||||||||||||| |  ||     |||||||| |||||||| ||   ||  ||||
Db     781 GCTTTTACAAAGCGGGTCCCTGGGTGANAAGTGGAGAAATGGATGCCCTTTCAAATCAGA 840

Qy    5666 --TGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTAC 5723
             | |    | |||||||||||||||| |||| || ||| |||    | || |  ||
Db     841 ATGGAAGATCGGGTTCATGGCTTCCAATCCCTCCAGGGGCTCTTATTGAGCCATTAACAC 900

Qy    5724 TACTTTAAAACGAAAACAAGAGGAAG 5749
            ||| | || ||  ||| ||| | ||
Db     901 CACTCTGAAGCGCCAACCAGAAGGAG 926


RESULT 4
BI488967
LOCUS       BI488967                735 bp    mRNA    linear   EST 28-AUG-2001
DEFINITION  603021693F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192182 5',
            mRNA sequence.
ACCESSION   BI488967
VERSION     BI488967.1  GI:15328195
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11480  row: j  column: 23
            High quality sequence stop: 728.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5192182"
                     /clone_lib="NIH_MGC_114"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      164 a    173 c    175 g    223 t
ORIGIN

  Query Match           10.5%;  Score 634.2;  DB 13;  Length 735;
  Best Local Similarity   92.6%;  Pred. No. 2.1e-139;
  Matches  677;  Conservative    0;  Mismatches   53;  Indels    1;  Gaps    1;

Qy    4894 CCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAA 4953
           |||||||||||||||||||||||||||||| |||||||| |||||||||| |||||||||
Db       1 CCTACCCTGTTCCGAGTGATCCGTCTTGCCAGGATTGG-CGAATCCTACGACTGATCAAA 59

Qy    4954 GGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTT 5013
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 GGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTT 119

Qy    5014 AACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAAC 5073
           |||||||||||||| || ||||| |||||||||||||||||||||| ||||||||||
Db     120 AACATCGGCCTCCTTCTTTTCCTGGTCATGTTCATCTACGCCATCTTAGGGATGTCCAAT 179

Qy    5074 TTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGC 5133
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 TTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGC 239

Qy    5134 AACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCA 5193
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     240 AACAGCATGATCTGCCTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCA 299

Qy    5194 CCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCA 5253
           || ||||| || |||    || || |||||||||||| | |||| | ||||||||||||
Db     300 CCTATTCTTAATAGTGGACCTCCAGACTGTGACCCTGACAAAGATCACCCTGGAAGCTCA 359

Qy    5254 GTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATC 5313
           ||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     360 GTTAAAGGAGACTGTGGGAACCCATCTGTTGGGATTTTCTTTTTTGTCAGTTACATCATC 419

Qy    5314 ATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTT 5373
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 ATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTT 479

Qy    5374 GCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTT 5433
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 GCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTG 539

Qy    5434 TGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTT 5493
           |||||||||||||||||||| || ||||| || || || |  ||| | ||| | |||
Db     540 TGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCGCCAAACTTTCTGATTTT 599

Qy    5494 GCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCC 5553
           |||| ||| || || || |||||     |  || |||| |||||| ||||||||||||||
Db     600 GCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTCCAGCTCATTGCC 659

Qy    5554 ATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTT 5613
           |||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     660 ATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATCTTATTTGCTTTT 719

Qy    5614 ACAAAGCGGGT 5624
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Db     720 ACAAAGCGTGT 730
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RESULT 5
BM718214
LOCUS       BM718214                579 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  UI-E-EJ1-ajf-a-09-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajf-a-09-0-UI 5', mRNA sequence.
ACCESSION   BM718214
VERSION     BM718214.1  GI:19036382
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 579)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      168 a    123 c    125 g    163 t
ORIGIN

  Query Match             9.5%;  Score 570.6;  DB 14;  Length 579;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-124;
  Matches  573;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 60

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 120

Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 180

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 240

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 300

Qy   5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 360

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 420

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 480

Qy   5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 540

Qy   5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGG 5846
           |||||||||||||||||| ||||| |||| ||||
Db    541 AAGCTTCCTTTACGTACAAAAAAAAAAAAAAAAAGG 577


RESULT 6
BG342331
LOCUS       BG342331                674 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602374246F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481819 5',
            mRNA sequence.
ACCESSION   BG342331
VERSION     BG342331.1  GI:13148769
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 674)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10317  row: l  column: 12
            High quality sequence stop: 672.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="IMAGE:4481819"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
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full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 146 a 167 c 161 g 200 t
ORIGIN

Query Match 9.2%; Score 557.4; DB 12; Length 674;
Best Local Similarity 90.1%; Pred. No. 3.5e-121;
Matches 608; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

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Qy   4594 GGAATGGTCTTTGACTTCGTAACCAGACAAGTTTTTGACATAAGCATCATGATTCTCATC 4653
          |||||||| |||||||| |||||||||||||| ||||| || |||||||||||| ||||||
Db      1 GGAATGGTTTTTGACTTTGTAACCAGACAAGTGTTTGATATCAGCATCATGATCCTCATC 60

Qy   4654 TGTCTTAACATGGTCACAATGATGGTGGAAACAGATGACCAGAGTGAATATGTGACTACC 4713
          ||||| |||||||| || |||||||||||||| |||||||||| || |||||||| | |
Db     61 TGTCTGAACATGGTGACCATGATGGTGGAAACGGATGACCAGAGCGATTATGTGACAAGC 120

Qy   4714 ATTTTGTCACGCATCAATCTGGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAA 4773
          |||||||||||||||| |||||||||| || || || || || |||||||| || ||
Db    121 ATTTTGTCACGCATCAACCTGGTGTTCATCGTCCTGTTCACCGGCGAGTGTGTGCTCAAG 180

Qy   4774 CTCATCTCTCTACGCCATTATTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTT 4833
          |||||||| || |||||||||||||| |||||||||||||| ||||| ||||||||||
Db    181 CTCATCTCGCTCCGCCATTATTATTTCACCATTGGATGGAACATTTTCGATTTTGTGGTG 240

Qy   4834 GTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCC 4893
          ||||| |||||||||||||| |||||||||| ||||| |||||||||||||| |||||
Db    241 GTCATCCTCTCCATTGTAGGGATGTTTCTTGCGGAGCTAATAGAAAAGTATTTTGTGTCT 300

Qy   4894 CCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAA 4953
          |||||||||||||||| ||||| || || |||||||| |||||||||| |||||||||
Db    301 CCTACCCTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAA 360

Qy   4954 GGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTT 5013
          || || |||||||||||||||||||||||||| |||||||||||||||||||| |||||
Db    361 GGTGCCAAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTT 420

Qy   5014 AACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAAC 5073
          ||||||||||||| || || || |||||||||||||||||||||||||||||||||||||
Db    421 AACATCGGCCTCCTGCTTTTTCTCGTCATGTTCATCTACGCCATCTTTGGGATGTCCAAC 480

Qy   5074 TTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGC 5133
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Db    481 TTTGCCTATGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTCGGC 540

Qy   5134 AACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCA 5193
          |||||||||||||||| |||||||| || |||||||| |||||||||||| |||| ||
Db    541 AACAGCATGATCTGCCTGTTCCAAATCACCACCTCTGCGGGCTGGGATGGACTGCTGGCC 600

Qy   5194 CCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCA 5253
          ||||| ||||| || || || || ||||||||||||||||||||||||||||||||||||
Db    601 CCCATCCTCAAAAGGAAACC-CCTGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCG 659

Qy   5254 GTTAAGGGAGACTGT 5268
          || ||||||||||||
Db    660 GTGAAGGGAGACTGT 674
```

RESULT 7
BM682680/c
LOCUS BM682680 562 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-EJ1-ajf-a-09-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone UI-E-EJ1-ajf-a-09-0-UI 3', mRNA sequence.
ACCESSION BM682680
VERSION BM682680.1 GI:18992576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 562)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ1-ajf-a-09-0-UI"
/clone_lib="UI-E-EJ1"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJ1
TAG_TISSUE=Foveal and Macular Retina
TAG_SEQ=GTCC"
BASE COUNT 161 a 121 c 118 g 162 t
ORIGIN

Query Match 9.2%; Score 555.8; DB 14; Length 562;
Best Local Similarity 99.6%; Pred. No. 8.1e-121;
Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 503

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 443

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 383

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 323

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db     322 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 263

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Db     262 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 203

Qy    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Db     202 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 143

Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Db     142 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 83

Qy    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Db      82 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 23

Qy    5821 ACGTACAATAAAAACAAAA 5839

Db      22 ACGTACAAAAAAAAAAAAA 4
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RESULT 8
BI488799

LOCUS	BI488799 774 bp mRNA linear EST 28-AUG-2001
DEFINITION	603021394F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192206 5', mRNA sequence.
ACCESSION	BI488799
VERSION	BI488799.1 GI:15328027
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 774)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11480 row: k column: 23 High quality sequence start: 19 High quality sequence stop: 763.

FEATURES	Location/Qualifiers
source	1. .774 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5192206" /clone_lib="NIH_MGC_114" /lab_host="DH10B" /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

BASE COUNT 173 a 175 c 203 g 223 t
ORIGIN

Query Match 9.1%; Score 548; DB 13; Length 774;
Best Local Similarity 89.7%; Pred. No. 6.1e-119;

Matches 700; Conservative 0; Mismatches 70; Indels 10; Gaps 10;

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Qy    4894 CCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGA-TTGGCCGAATCCTACGTCTGATCAA 4952

Db       1 CCTAGCCTGTTCCGAGTGATCCGTCTTGCCAGGAGTGGGGCGAATCCTACGACTGATCAA 60

Qy    4953 AGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTT 5012

Db       61 GGGAGCAAAGGGGATCCGCAGGCTGCTCTTGGCGTTGATGATGTCCCTTCCGGCG-TGTT 119

Qy    5013 TAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAA 5072

Db      120 TAACATCGGCCTCCTTCTTTTCCTGGTCATGTTCATCTACGCCATCTTAGGGATGTCCAA 179

Qy    5073 CTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGG 5132

Db      180 TTGTGCCTATGTTAAGAGGGAAG-TGGGATCGATGACATGTTCAACTTTGAGACCTGTGG 238

Qy    5133 CAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGC 5192

Db      239 CAACAGCATGATCTGCCTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGA-TGCTAGC 297

Qy    5193 ACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTC 5252

Db      298 ACCTATTCTTAATAGTGGACCTCCAGACTGTGACCCTGACAAAGATCACCCTGGAAGCTC 357

Qy    5253 AGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCAT 5312

Db      358 AGTTAAAGGAGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGTTACATCAT 417

Qy    5313 CATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGT 5372

Db      418 CATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGT 477

Qy    5373 TGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGT 5432

Db      478 TGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGT 537

Qy    5433 TTGGGAGA-AGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGT 5491

Db      538 TTGGGAGACAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTTGCAAACTT-TCTGATT 596

Qy    5492 TTGCAGCTGCGCTTGAACCGCCTC-TCAATCTGCCACAACCAAACAAACTCCAGCTCATT 5550

Db      597 TTGCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAAACCAAGCAAAGTCCAGCTCATT 656

Qy    5551 GCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCT 5610

Db      657 GCCATGGATCTGGCCATGGTGAGTGGTGACCGGATCCACTGTC-TGACATCTTCATTGCT 715

Qy    5611 TTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGAT-GGATGCTCTACGAATACAGATGGA 5669

Db      716 TTTACAAAGCGTGGT-TTGGTGAGAGTGGAGAGATGGGATGCCCTTCGATTACGCATGGA 774
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RESULT 9
BB622500

LOCUS	BB622500 618 bp mRNA linear EST 31-AUG-2001
DEFINITION	BB622500 RIKEN full-length enriched, adult male olfactory brain Mus musculus cDNA clone 6430408L10 5', mRNA sequence.
ACCESSION	BB622500
VERSION	BB622500.1 GI:15397780
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 618)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,

Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .618
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="6430408L10"
/clone_lib="RIKEN full-length enriched, adult male olfactory brain"
/sex="male"
/tissue_type="olfactory brain"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 133 a 155 c 157 g 173 t
ORIGIN

Query Match 8.6%; Score 518.8; DB 10; Length 618;
Best Local Similarity 90.0%; Pred. No. 5e-112;
Matches 556; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Qy   4840 CTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACC 4899
          ||||||||||||| |||||||| || |||||||||| ||||||||||||||||||||||
Db      1 CTCTCCATTGTAGGGATGTTTCTCGCGGAGCTGATAGAGAAGTATTTCGTGTCCCCTACC 60

Qy   4900 CTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCA 4959
          |||||||||| ||||| || || |||||||| |||||||||| |||||||||| ||
Db     61 CTGTTCCGAGTCATCCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGCC 120

Qy   4960 AAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATC 5019
          |||||||||||||||||||||||||| |||||||||||||||||| ||||||||||
Db    121 AAGGGGATCCGCACGCTGCTCTTTGCTCTGATGATGTCCCTTCCTGCGCTGTTTAACATC 180

Qy   5020 GGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 5079
          |||||||| || ||||| ||||||||||||||||||||||||||||||||||||||||||
Db    181 GGCCTCCTGCTTTTCCTGGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCC 240

Qy   5080 TATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGC 5139
          || ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    241 TACGTTAAGAGGGAAGTTGGGATTGATGACATGTTCAACTTTGAGACCTTTGGCAACAGC 300

Qy   5140 ATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATT 5199
          |||||||||| |||||||| || || ||||| |||||||||||| |||| || || ||
Db    301 ATGATCTGCCTGTTCCAAATCACCACTTCTGCGGGCTGGGATGGACTGCTGGCCCCTATA 360

Qy   5200 CTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAG 5259
          || || |||   || ||||| |||||||||| | |||| | | ||||||||||| || |||
Db    361 CTAAATAGTGGACCTCCCGATTGTGACCCTGAAAAAGATCATCCTGGAAGCTCGGTGAAG 420

Qy   5260 GGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCC 5319
          |||||||||||||||||||||| || ||||||||||||||| ||||||||||||||||||
Db    421 GGAGACTGTGGGAACCCATCTGTGGGGATTTTCTTTTTTGTCAGCTACATCATCATATCC 480

Qy   5320 TTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACT 5379
          |||||||||||||||||||||||||| || |||||||||||||||||| ||||| ||
Db    481 TTCCTGGTTGTGGTGAACATGTACATTGCTGTCATCCTGGAGAACTTCAGCGTTGCCACA 540

Qy   5380 GAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAG 5439
          ||||||| |||||||||||||||||||| |||||||||||||||| || || ||||||
Db    541 GAAGAAAATGCAGAGCCTCTGAGTGAGGACGACTTTGAGATGTTCTACGAAGTCTGGGAG 600

Qy   5440 AAGTTTGATCCCGATGCA 5457
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Db    601 AAAGTCGACCCTGACGCA 618
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RESULT 10
AL706368
LOCUS AL706368 602 bp mRNA linear EST 22-MAR-2002
DEFINITION DKFZp686H1140_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686H1140 5', mRNA sequence.
ACCESSION AL706368
VERSION AL706368.1 GI:19689723
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Ansorge W
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686H1140) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```
          Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686H1140"
                     /clone_lib="686 (synonym: hlcc3)"
                     /tissue_type="human skeletal muscle"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
BASE COUNT      127 a    141 c    138 g    196 t
ORIGIN

  Query Match             8.5%;  Score 511.6;  DB 9;  Length 602;
  Best Local Similarity   91.0%;  Pred. No. 2.5e-110;
  Matches  544;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy   4750 TTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACCATTGGA 4809
          || |||||||| | ||| ||||| ||| |||| ||  | || || || || || || ||
Db      5 TTCACTGGAGAATTTGTGCTGAAGCTCGTCTCCCTCAGACACTACTACTTCACTATAGGC 64

Qy   4810 TGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAG 4869
          ||||| || |||| |||||||| || ||||||||||||||||||||||||| || |||
Db     65 TGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGTATGTTTCTGGCTGAG 124

Qy   4870 CTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATT 4929
          ||||||||||||||| |||||||||||| |||||||||||||||||||| ||||||
Db    125 ATGATAGAAAAGTATTTTGTGTCCCCTACCTTGTTCCGAGTGATCCGTCTTGCCAGGATT 184

Qy   4930 GGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTG 4989
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Db    185 GGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTG 244

Qy   4990 ATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATC 5049
          |||| |||||||||||||||||||||||||||||| |||||||| |||||||| |||
Db    245 ATGACGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTGCTCTTCCTGGTCATGTTTATC 304

Qy   5050 TACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGAC 5109
          || |||||||||||||||||||||||||||||| | ||||| ||| || ||||||
Db    305 TATGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAAAAGGAAGCTGGAATTGATGAC 364

Qy   5110 ATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCT 5169
          |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Db    365 ATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCTTGTTCCAAATTACAACCTCT 424

Qy   5170 GCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCT 5229
          |||||||||||||||||||||||||| ||||| || |||   ||||||||||||||||||
Db    425 GCTGGCTGGGATGGATTGCTAGCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCT 484

Qy   5230 AATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATT 5289
          | | | || ||||||| || |||||||||||||||||||||||||||||||||||| |||
Db    485 GACACAATTCACCCTGGCAGTTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGGATT 544

Qy   5290 TTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCG 5347
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Db    545 TTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCG 602


RESULT 11
AU035605
LOCUS       AU035605                778 bp    mRNA    linear   EST 12-JUL-2000
DEFINITION  AU035605 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-0634,
            mRNA sequence.
ACCESSION   AU035605
VERSION     AU035605.1  GI:3718608
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
            Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
  TITLE     Construction of mouse full length-enriched cDNA libraries
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Katsuyuki Hashimoto
            Division of Genetic Resources
            National Institute of Infectious Diseases
            23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
            Email: khashi@nih.go.jp
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="MNCb-0634"
                     /clone_lib="Sugano mouse brain mncb"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="TOP10"
                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
                     was primed with an oligo(dT) primer
                     ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
                     cloned into distinct DraIII sites of the pME18S-FL3. XhoI
                     sites just outside the DraIII sites can be used to isolate
                     the cDNA insert. Size selection was performed to exclude
                     fragments <1.5 kb. Library was constructed by Sugano et
                     al.(University of Tokyo, Institute of Medical Science).
                     Custom primer used for sequencing: 5' end primer
                     [CTTCTGCTCTAAAAGCTGCG], 3' end primer
                     [CGACCTGCAGCTCGAGCACA]"
BASE COUNT      196 a    192 c    165 g    223 t      2 others
ORIGIN

  Query Match             8.2%;  Score 495.8;  DB 9;  Length 778;
  Best Local Similarity   81.5%;  Pred. No. 1.5e-106;
  Matches  635;  Conservative    0;  Mismatches  134;  Indels   10;  Gaps    5;

Qy   4374 CATGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTT 4433
          |||||||| |||||||| || |||||||||||||||| ||||||||  | || || ||
Db      1 CATGTATCTGTACTTTGTCATCTTCATCATCTTTGGGTCGTTCTTCACTCTAAATCTATT 60

Qy   4434 TATTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACAT 4493
          || || |||||||||||| || |||||||||||||| ||||||||||||||||||||||
Db     61 CATCGGCGTCATCATAGACAACTTCAACCAGCAGAAGAAGAAGTTTGGAGGTCAAGACAT 120

Qy   4494 CTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAA 4553
          |||||||||||||||| ||||| || ||||| |||||||||| ||| | || || |||||
Db    121 CTTTATGACAGAAGAGCAGAAAAAGTACTACAATGCAATGAAGAAACTTGGCTCCAAAAA 180

Qy   4554 ACCGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGT 4613
          ||| || ||||| || |||||||| | ||||||||||||||||||||||||||||||| ||
Db    181 ACCTCAGAAGCCCATCCCTCGACCTGCAAACAAATTTCAAGGAATGGTCTTTGACTTTGT 240

Qy   4614 AACCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAAT 4673
          |||||||||||| |||||||| |||||||||| |||||||| || |||||||| || ||
Db    241 AACCAGACAAGTGTTTGACATCAGCATCATGATCCTCATCTGCCTCAACATGGTGACCAT 300

Qy   4674 GATGGTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCT 4733
          |||||||||||| || |||||||  ||||  ||||     ||||||| || ||||| ||
Db    301 GATGGTGGAAACGGACGACCAGAGCAAATACATGACCCTGGTTTTGTCCCGAATCAACCT 360

Qy   4734 GGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTA 4793
          ||| ||||| || || || |||| |||| | | ||||| ||||||||||  |  | ||
Db    361 GGTATTCATCGTCCTCTTCACTGGGGAGTTTCTGCTGAAGCTCATCTCTCTCAGATACTA 420

Qy   4794 TTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGG 4853
          || || || ||||| || ||||| |||||||| || |||||||| ||||||||
Db    421 CTACTTCACGATTGGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCAATTGTAGG 480

Qy   4854 TATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGAT 4913
          ||||| ||||| |||||||||||| |||||||| ||||| |||||||||||||||||| ||
```

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Db    481 AATGTTCCTTGCTGAGCTGATAGAGAAGTATTTTGTGTCTCCTACCCTGTTCCGAGTCAT 540

Qy   4914 CCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCAC 4973
          ||| || || |||||||| |||||||||| |||||||||| ||  ||||||||||||
Db    541 CCGCCTGGCCAGGATTGGACGAATCCTACGCCTGATCAAAGGCGC-CAGGGGATCCGCAC 599

Qy   4974 GCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTT 5033
          |||||||||||||| ||| |||||||||| ||||| || | ||||   |   |     |||
Db    600 GCTGCTCTTTGCTCTGACCATGTCCCTTTCTGCGCTGGTCAACAATCGGGCCTCCTGCTT 659

Qy   5034 CCTAGTC----ATGTTCATCTACGCCATCTTTGGGATGT---CCAACTTTGCCTATGTTA 5086
            |  ||       | |||||||| ||||||||||    |   | |  |||||||||| ||
Db    660 TTTCCTCGGCATGGGTCATCTACCCCATCTTTGGGGANTGTCCAACTTTTGCCTATGGTA 719

Qy   5087 AGAGGGAAGTTGGG-ATCGATGACATGTTCAACTTTGAG-ACCTTTGGCAACAGCATGA 5143
          | |  || | |||| ||  |||||||||||||||||||| || ||||||||| ||||||
Db    720 AAAAAGAGGCTGGGAATTTATGACATGTTCAACTTTGAGAACNTTTGGCAACCGCATGA 778


RESULT 12
AI796228/c
LOCUS       AI796228                731 bp    mRNA    linear   EST 20-DEC-1999
DEFINITION  wh44d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383595 3'
            similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT
            (HUMAN);, mRNA sequence.
ACCESSION   AI796228
VERSION     AI796228.1  GI:5361702
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 806   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2383595"
                     /clone_lib="NCI_CGAP_Kid11"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
BASE COUNT      188 a    167 c    160 g    215 t      1 others
ORIGIN

  Query Match             7.8%;  Score 468.4;  DB 9;  Length 731;
  Best Local Similarity   80.0%;  Pred. No. 4.8e-100;
  Matches  588;  Conservative    0;  Mismatches  142;  Indels    5;  Gaps    3;
```

```
Qy   5242 CCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTC 5301
          |||||||||||||| || |||||||| |||||||||| ||| ||||||||||||||
Db    731 CCTGGAAGCTCAGTAAAAGGAGACTGT-GGAACCCATCTG-TGGGATTTTCTTTTTTGTC 674

Qy   5302 AGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAG 5361
          || ||||||||||||||||||||||||  ||||||  ||||||||||||||||||||||||
Db    673 AGGTACATCATCATATCCTTCCTGGTGNTGGTGACAATGTACATCGCGGTCATCCTGGAG 614

Qy   5362 AACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATG 5421
          |     |||||         ||||||||||||||||||||||||||||||||||||||||
Db    613 ACTCAAAGTGTGCTACTGAAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATG 554

Qy   5422 TTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAA 5481
          ||||||||||||||||||||||||||||||||| || ||||| || || ||||  |||
Db    553 TTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTTGCCAAA 494

Qy   5482 TTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTC 5541
            | ||| | ||||||| ||| || || || ||||      |  || |||| ||||||||
Db    493 CTTTCTGATTTTGCAGATGCCCTGGATCCTCCTCTTCTCATAGCAAAACCCAACAAAGTC 434

Qy   5542 CAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATC 5601
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||| |||
Db    433 CAGCTCATTGCCATGGATCTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGACATC 374

Qy   5602 TTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATA 5661
          |||||||||||||||||| ||| | || ||||||||||||||||||| || ||||||
Db    373 TTATTTGCTTTTACAAAGCGTGTTTTGGGTGAGAGTGGAGAGATGGATGCCCTTCGAATA 314

Qy   5662 CAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACT 5721
          |||||||||||||||||||||||||| || || || ||||| ||||| ||| |||| || ||
Db    313 CAGATGGAAGAGCGATTCATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCCATTACG 254

Qy   5722 ACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGA 5781
          || || || ||||| |||||||||| || |||||| | ||||| ||| | |||||||||
Db    253 ACCACGTTGAAACGCAAACAAGAGGAGGTGTCTGCTATTATTATCCAGAGGGCTTACAGA 194

Qy   5782 CGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAAACAAAATC 5841
          ||| ||||| || |||| ||  || ||| | |  ||   ||  ||||| ||| |||||  |
Db    193 CGCTACCTCTTGAAGCAAAAAGTTAAAAAGGTATCAAGTATATACAAGAAAGACAAAGGC 134

Qy   5842 AAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGACAGAATAAATGAAAAC 5901
          ||||   | | |       |  || |||||||| |   | ||||| | | | ||||| ||
Db    133 AAAGAATGTGATGGAACACCCATCAAAGAAGATACTCTCATTGATAAACTGAATGAGAAT 74

Qy   5902 TCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGTCCACCTTCCTATGAC 5961
          || | | |||| ||||| ||| ||||    ||||   |  | | |||||| || |||||
Db     73 TCAACTCCAGAGAAAACCGATATGACGCCTTCCA---CCACGTCTCCACCCTCGTATGAT 17

Qy   5962 CGGGTGACAAAGCCA 5976
            | ||||| || |||
Db     16 AGTGTGACCAAACCA 2


RESULT 13
BQ444145
LOCUS       BQ444145                816 bp    mRNA    linear   EST 29-MAY-2002
DEFINITION  UI-M-EX0-bxj-d-14-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone
            IMAGE:5708893 5', mRNA sequence.
ACCESSION   BQ444145
VERSION     BQ444145.1  GI:21247257
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James Lin, Univeristy of Iowa
```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.

```
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Mus musculus"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5708893"
                     /clone_lib="NIH_BMAP_EX0"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 15.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured mRNa was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was size selected according to mRNA size fraction,
                     ligated with EcoR I adaptor, digested with Not I, and then
                     cloned directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     , is GTGCGTGGAA. This library was created for the
                     University of Iowa Mouse Brain Molecular Anatomy Project
                     (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                     System', supported by National Instututes of Mental Health
                     (NIMH), Hemin Chin, Ph.D., program coordinator."
BASE COUNT      192 a    209 c    208 g    205 t      2 others
ORIGIN
```

Query Match 7.5%; Score 454.8; DB 14; Length 816;
Best Local Similarity 73.1%; Pred. No. 8.3e-97;
Matches 595; Conservative 1; Mismatches 215; Indels 3; Gaps 1;

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Qy   2071 AAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAAAGG 2130
          |||| | |  |  | ||  ||   || ||||||||    || |          |  | |
Db      3 AAGAAAGGCCCTGGATCGCTCTTAGTCTCCATGGAACAACTCGCCTCCTACGGACGGAAG 62

Qy   2131 CAACGAGCAATGAGTATAGCCAGCATTCTAACAAATAC---AGTAGAAGAACTTGAAGAA 2187
            |  ||   |  ||||||   ||| || | ||||| ||   ||| ||||| || |||||
Db     63 GACAGAATCAACAGTATAATGAGCGTTGTCACAAACACACTAGTGGAAGAGCTGGAAGAG 122

Qy   2188 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2247
          ||   |   || |||||||| || |||||||| ||| |||| |  ||| | ||||||||
Db    123 TCTCAGAGAAAGTGCCCACCATGCTGGTATAAGTTTGCCAATACTTTCCTCATCTGGGAG 182

Qy   2248 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTYGTGATGGACCCATTT 2307
          |||   || || ||| ||||| ||||  |  |||| |||||| |:|| |||||||| ||
Db    183 TGTCACCCCTACTGGATAAAACTGAAGGAGATTGTGAACCTGATCGTCATGGACCCTTTC 242

Qy   2308 GTTGACCTGGCCATCACCATCTGTATTGTCTTAAATACTCTTTTCATGGCCATGGAGCAC 2367
          || ||| | ||||| |||||||| |||||| | || || || || ||||| |||||||||
Db    243 GTAGACTTAGCCATAACCATCTGCATTGTCCTGAACACACTATTTATGGCAATGGAGCAC 302

Qy   2368 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2427
           |||| ||||||   || ||| |  |||| ||  | ||||| ||| |||| |||||||||
Db    303 CATCCCATGACGCCACAATTCGAACATGTCCTGGCCGTAGGGAACCTGGTGTTCACTGGG 362

Qy   2428 ATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAA 2487
          ||||| || || |||||||| |||||  | || |||||||||| |||||||| ||||||
Db    363 ATCTTCACGGCGGAAATGTTCCTGAAGCTCATAGCCATGGATCCCTACTATTACTTCCAA 422

Qy   2488 GAAGGCTGGAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTC 2547
          |||||||||| || |||||||| ||||| ||  | || ||  |  | || || || ||
Db    423 GAAGGCTGGAACATTTTTGACGGATTTATCGTCTCCCTCAGTTTAATGGAGCTGGGCCTT 482
```

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Qy   2548 GCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTG 2607
          ||  | ||||| ||  | || || || || || || |||||||| ||||| ||||  |||
Db    483 GCAGACGTGGAGGGGCTCTCAGTGCTGCGATCTTTCCGATTGCTCCGAGTCTTCANATTG 542

Qy   2608 GCAAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCT 2667
          || || || ||||| ||  | || ||||| || |||||||| || || ||||| || ||
Db    543 GCCAAGTCCTGGCCCACCCTGAACATGCTGATCAAGATCATTGGGAACTCCGTTGGCGCC 602

Qy   2668 CTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATG 2727
          ||| | ||  | ||||| ||  |||||||||| |||||||| |||||||||| || |||
Db    603 CTGNGCAACCTGACCCTGGTGCTGGCCATCATTGTCTTCATCTTTGCCGTGGTGGGGATG 662

Qy   2728 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 2787
          |||||||||| || |||||||| || || ||||| ||||||  |   || ||  | |||
Db    663 CAGCTCTTTGGAAAGAGCTACAAGGAGTGCGTCTGTAAGATCAGCCAGGAGTGCAAGCTC 722

Qy   2788 CCACGCTGGCACATGAATGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGT 2847
          || |||||||||||||| |||||||||||||||||||| || || ||||| |||||||||
Db    723 CCGCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTCATCGTCTTCCGAGTGCTGTGT 782

Qy   2848 GGGGAGTGGATAGAGACCATGTGGGACTGTATGG 2881
          |||||||||| |||||    ||   || ||||
Db    783 GGGGAGTGGATCGAGACATGTGGGATTTGCATGG 816
```

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RESULT 14
AA984063/c
LOCUS       AA984063                706 bp    mRNA    linear   EST 27-MAY-1998
DEFINITION  am76b09.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone
            IMAGE:1616345 3' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN
            II ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AA984063
VERSION     AA984063.1  GI:3162588
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 706)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 425.
FEATURES             Location/Qualifiers
     source          1. .706
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1616345"
                     /clone_lib="Stratagene schizo brain S11"
                     /sex="male"
                     /tissue_type="schizophrenic brain S-11 frontal lobe"
                     /dev_stage="34 years old"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: Bluescript SK-; Site_1: EcoRI;  Library
                     constructed from S-11 frontal lobe, male, 34 years old,
                     50% caucasian, 50% Aleutian.  Schizophrenic suicide.
                     Random primed into EcoRI site of ZAP II Vector.  Mass
                     excised. Custom library. Avg insert length 1.4kb.
                     Material obtained by Johnston N., Torrey, E.F., Yolken R.,
                     and the Stanley Neuropathology Consortium - Analysis of
                     RNAs from the Brains of Individuals with Psychiatric
```

Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
BASE COUNT 232 a 155 c 135 g 184 t
ORIGIN

Query Match 7.4%; Score 447.8; DB 9; Length 706;
Best Local Similarity 79.9%; Pred. No. 3.7e-95;
Matches 565; Conservative 0; Mismatches 137; Indels 5; Gaps 3;

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Qy    538 TTAGAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACA 597
          ||||| ||||| || ||  | ||||||||||| || ||| | |||||||| ||||||||
Db    706 TTAGAGGATTTCACATTTTTACGGGATCCATGAAATTGGTTGGATTTCACAGTCATTACT 647

Qy    598 TTTGCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGA 657
          |||| || || |||||||||||||||||||  |||||||| || ||||||||||||||||
Db    646 CTTGCATATGTGACAGAGTTTGTGGACCTGGCAAATGTCTCAGCGTTGAGAACATTCAGA 587

Qy    658 GTTCTCCGAGCATTG-AAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGC 716
          |||||||||||||| || || |||||||||||||||||||||| |||||||| || ||
Db    586 GTTCTCCGAGCATTGAAAAACAATTTCAGTCATTCCAGGCCTGAAGACCATTGT-GGTGC 528

Qy    717 CCTGATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAG 776
          |||||||||||| |||||||||| || ||||| |||||| ||||||||||||||||| ||
Db    527 CCTGATCCAGTCAGTGAAGAAGCTTTCTGATGTCATGATCTTGACTGTGTTCTGTCTAAG 468

Qy    777 CGTATTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACA 836
          ||| ||||| ||||| ||  ||||| |||||||||||||||  | |||||||| | ||
Db    467 CGTGTTTGCGCTAATAGGATTGCAGTTGTTCATGGGCAACCTACGAAATAAATGTTTGCA 408

Qy    837 ATGGCCTCCCACCAATGCTTCCTTGGAGGAACAT---AGTATAGAAAAGAATATAACTGT 893
          |||||||||    ||| ||||||| ||   | ||   | |          || |   | |
Db    407 ATGGCCTCCAGATAATTCTTCCTTTGAAATAAATATCACTTCCTTCTTTAACAATTCATT 348

Qy    894 GAATTATAATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATAT 953
          | ||   ||||||||   | | |||   || ||       ||| ||||| |   ||||||
Db    347 GGATGGGAATGGTACTACTTTCAATAGGACAGTGAGCATATTTAACTGGGATGAATATAT 288

Qy    954 TCAAGATTCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAA 1013
          | | |||  |||  |   ||||||  | |||||       ||||| || || ||||| ||
Db    287 TGAGGATAAAAGTCACTTTTATTTTTTAGAGGGGCAAAATGATGCTCTGCTTTGTGGCAA 228

Qy   1014 TAGCTCTGATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCC 1073
          |||||  |||||||||||| ||||| || ||||| || |||||||| |||||||||| ||
Db    227 CAGCTCAGATGCAGGCCAGTGTCCTGAAGGATACATCTGTGTGAAGGCTGGTAGAAACCC 168

Qy   1074 CAATTATGGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACT 1133
          ||| |||||||||||  |||||||| |||||  |||||||  |||||||||||  |||||  ||
Db    167 CAACTATGGCTACACGAGCTTTGACACCTTTAGTTGGGCCTTTTTGTCCTTATTTCGTCT 108

Qy   1134 AATGACTCAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAAC 1193
          ||||||||  ||||||||||||||  ||||||||||||||||  ||||||||||||||||||
Db    107 CATGACTCAAGACTTCTGGGAAAACCTTTATCAACTGACACTACGTGCTGCTGGGAAAAC 48

Qy   1194 GTACATGATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACC 1240
          |||||||||||||||||| |||||||||||||||||||||||||| |
Db     47 GTACATGATATTTTTTGTGCTGGTCATTTTCTTGGGCTCATTCTATC 1
```

RESULT 15
BF470392
LOCUS BF470392 547 bp mRNA linear EST 04-DEC-2000
DEFINITION UI-M-BH3-avc-c-07-0-UI.r1 NIH_BMAP_M_S4 Mus musculus cDNA clone UI-M-BH3-avc-c-07-0-UI 5', mRNA sequence.
ACCESSION BF470392
VERSION BF470392.1 GI:11539575
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 547)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
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/strain="C57BL/6J"
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/clone="UI-M-BH3-avc-c-07-0-UI"
/clone_lib="NIH_BMAP_M_S4"
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"
BASE COUNT 110 a 143 c 128 g 166 t
ORIGIN

Query Match 7.3%; Score 438.8; DB 12; Length 547;
Best Local Similarity 87.7%; Pred. No. 4.8e-93;
Matches 479; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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14676.674 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3544.8	58.8	6404	3	US-08-836-325-14	Sequence 14, Appl
2	3476.8	57.7	6371	3	US-08-836-325-13	Sequence 13, Appl
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ALIGNMENTS

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; Sequence 14, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and U
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6404 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
US-08-836-325-14

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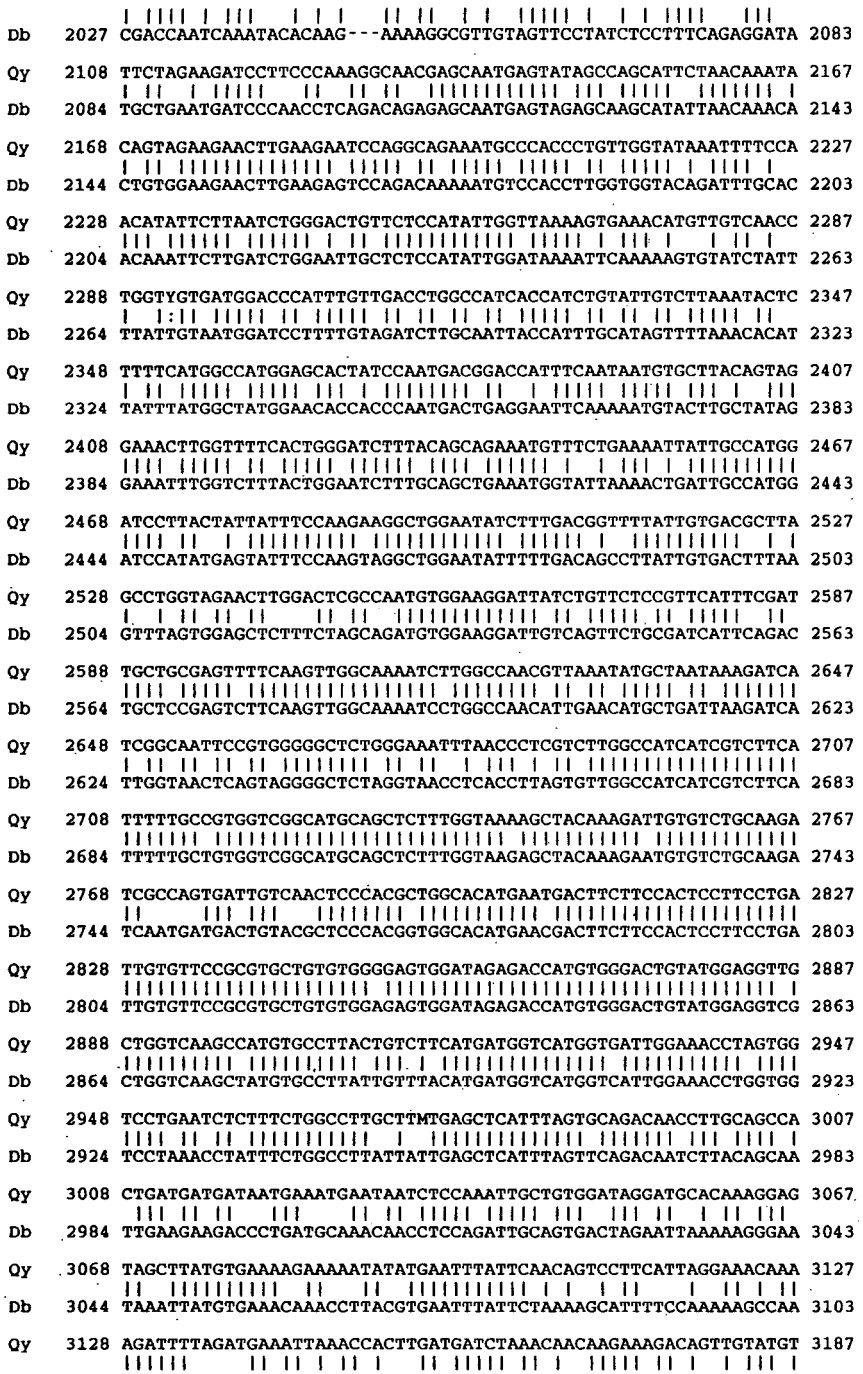
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Qy 3008 CTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAAGGAG 3067
Db 2984 TTGAAGAAGACCCTGATGCAAACAACCTCCAGATTGCAGTGACTAGAATTAAAAAGGGAA 3043
Qy 3068 TAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAA 3127
Db 3044 TAAATTATGTGAAACAAACCTTACGTGAATTTATTCTAAAAGCATTTTCCAAAAAGCCAA 3103
Qy 3128 AGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGT 3187
Db 3104 AGATTTCCAGGGAGATAAGACAAGCAGAAGATCTGAATACTAAGAAGGAAAACTATATTT 3163
Qy 3188 CCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTA 3247
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Qy 3248 CAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACA 3307
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Qy 3308 TGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTG 3367
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Qy 3368 ACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGCAAAG 3427
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Qy 3428 AGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCACCTG 3487
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Qy 3488 TAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTCACTG 3547
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Qy 3548 AAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAAC 3607
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Qy 3608 AATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAGACCT 3667
Db 3578 TCTGGTGGAACATCAGGAAAACCTGCTACAAGATTGTTGAACACAGTTGGTTTGAAAGCT 3637
Qy 3668 TCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATATATTG 3727
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Db 3818 CCTGGTGTTGGCTGGATTTCCTAATTGTTGATGTTTCTTTGGTTACTTTAGTGGCAAACA 3877
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Qy 3968 CTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTAGGAG 4027
Db 3938 CTCTAAGAGCCTTATCTAGATTTGAAGGAATGAGGGTCGTTGTGAATGCACTCATAGGAG 3997
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Qy 4088 TCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACTGGTG 4147
Db 4058 TCATGGGAGTAAATTTGTTTGCTGGCAAGTTCTATGAGTGTATTAACACCACAGATGGGT 4117
Qy 4148 ACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAAAGAA 4207
Db 4118 CACGGTTTCCTGCAAGTCAAGTTCCAAATCGTTCCGAATGTTTTGCCCTTATGAATGTTA 4177
Qy 4208 ATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGGTATC 4267
Db 4178 GTCAAAATGTGCGATGGAAAAACCTGAAAGTGAACTTTGATAATGTCGGACTTGGTTACC 4237

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Qy   4268 TCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTG 4327
Db   4238 TATCTCTGCTTCAAGTTGCAACTTTTAAGGGATGGACGATTATTATGTATGCAGCAGTGG 4297

Qy   4328 ATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTTTACT 4387
Db   4298 ATTCTGTTAATGTAGACAAGCAGCCCAAATATGAATATAGCCTCTACATGTATATTTATT 4357

Qy   4388 TTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTCATCA 4447
Db   4358 TTGTCGTCTTTATCATCTTTGGGTCATTCTTCACTTTGAACTTGTTCATTGGTGTCATCA 4417

Qy   4448 TAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAG 4507
Db   4418 TAGATAATTTCAACCAACAGAAAAAGAAGCTTGGAGGTCAAGACATCTTTATGACAGAAG 4477

Qy   4508 AACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAGCCTA 4567
Db   4478 AACAGAAGAAATACTATAATGCAATGAAAAAGCTGGGGTCCAAGAAGCCACAAAAGCCAA 4537

Qy   4568 TACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAAGTTT 4627
Db   4538 TTCCTCGACCAGGGAACAAAATCCAAGGATGTATATTTGACCTAGTGACAAATCAAGCCT 4597

Qy   4628 TTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAAACAG 4687
Db   4598 TTGATATTAGTATCATGGTTCTTATCTGTCTCAACATGGTAACCATGATGGTAGAAAAGG 4657

Qy   4688 ATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATTGTGC 4747
Db   4658 AGGGTCAAAGTCAACATATGACTGAAGTTTTATATTGGATAAATGTGGTTTTTATAATCC 4717

Qy   4748 TATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACCATTG 4807
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Qy   4808 GATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCG 4867
Db   4778 GATGGAATATTTTTGATTTTGTGGTTGTGATTATCTCCATTGTAGGTATGTTTCTAGCTG 4837

Qy   4868 AGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGA 4927
Db   4838 ATTTGATTGAAACGTATTTTGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCCAGGA 4897

Qy   4928 TTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTT 4987
Db   4898 TTGGCCGAATCCTACGTCTAGTCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTT 4957

Qy   4988 TGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCA 5047
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Qy   5288 TTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCG 5347
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Qy   5348 CGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGG 5407
Db   5318 CAGTCATACTGGAGAATTTTAGTGTTGCCACTGAAGAAAGTACTGAACCTCTGAGTGAGG 5377

Qy   5408 ATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCA 5467
Db   5378 ATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCGACCCAGTTTA 5437

Qy   5468 TGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCAC 5527
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Qy   5528 AACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCC 5587
Db   5498 AACCCAACAAAGTCCAGCTCATTGCCATGGATCTGCCCATGGTTAGTGGTGACCGGATCC 5557

Qy   5588 ACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGG 5647
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Qy   5648 ATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCT 5707
Db   5618 ATTCTCTTCGTTCACAGATGGAAGAAAGGTTCATGTCTGCAAATCCTTCCAAAGTGTCCT 5677

Qy   5708 ATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTC 5767
Db   5678 ATGAACCCATCACAACCACACTAAAACGGAAACAAGAGGATGTGTCTGCTACTGTCATTC 5737

Qy   5768 AGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACA 5827
Db   5738 AGCGTGCTTATAGACGTTACCGCTTAAGGCAAAATGTCAAAAATATATCAAGTATATACA 5797

Qy   5828 ATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGACA 5887
Db   5798 TAAAAGATGGAGACAGAGAT---GATGATTTACTCAATAAAAAAGATATGGCTTTTGATA 5854

Qy   5888 GAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGTC 5947
Db   5855 ATGTTAATGAGAACTCAAGTCCAGAAAAAACAGAT---GCCACTTCATCCACCACCTCTC 5911

Qy   5948 CACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAAG 6007
Db   5912 CACCTTCATATGATAGTGTAACAAAGCCAGACAAAGAGAAATATGAACAAGACAGAACAG 5971

Qy   6008 ATGAAAAAGCCAAAGGGAAATA 6029
Db   5972 AAAAGGAAGACAAAGGGAAAGA 5993
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RESULT 2
US-08-836-325-13
; Sequence 13, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Usi
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
US-08-836-325-13

  Query Match           57.7%;  Score 3476.8;  DB 3;  Length 6371;
  Best Local Similarity  75.0%;  Pred. No. 0;
  Matches 4516;  Conservative    1;  Mismatches 1388;  Indels  117;  Gaps    9;

Qy      11 CAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAATCTCTTGCGG 70
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Db      53 CAATGTTGCCTCCCCCAGGACCTCAGAGCTTTGTCCATTTCACAAAACAGTCTCTTGCCC 112

Qy      71 CTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGACAAAAAAGATG 130
             ||||||  |||||||| |||  ||| |||||  | ||||||  ||| || |||||||
Db     113 TCATTGAACAACGCATTGCTGAAAGAAAATCAAAGGAACCCAAAGAAGAAAAGAAAGATG 172

Qy     131 ACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAACCTTCCATTTA 190
           | || ||| | | ||||||||||  ||||||||||||||||  ||   | || || || | |
Db     173 ATGATGAAGAAGCCCCAAAGCCAAGCAGTGACTTGGAAGCTGGCAAACAACTGCCCTTCA 232

Qy     191 TTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTGGACCCCTACT 250
           | ||||| ||||||||||| |  ||||||||||||||||||||||| ||||||||||||
Db     233 TCTATGGGGACATTCCTCCCGGCATGGTGTCAGAGCCCCTGGAGGACTTGGACCCCTACT 292

Qy     251 ATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTCCGGTTCAGTG 310
           ||    | || || ||||| |||||||||| ||||||||  | ||||||| |||| ||
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Qy     311 CCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATAGCTATTAAGA 370
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Db     353 CCACACCTGCTTTATATATGCTTTCTCCTTTCAGTCCTCTAAGAAGAATATCTATTAAGA 412

Qy     371 TTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACAAACTGTGTGT 430
           |||| ||||| || ||||||||||||| || |||||||||||| ||||||||||  | |
Db     413 TTTTAGTACACTCCTTATTCAGCATGCTCATCATGTGCACTATTCTGACAAACTGCATAT 472

Qy     431 TTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACCTTCACAGGAA 490
           ||||||| |||| |||||| || || ||||| || ||||| || ||||| || || ||||
Db     473 TTATGACCATGAATAACCCGCCGGACTGGACCAAAAATGTCGAGTACACTTTTACTGGAA 532

Qy     491 TATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTAGAAGATTTTA 550
           ||||||||||||||||||| |||||||  |||||| || |||||| ||| ||| || | |
Db     533 TATATACTTTTGAATCACTTGTAAAAATCCTTGCAAGAGGCTTCTGTGTAGGAGAATTCA 592

Qy     551 CTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTTGCGTACGTCA 610
           |||| ||||| || || |||||||||| |||||   ||||||  ||||||||  | |

Db     593 CTTTTCTTCGTGACCCGTGGAACTGGCTGGATTTTGTCGTCATTGTTTTTGCGTATTTAA 652

Qy     611 CAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTTCTCCGAGCAT 670
           |||| |||||  |||| |||||||| || ||  |  |||| |||||||| |  |||| |
Db     653 CAGAATTTGTAAACCTAGGCAATGTTTCAGCTCTTCGAACTTTCAGAGTATTGAGAGCTT 712

Qy     671 TGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTG 730
           |||| || ||||| || || |||||||||| || ||||| || ||  |||||||||| |
Db     713 TGAAAACTATTTCTGTAATCCCAGGCCTGAAGACAATTGTAGGGGCTTTGATCCAGTCAG 772

Qy     731 TGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAA 790
           |||||||||| || ||||| |||||||||||||||||||||||||| || ||||| ||||
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Qy     791 TTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCA 850
           |||| || |||||||||||||| |||||| | |||||||| | | |
Db     833 TTGGACTACAGCTGTTCATGGGAAACCTGAAGCATAAATGTTTTCGA---------- 879

Qy     851 ATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACAC 910
                       ||   | |  | || |    |  | |   ||  ||||||    |
Db     880 --------------AATTCACTTGAAAATAATGAAACATTAGAAAGCATAATGAATACC 924

Qy     911 TTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATC 970
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Qy     971 ATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCC 1030
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Qy    1031 AATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAA 1090
           | |||||||||||  || |  |||||||||  ||| |||||  ||  ||||||||||||| |
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Qy    1091 GCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACTCAGGACTTCT 1150
           |||||||  || |||||  |||||  || ||  ||||||||  | ||||||| || || | ||
Db    1076 GCTTTGACACTTTCAGCTGGGCCTTCTTAGCCTTGTTTAGGCTAATGACCCAAGATTACT 1135

Qy    1151 GGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTG 1210
           |||||||  |||||  |||| |||  | ||||||||||  |||||  |||||||  || ||||
Db    1136 GGGAAAACCTTTACCAACAGACGCTGCGTGCTGCTGGCAAAACCTACATGATCTTCTTTG 1195

Qy    1211 TGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCA 1270
           |  | || |||||| |||||||  || || |||||||| ||||||||||||||||  ||||
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Qy    1271 TGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAAGAGGCCGAAT 1330
           |||| || ||||||||  |||| | | |||||||  ||||||||||    ||||
Db    1256 TGGCATATGAAGAACAGAACCAGGCAAACATTGAAGAAGCTAAACAGAAAGAATTAGAAT 1315

Qy    1331 TTCAGCAGATGATTGAACAGCTTAAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGG 1390
           |||| ||||||  | || |  ||||||||  | || || | |||| ||      ||| |||
Db    1316 TTCAACAGATGTTAGACCGTCTTAAAAAAGAGCAAGAAGAAGCTGAGGCAATTGCAGCGG 1375

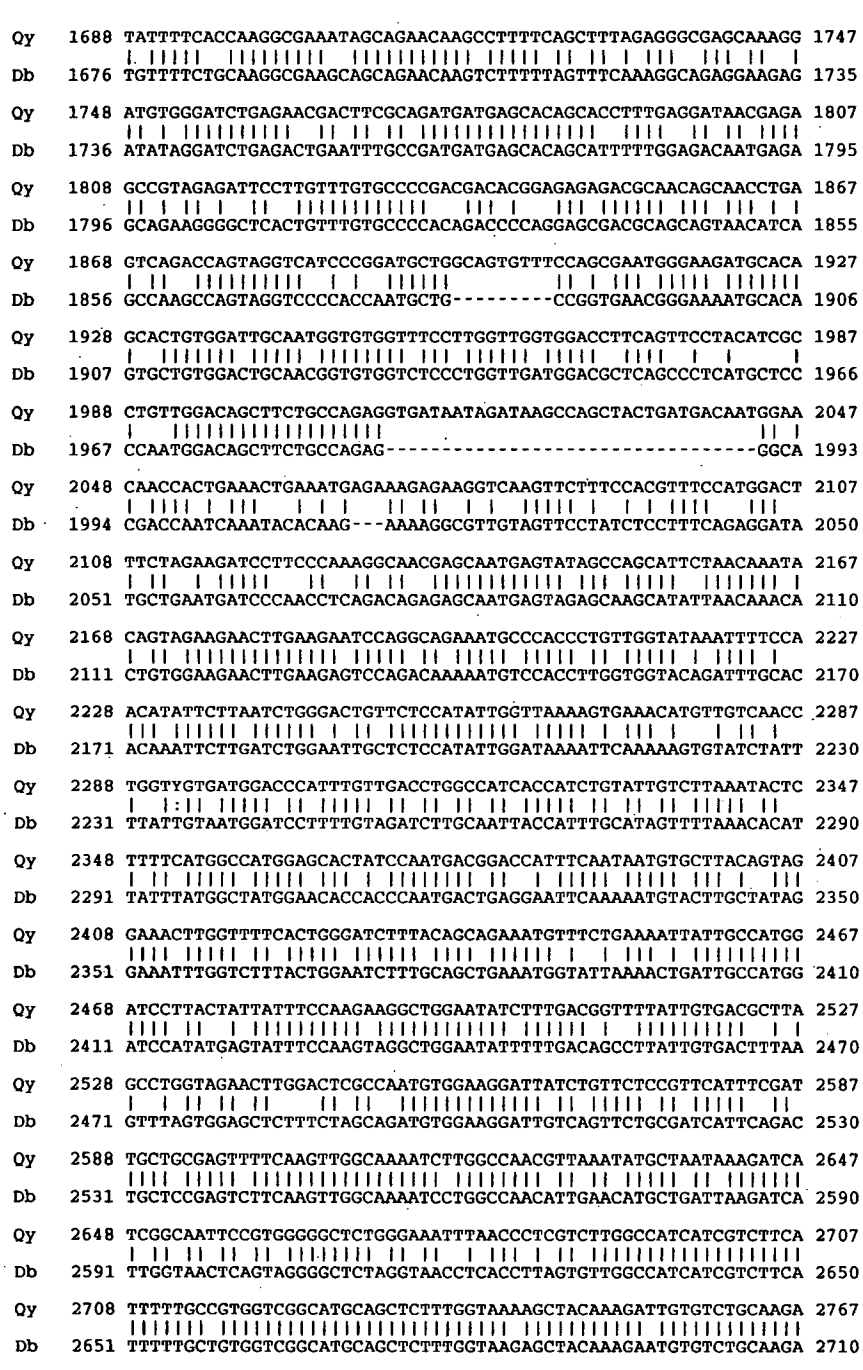
Qy    1391 CAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCAT 1450
           || | ||   | |      |   |   ||  |     | |||||||| || || |
Db    1376 CAGCGGCTGAATATACAAGTATTAGGAGAAGCAGAATTATGGGCCTCTCAGAGAGTTCTT 1435

Qy    1451 CTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGGAGGAAGAAAA 1510
           ||||| | || ||  |||| || ||||||| ||||||||||  | || |||||||
Db    1436 CTGAAACATCCAAACTGAGCTCTAAAAGTGCTAAAGAAAGAAGAAACAGAAGAAAGAAAA 1495

Qy    1511 GAAAACAGAAAGAGCAGTC---TGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAAT 1567
             || || ||  |||  ||   ||| | |||| ||  |||||  ||  ||||    ||||
Db    1496 AGAATCAAAAGAAGCTCTCCAGTGGAGAGGAAAAGGGAGATGCTGAGAAATTGTCGAAAT 1555

Qy    1568 CTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGGAACCGAT 1627
           | |||||  |||||||||||||| || ||| |||| | | |     | ||||||  |  |
Db    1556 CAGAATCAGAGGACAGCATCAGAAGAAAAAGTTTCCACCTTGGTGTCGAAGGGCATAGGC 1615

Qy    1628 TGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGTGGCTCCC 1687
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Db    1616 GAGCACATGAAAAGAGGTTGTCTACCCCCAATCAGTCACCACTCAGCATTCGTGGCTCCT 1675
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Qy 1688 TATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGAGCAAAGG 1747
Db 1676 TGTTTTCTGCAAGGCGAAGCAGCAGAACAAGTCTTTTTAGTTTCAAAGGCAGAGGAAGAG 1735
Qy 1748 ATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGATAACGAGA 1807
Db 1736 ATATAGGATCTGAGACTGAATTTGCCGATGATGAGCACAGCATTTTTGGAGACAATGAGA 1795
Qy 1808 GCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGCAACCTGA 1867
Db 1796 GCAGAAGGGGCTCACTGTTTGTGCCCCACAGACCCCAGGAGCGACGCAGCAGTAACATCA 1855
Qy 1868 GTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACA 1927
Db 1856 GCCAAGCCAGTAGGTCCCCACCAATGCTG---------CCGGTGAACGGGAAAATGCACA 1906
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Db 1967 CCAATGGACAGCTTCTGCCAGAG----------------------------------GGCA 1993
Qy 2048 CAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACT 2107
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Db 2051 TGCTGAATGATCCCAACCTCAGACAGAGAGCAATGAGTAGAGCAAGCATATTAACAAACA 2110
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Db 2111 CTGTGGAAGAACTTGAAGAGTCCAGACAAAAATGTCCACCTTGGTGGTACAGATTTGCAC 2170
Qy 2228 ACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACC 2287
Db 2171 ACAAATTCTTGATCTGGAATTGCTCTCCATATTGGATAAAATTCAAAAAGTGTATCTATT 2230
Qy 2288 TGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAATACTC 2347
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Qy 2708 TTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGA 2767
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RESULT 3
US-08-836-325-9
; Sequence 9, Application US/08836325
; Patent No. 6110672
;  GENERAL INFORMATION:
;    APPLICANT:  Mandel, Gail
;    APPLICANT:  Halegoua, Simon
;    APPLICANT:  Borden, Laurence A.
;    TITLE OF INVENTION:  Peripheral Nervous System Specific
;    TITLE OF INVENTION:  Sodium Channels, DNA Encoding Therefor, Crystallization,
;    TITLE OF INVENTION:  X-ray Diffraction, Computer Molecular Modeling, Rational
;    TITLE OF INVENTION:  Drug Design, Drug Screening, and Methods of Making and Using
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
;      STREET:  1100 New York Ave., N. W., Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,325
;      FILING DATE:  2-MAY-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14251
;      FILING DATE:  02-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/482,401
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/334,029
;      FILING DATE:  02-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ludwig, Steven R.
;      REGISTRATION NUMBER:  36,203
;      REFERENCE/DOCKET NUMBER:  0917.0240002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6452 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  both
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  326..6277
US-08-836-325-9

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  Matches 4457;  Conservative    2;  Mismatches 1473;  Indels   84;  Gaps    8;

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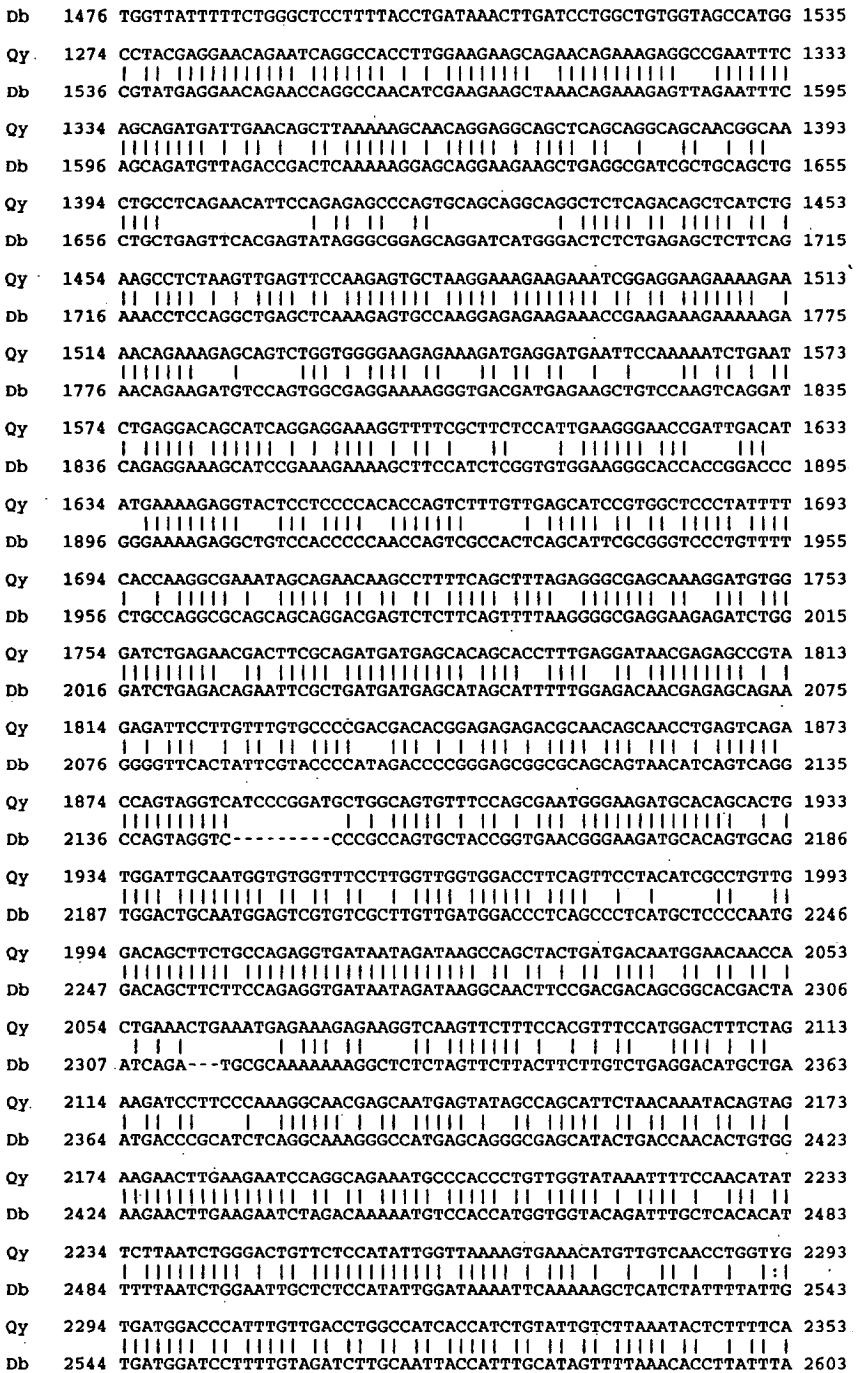
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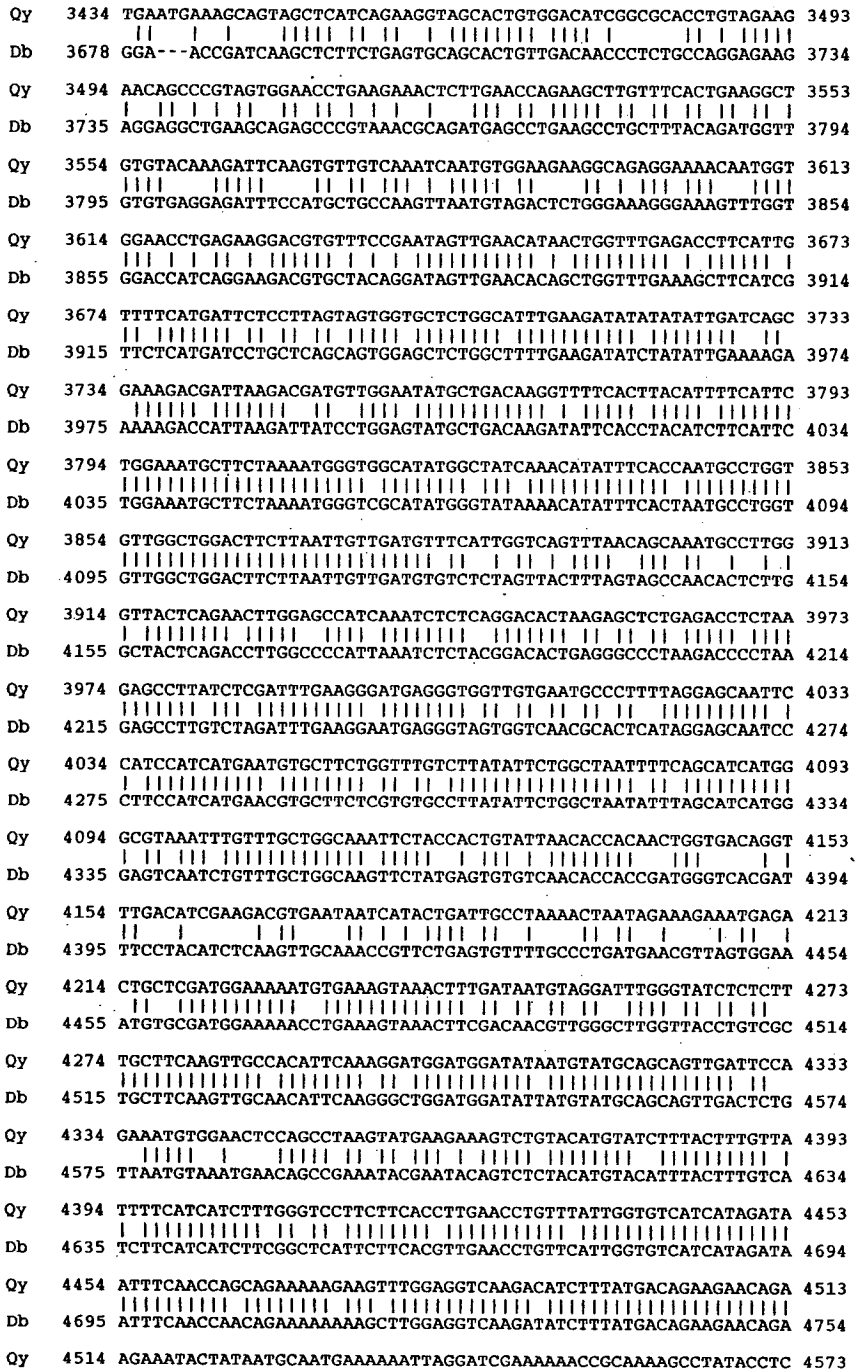
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Qy 1394 CTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCATCTG 1453
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Db 2016 GATCTGAGACAGAATTCGCTGATGATGAGCATAGCATTTTTGGAGACAACGAGAGCAGAA 2075
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Qy 1934 TGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTG 1993
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RESULT 4
US-09-024-020B-2
; Sequence 2, Application US/09024020B
; Patent No. 6030810
; GENERAL INFORMATION:
;   APPLICANT:  DELGADO, STEPHEN G.
;   APPLICANT:  DIETRICH, PAUL S.
;   APPLICANT:  FISH, LINDA M.
;   APPLICANT:  HERMAN, RONALD C.
;   APPLICANT:  SANGAMESWARAN, LAKSHMI
;   TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;   TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;   NUMBER OF SEQUENCES:  43
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  JANET PAULINE CLARK
;     STREET:  3401 HILLVIEW AVENUE, MS A2-250
;     CITY:  PALO ALTO
;     STATE:  CA
;     COUNTRY:  U.S.A.
;     ZIP:  94304-1397
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/024,020B
;     FILING DATE:  16-FEB-1998
;     CLASSIFICATION:  536
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/039,447
;     FILING DATE:  26-FEB-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  CLARK, JANET P.
;     REGISTRATION NUMBER:  34,799
;     REFERENCE/DOCKET NUMBER:  R0020B-REG
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (650) 852-3097
;     TELEFAX:  (650) 855-5322
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  6007 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-2

  Query Match             46.2%;  Score 2787.6;  DB 3;  Length 6007;
  Best Local Similarity   69.9%;  Pred. No. 0;
  Matches 4086;  Conservative    3;  Mismatches 1597;  Indels  162;  Gaps   18;

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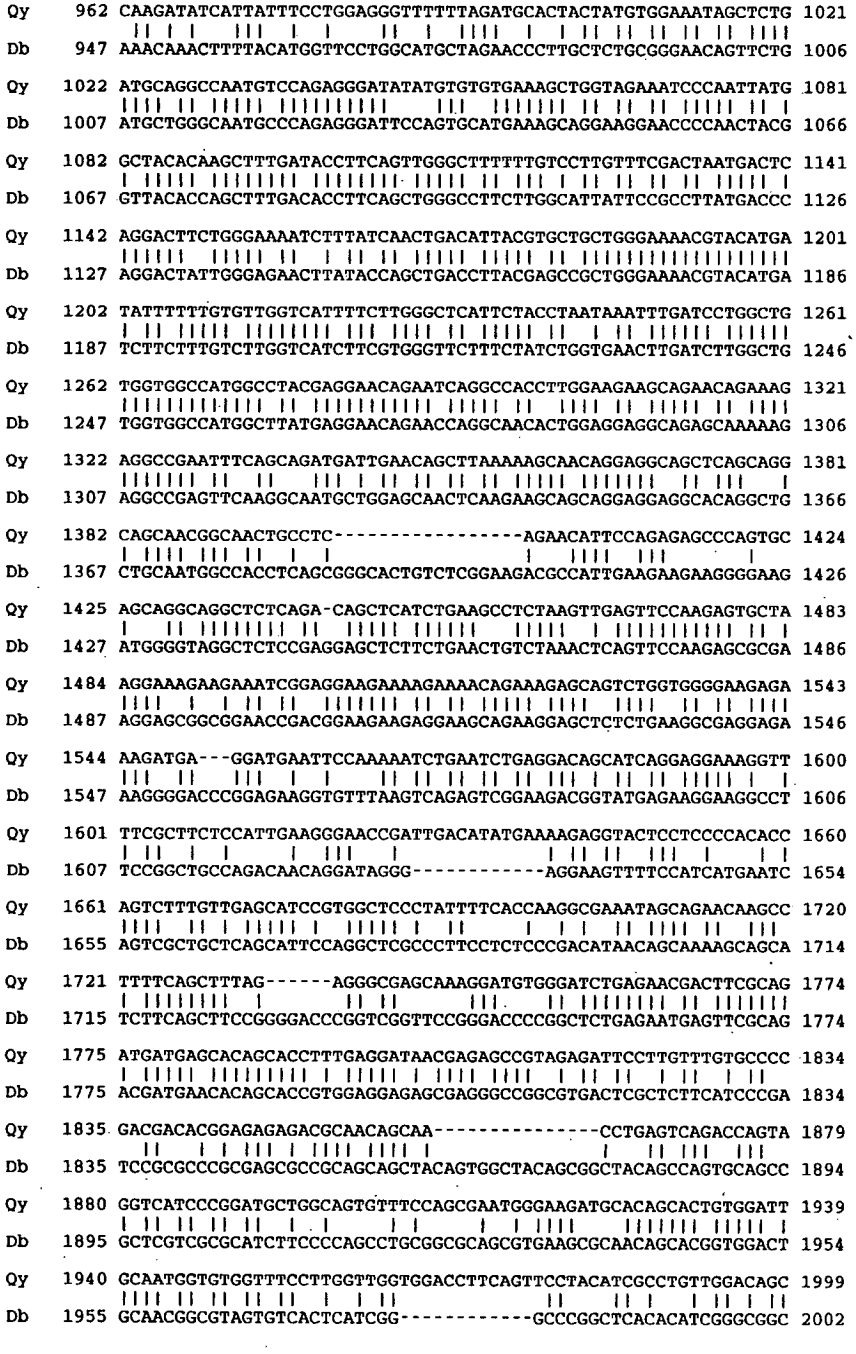
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Qy 2120 CTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATAC---AGTAGAAG 2176
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RESULT 5
US-09-425-043-2
; Sequence 2, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6007 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-2

  Query Match             46.2%;  Score 2787.6;  DB 4;  Length 6007;
  Best Local Similarity   69.9%;  Pred. No. 0;
  Matches 4086;  Conservative    3;  Mismatches 1597;  Indels  162;  Gaps   18;

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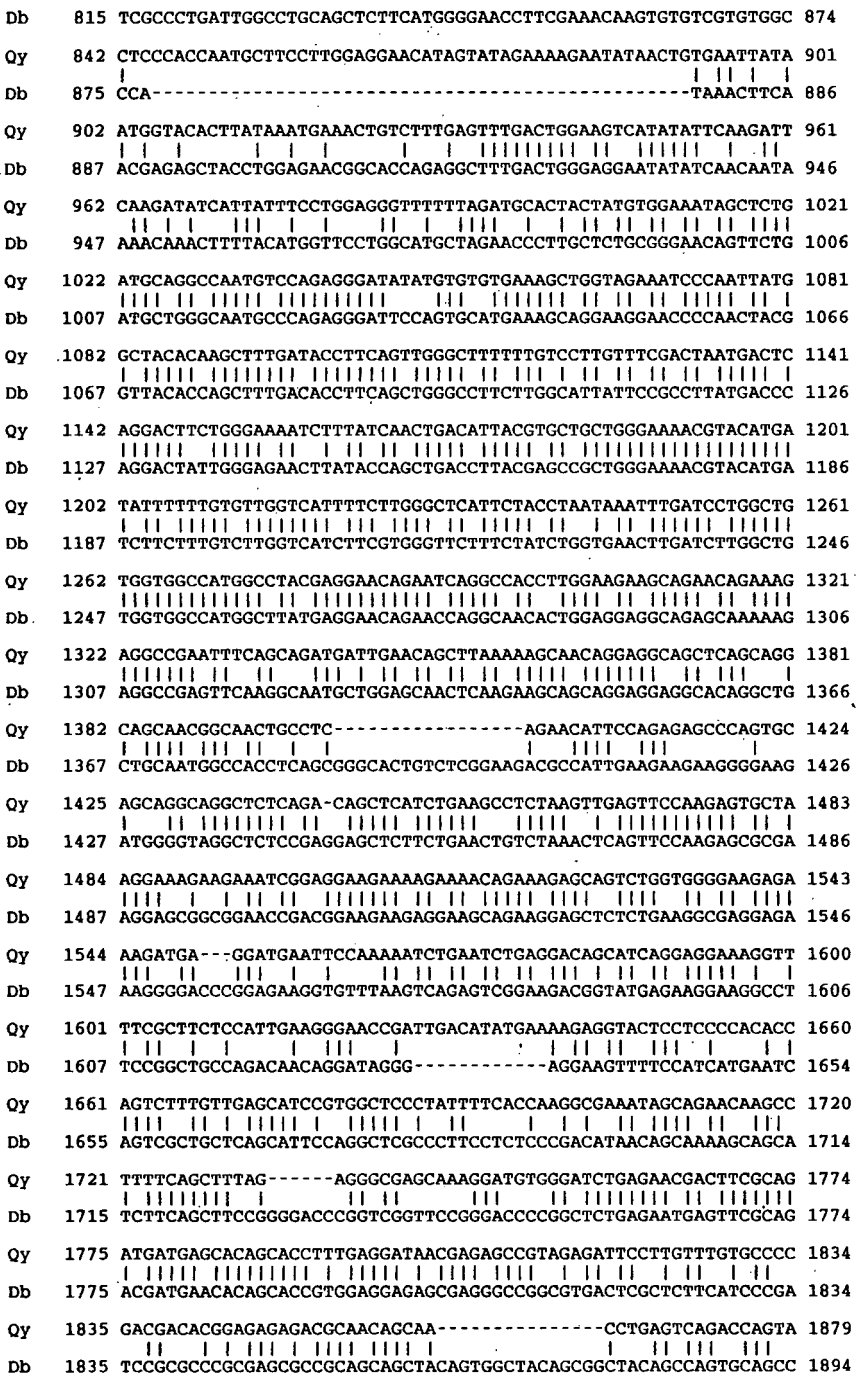
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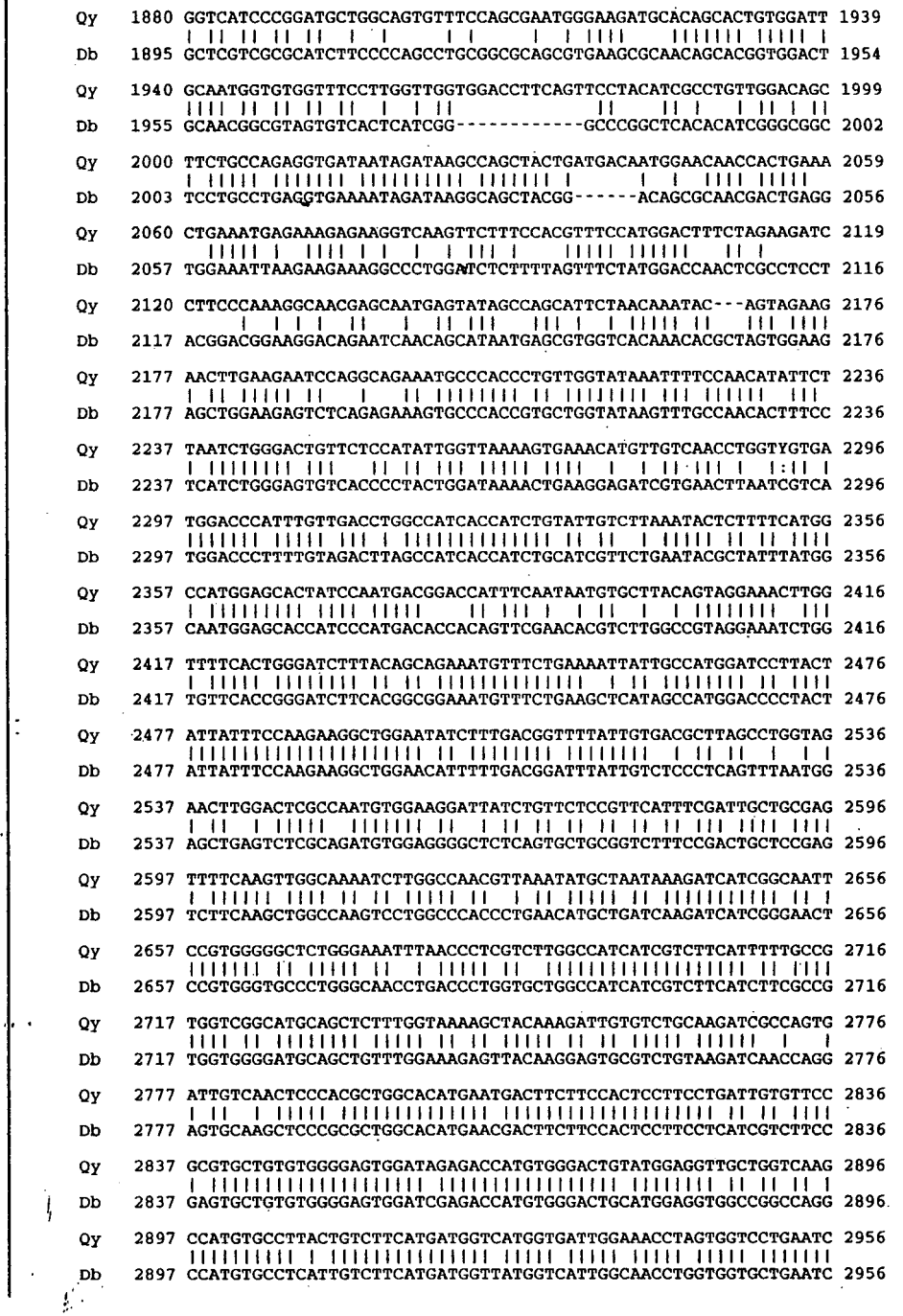
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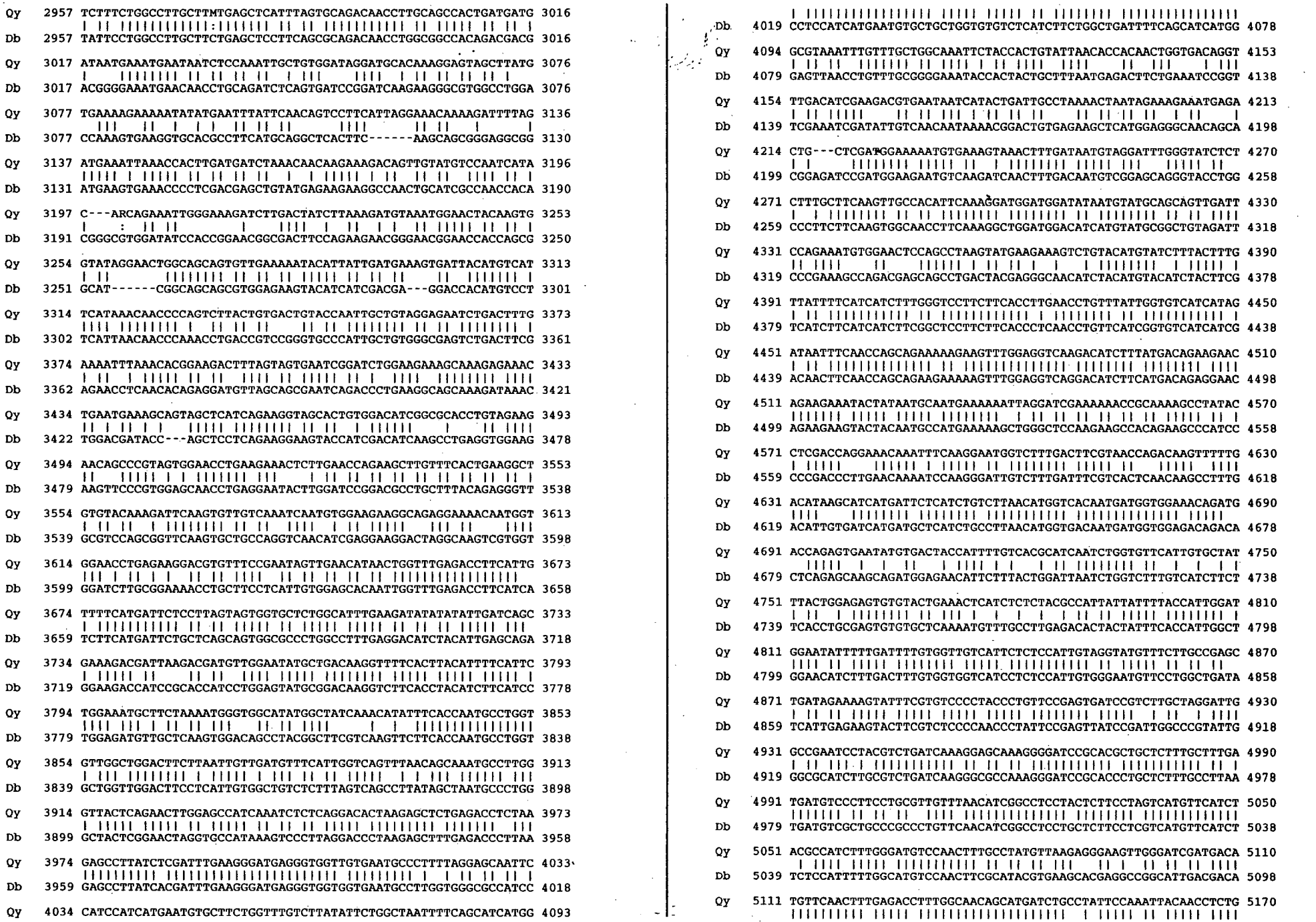
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Db    755 TCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTTT 814

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Qy    5471 AATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAAC 5530
           | |     ||  |  |  | ||||| |  || || || |  || |||    | ||  | |
Db    5456 AGTACTGTAAGCTGGCAGACTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGC 5515

Qy    5531 CAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACT 5590
           | ||||   || |||||||| ||||||||  |||||||||||||| || || || |||||||
Db    5516 CCAACACCATCGAGCTCATCGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACT 5575

Qy    5591 GTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATG 5650
           |  | || ||| | || || || || |||| || || |||| |||| ||| ||||
Db    5576 GCTTGGACATCCTTTTCGCCTTCACCAAGCGAGTCCTGGGAGACAGTGGGGAGTTGGACA 5635

Qy    5651 CTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATC 5710
             || ||    |||||||| |||| ||| |||| |||||||||||||| || || ||
Db    5636 TCCTGCGGCAGCAGATGGAGGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACG 5695

Qy    5711 AGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGC 5770
           |||| ||||| || ||| |    || || || ||||| || ||||| ||  |  | ||||
Db    5696 AGCCTATCACAACCACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGCAGTGGTCCTGCAGC 5755

Qy    5771 GTGCTTACAGACGCCACCTTTTAAAGCG 5798
           |||| |||||  | ||| |    | |||
Db    5756 GTGCCTACAGGGGACACTTGGCTAGGCG 5783


RESULT 6
US-09-024-020B-43
; Sequence 43, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6586 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-43

  Query Match             45.7%;  Score 2758.2;  DB 3;  Length 6586;
  Best Local Similarity   69.4%;  Pred. No. 0;
  Matches 4050;  Conservative    3;  Mismatches 1646;  Indels  136;  Gaps   17;

Qy     14 TGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAATCTCTTGCGGCTA 73
          |||| | |||||||| ||||| || |||||     ||||||    || || || ||    |
Db    182 TGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAGTCGCTGGCAAACA 241

Qy     74 TTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAG------------ACA 121
          | || || || ||||| ||     |||   ||||| ||    |   |             ||
Db    242 TCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCGGATGGCAGCCACC 301

Qy    122 AAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAACC 181
            | || || || || |     || |||||||| |||||| |||| ||||| ||||
Db    302 GGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAGGCTGGGAAGAGTT 361

Qy    182 TTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTGG 241
          | || || || || || ||||| || | ||   ||||  | |  ||||||||||| | |
Db    362 TGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTTG 421

Qy    242 ACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTCC 301
          |||| |||||  | |   ||||||| ||| ||||||| || | ||||||   |  |||||
Db    422 ACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGGAAAACTCTCTTCA 481

Qy    302 GGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATAG 361
          | || ||||||||  |||||  |||||||||||  || || || |   | || | |||||
Db    482 GATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTGATAAGAAGAATAG 541

Qy    362 CTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACAA 421
          |||||||  |||||| |||| ||| | |||||||||  | || ||||||||  ||  |||| |
Db    542 CTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGCACCATCCTGACCA 601

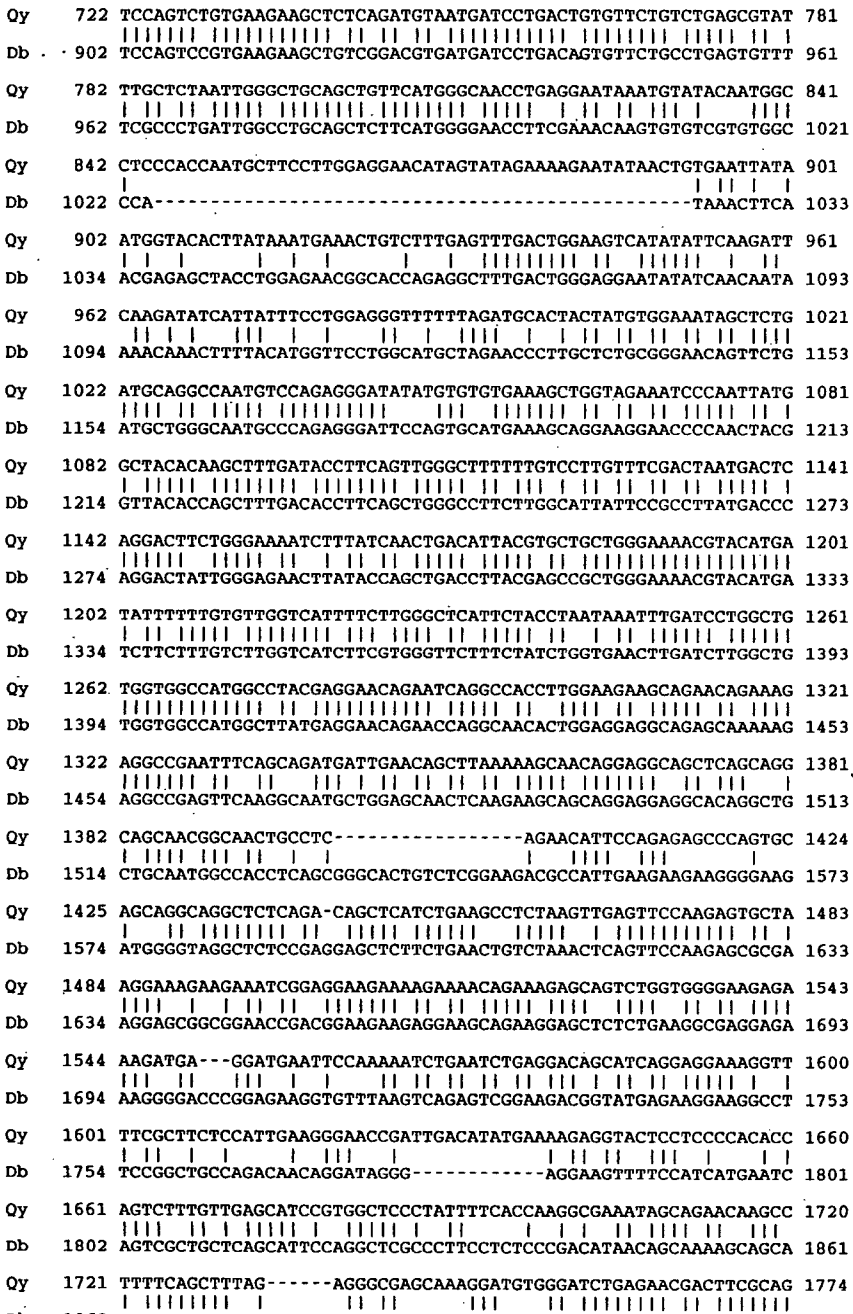
Qy    422 ACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACCT 481
          ||||||||||  |||||  | ||||||||||  || ||| | ||||||||  |||||  |
Db    602 ACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAATGTGGAGTACACAT 661

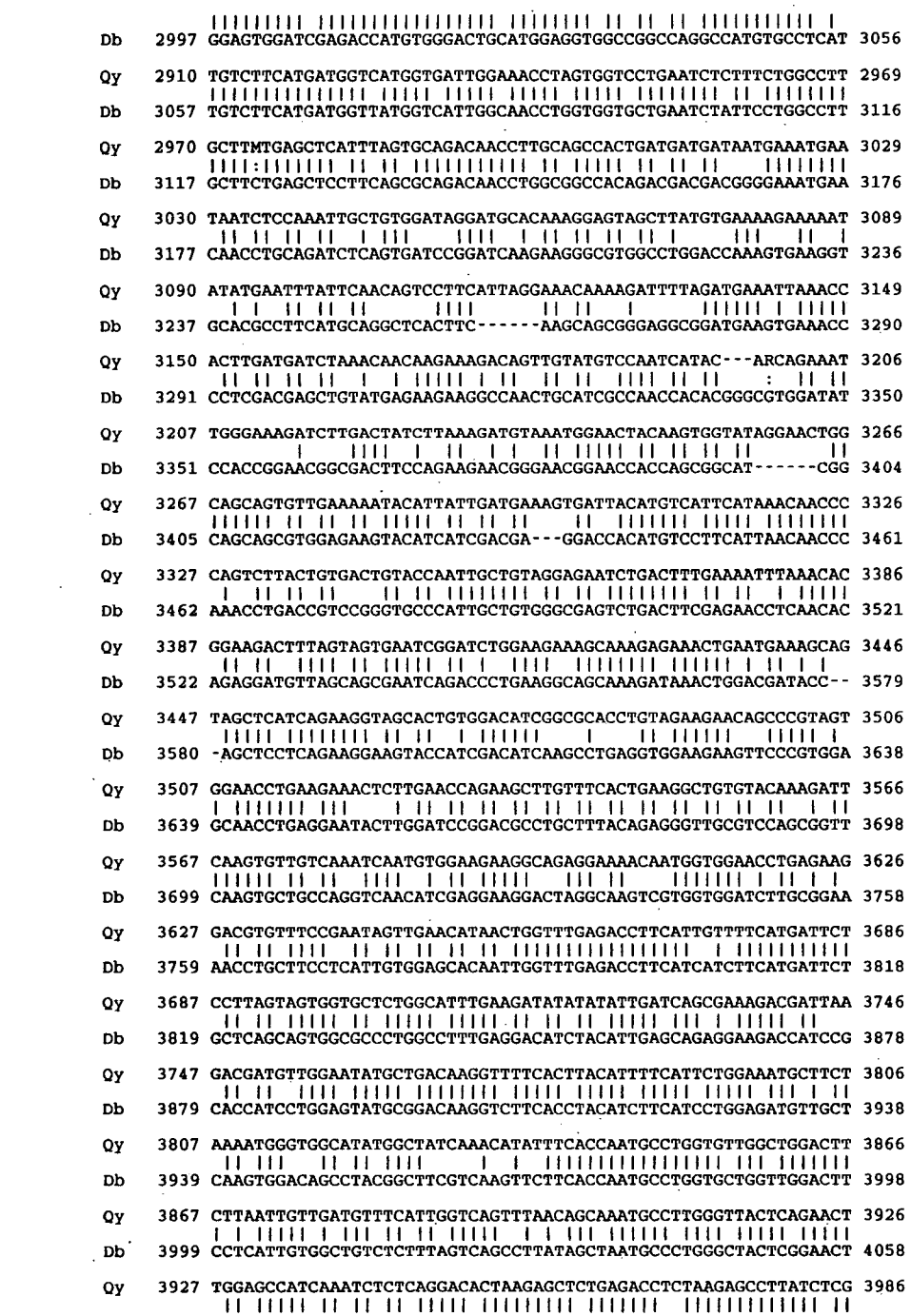
Qy    482 TCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTAG 541
          |||||||  || || ||  ||||||||||  | |||||  || |||||  || |||||  |||
Db    662 TCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGAGGTTTCTGCATAG 721

Qy    542 AAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTTG 601
          | |  || || ||| | || || || |||||||| | || |||| ||||||  |  | |
Db    722 ACGGCTTCACCTTCTTGCGAGACCCGTGGAACTGGTTAGACTTCAGTGTCATCATGATGG 781

Qy    602 CGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTTC 661
          | || || ||||||||||||||||||||||||||||||  ||  ||||||||||||| ||||
Db    782 CATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTTC 841

Qy    662 TCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGA 721
          |||||||  |||| || || || || ||||||||||||| || || |||||  |||| |
Db    842 TCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTAA 901
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Qy 722 TCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTAT 781
Db 902 TCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTTT 961
Qy 782 TTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGGC 841
Db 962 TCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGTGTCGTGTGGC 1021
Qy 842 CTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTATA 901
Db 1022 CCA----------TAAACTTCA 1033
Qy 902 ATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGATT 961
Db 1034 ACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAATATATCAACAATA 1093
Qy 962 CAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCTG 1021
Db 1094 AAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGCGGGAACAGTTCTG 1153
Qy 1022 ATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTATG 1081
Db 1154 ATGCTGGGCAATGCCCAGAGGGATTCCAGTGCATGAAAGCAGGAAGGAACCCCAACTACG 1213
Qy 1082 GCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACTC 1141
Db 1214 GTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTCCGCCTTATGACCC 1273
Qy 1142 AGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATGA 1201
Db 1274 AGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGGAAAACGTACATGA 1333
Qy 1202 TATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCTG 1261
Db 1334 TCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCTGGTGAACTTGATCTTGGCTG 1393
Qy 1262 TGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAAG 1321
Db 1394 TGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAGGCAGAGCAAAAAG 1453
Qy 1322 AGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGG 1381
Db 1454 AGGCCGAGTTCAAGGCAATGCTGGAGCAACTCAAGAAGCAGCAGGAGGAGGCACAGGCTG 1513
Qy 1382 CAGCAACGGCAACTGCCTC----------AGAACATTCCAGAGAGCCCAGTGC 1424
Db 1514 CTGCAATGGCCACCTCAGCGGGCACTGTCTCGGAAGACGCCATTGAAGAAGAAGGGGAAG 1573
Qy 1425 AGCAGGCAGGCTCTCAGA-CAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTA 1483
Db 1574 ATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAGTTCCAAGAGCGCGA 1633
Qy 1484 AGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGA 1543
Db 1634 AGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTCTGAAGGCGAGGAGA 1693
Qy 1544 AAGATGA---GGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTT 1600
Db 1694 AAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAAGACGGTATGAGAAGGAAGGCCT 1753
Qy 1601 TTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACC 1660
Db 1754 TCCGGCTGCCAGACAACAGGATAGGG----------AGGAAGTTTTCCATCATGAATC 1801
Qy 1661 AGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCC 1720
Db 1802 AGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAACAGCAAAAGCAGCA 1861
Qy 1721 TTTTCAGCTTTAG------AGGGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAG 1774
Db 1862 TCTTCAGCTTCCGGGGACCCGGTCGGTTCCGGGACCCCGGCTCTGAGAATGAGTTCGCAG 1921
Qy 1775 ATGATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCC 1834
Db 1922 ACGATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTCGCTCTTCATCCCGA 1981
Qy 1835 GACGACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAG--TAGGTCATCCCCGGAT 1892
Db 1982 TCCGCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTACAGCCAGTGCAGCC 2041
Qy 1893 GCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGT 1952
Db 2042 GCTCGTCGCGTGAAAATAGATAAGGCAGCTACGGACAGCGCATCTTCCCCAGCCTGCGGC 2101
Qy 1953 TTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGT 2012
Db 2102 GCAGCGTGAAGCGCAACAGCACGGTGGACTGCAACGGCGTAGTGTCACTCATCGGGCCCG 2161
Qy 2013 GATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATGAGAAA 2072
Db 2162 GCTCACACATCGGGCGGCTCCTG-----CCTGAGGCAACGACTGAGGTGGAAATTAAGAA 2216
Qy 2073 GAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAAAGGCA 2132
Db 2217 GAAAGGCCCTGGATCTCTTTTAGTTTCTATGGACCAACTCGCCTCCTACGGACGGAAGGA 2276
Qy 2133 ACGAGCAATGAGTATAGCCAGCATTCTAACAAATAC---AGTAGAAGAACTTGAAGAATC 2189
Db 2277 CAGAATCAACAGCATAATGAGCGTGGTCACAAACACGCTAGTGGAAGAGCTGGAAGAGTC 2336
Qy 2190 CAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGACTG 2249
Db 2337 TCAGAGAAAGTGCCCACCGTGCTGGTATAAGTTTGCCAACACTTTCCTCATCTGGGAGTG 2396
Qy 2250 TTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTYGTGATGGACCCATTTGT 2309
Db 2397 TCACCCCTACTGGATAAAACTGAAGGAGATCGTGAACTTAATCGTCATGGACCCTTTTGT 2456
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Db 2457 AGACTTAGCCATCACCATCTGCATCGTTCTGAATACGCTATTTATGGCAATGGAGCACCA 2516
Qy 2370 TCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGGAT 2429
Db 2517 TCCCATGACACCACAGTTCGAACACGTCTTGGCCGTAGGAAATCTGGTGTTCACCGGGAT 2576
Qy 2430 CTTTACAGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAAGA 2489
Db 2577 CTTCACGGCGGAAATGTTTCTGAAGCTCATAGCCATGGACCCCTACTATTATTTCCAAGA 2636
Qy 2490 AGGCTGGAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTCGC 2549
Db 2637 AGGCTGGAACATTTTTGACGGATTTATTGTCTCCCTCAGTTTAATGGAGCTGAGTCTCGC 2696
Qy 2550 CAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTGGC 2609
Db 2697 AGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTTCCGACTGCTCCGAGTCTTCAAGCTGGC 2756
Qy 2610 AAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCTCT 2669
Db 2757 CAAGTCCTGGCCCACCCTGAACATGCTGATCAAGATCATCGGGAACTCCGTGGGTGCCCT 2816
Qy 2670 GGGAAATTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCA 2729
Db 2817 GGGCAACCTGACCCTGGTGCTGGCCATCATCGTCTTCATCTTCGCCGTGGTGGGGATGCA 2876
Qy 2730 GCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTCCC 2789
Db 2877 GCTGTTTGGAAAGAGTTACAAGGAGTGCGTCTGTAAGATCAACCAGGAGTGCAAGCTCCC 2936
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Db 2937 GCGCTGGCACATGAACGACTTCTTCCACTCCTTCCTCATCGTCTTCCGAGTGCTGTGTGG 2996
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Db 2997 GGAGTGGATCGAGACCATGTGGGACTGCATGGAGGTGGCCGGCCAGGCCATGTGCCTCAT 3056
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Db 3057 TGTCTTCATGATGGTTATGGTCATTGGCAACCTGGTGGTGCTGAATCTATTCCTGGCCTT 3116
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Db 3117 GCTTCTGAGCTCCTTCAGCGCAGACAACCTGGCGGCCACAGACGACGACGGGGAAATGAA 3176
Qy 3030 TAATCTCCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAAT 3089
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Qy 3090 ATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACC 3149
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Qy 3150 ACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATAC---ARCAGAAAT 3206
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Qy 3867 CTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCAAATGCCTTGGGTTACTCAGAACT 3926
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Qy 3987 ATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTAGGAGCAATTCCATCCATCATGAA 4046
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Qy 4284 TGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTGGA 4343
Db 4419 GGCAACCTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCCCGAAAGCCAGA 4478
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Qy 4464 GCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTA 4523
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Qy 4524 TAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAGCCTATACCTCGACCAGGAAA 4583
Db 4659 CAATGCCATGAAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCCCGACCCTTGAA 4718
Qy 4584 CAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAAGTTTTTGACATAAGCATCAT 4643
Db 4719 CAAAATCCAAGGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGACATTGTGATCAT 4778
Qy 4644 GATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAAACAGATGACCAGAGTGAATA 4703
Db 4779 GATGCTCATCTGCCTTAACATGGTGACAATGATGGTGGAGACAGACACTCAGAGCAAGCA 4838
Qy 4704 TGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATTGTGCTATTTACTGGAGAGTG 4763
Db 4839 GATGGAGAACATTCTTTACTGGATTAATCTGGTCTTTGTCATCTTCTTCACCTGCGAGTG 4898
Qy 4764 TGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACCATTGGATGGAATATTTTTGA 4823
Db 4899 TGTGCTCAAAATGTTTGCCTTGAGACACTACTATTTCACCATTGGCTGGAACATCTTTGA 4958
Qy 4824 TTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTA 4883
Db 4959 CTTTGTGGTGGTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTA 5018
Qy 4884 TTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACG 4943
Db 5019 CTTCGTCTCCCCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGGCGCATCTTGCG 5078
Qy 4944 TCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCC 5003
Db 5079 TCTGATCAAGGGCGCCAAAGGGATCCGCACCCTGCTCTTTGCCTTAATGATGTCGCTGCC 5138
Qy 5004 TGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGG 5063
Db 5139 CGCCCTGTTCAACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTTCTCCATTTTTGG 5198

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Qy   5064 GATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGA 5123
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Db   5199 CATGTCCAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATGTTCAACTTCGA 5258

Qy   5124 GACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGG 5183
          ||| ||||||||||||||||||||  | ||||| || ||||| ||||||||||||||||
Db   5259 GACATTTGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCTGGCTGGGATGG 5318

Qy   5184 ATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCC 5243
            ||||    || || || ||| |    || || |||||   |    | ||||   ||||
Db   5319 CCTGCTGCTGCCAATCCTGAACCG---CCCCCCTGACTGCAGCTTGGACAAAGAGCACCC 5375

Qy   5244 TGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAG 5303
          || ||  -. | || || ||||||||||||||| || || || || ||||| ||||| ||
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Qy   5304 TTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAA 5363
          |||||||||| |||||||| ||||||||||||||||||||  ||||||||||||
Db   5436 CTACATCATCATCTCCTTCCTGATTGTGGTGAACATGTACATCGCCATCATCCTGGAGAA 5495

Qy   5364 CTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTT 5423
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Db   5496 CTTCAGCGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGACTTCGAGACTTT 5555

Qy   5424 CTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATT 5483
          ||||||| | |||||||||||||| || || || || |||||||| || |     ||  |
Db   5556 CTATGAGATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAGTACTGTAAGCT 5615

Qy   5484 ATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCA 5543
            | | ||||| |  || || || |  || |||    | ||  | || ||||   || |
Db   5616 GGCAGACTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCCAACACCATCGA 5675

Qy   5544 GCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTT 5603
          |||||| ||||||||  |||||||||||||| || || || ||||||||  | || ||| |
Db   5676 GCTCATCGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGCTTGGACATCCT 5735

Qy   5604 ATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACA 5663
          || || || || ||||| || || ||||| ||||| ||| ||||    || ||   ||
Db   5736 TTTCGCCTTCACCAAGCGAGTCCTGGGAGACAGTGGGGAGTTGGACATCCTGCGGCAGCA 5795

Qy   5664 GATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTAC 5723
          |||||| ||||| ||| |||| |||||||||||||| || || ||  |||| ||||| ||
Db   5796 GATGGAGGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACGAGCCTATCACAAC 5855

Qy   5724 TACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACG 5783
          ||| |    || || || ||||| || ||||| ||  |  | |||||||| |||||  |
Db   5856 CACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGTGCCTACAGGGG 5915

Qy   5784 CCACCTTTTAAAGCG 5798
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Db   5916 ACACTTGGCTAGGCG 5930


RESULT 7
US-09-425-043-43
; Sequence 43, Application US/09425043
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6586 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-43

  Query Match             45.7%;  Score 2758.2;  DB 4;  Length 6586;
  Best Local Similarity   69.4%;  Pred. No. 0;
  Matches 4050;  Conservative    3;  Mismatches 1646;  Indels  136;  Gaps   17;

Qy      14 TGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAATCTCTTGCGGCTA 73
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Qy     122 AAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAACC 181
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Db     302 GGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAGGCTGGGAAGAGTT 361

Qy     182 TTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTGG 241
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Db     362 TGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTTG 421

Qy     242 ACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTCC 301
           |||| |||||| | |   ||||||| ||| ||||||| || | ||||||  |  |||||
Db     422 ACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGGAAAACTCTCTTCA 481

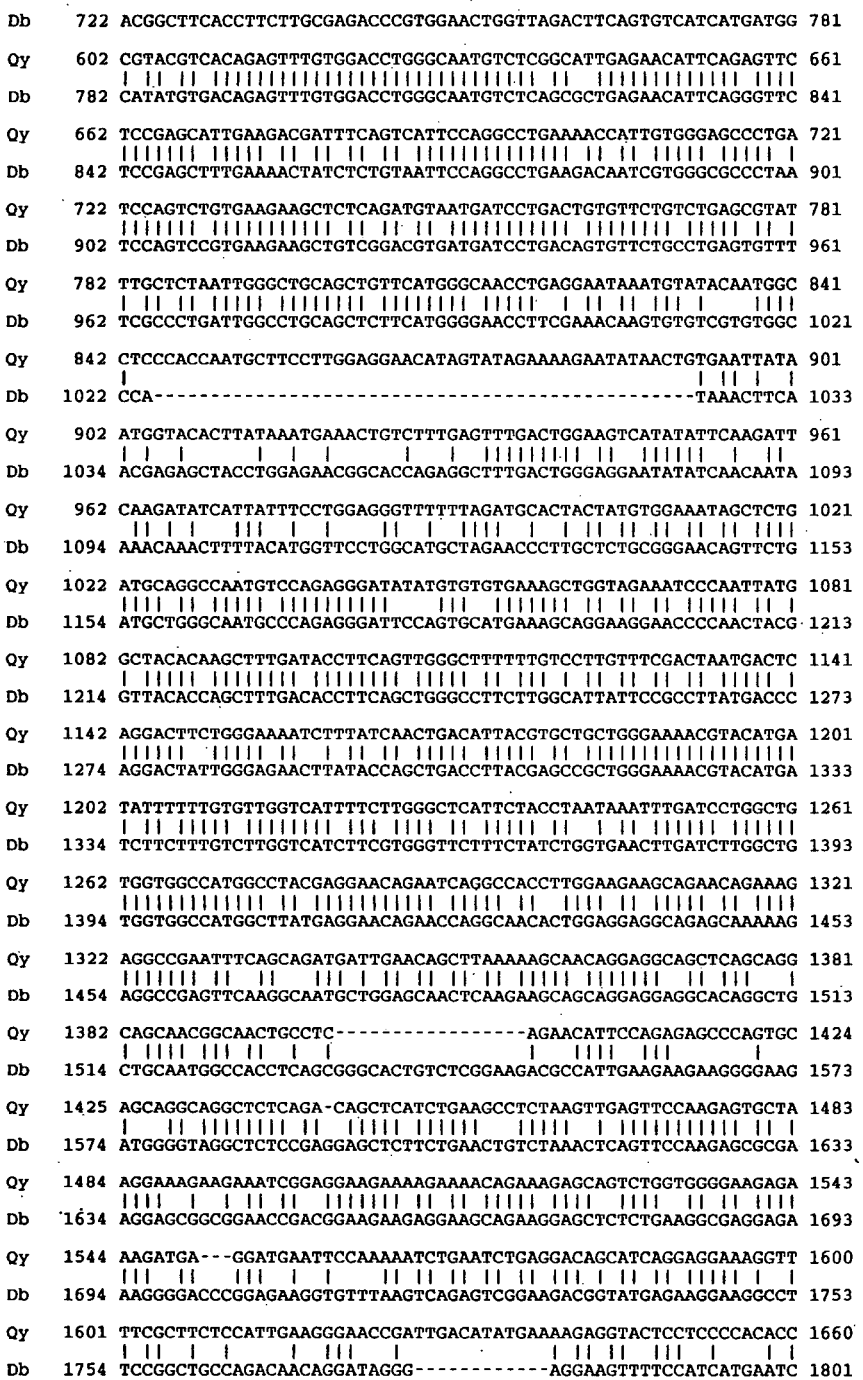
Qy     302 GGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATAG 361
           | || |||||||  ||||| ||||||||||||  || || || |   | || | |||||
Db     482 GATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTGATAAGAAGAATAG 541

Qy     362 CTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACAA 421
           ||||||| |||||| |||| ||| | |||||||| | || |||||||| ||  |||| |
Db     542 CTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGCACCATCCTGACCA 601

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Db     602 ACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAATGTGGAGTACACAT 661

Qy     482 TCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTAG 541
           ||||||| || || || ||||||||||  | ||||| || ||||| || |||||  |||
Db     662 TCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGAGGTTTCTGCATAG 721

Qy     542 AAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTTG 601
           | |  || || ||| | || || || |||||||||| | || |||| |||||| |   | |
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Db 722 ACGGCTTCACCTTCTTGCGAGACCCGTGGAACTGGTTAGACTTCAGTGTCATCATGATGG 781
Qy 602 CGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTTC 661
Db 782 CATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTTC 841
Qy 662 TCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGA 721
Db 842 TCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTAA 901
Qy 722 TCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTAT 781
Db 902 TCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTTT 961
Qy 782 TTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGGC 841
Db 962 TCGCCCTGATTGGCCTGCAGCTCTTCATGGGGAACCTTCGAAACAAGTGTGTCGTGTGGC 1021
Qy 842 CTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTATA 901
Db 1022 CCA----------TAAACTTCA 1033
Qy 902 ATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGATT 961
Db 1034 ACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAATATATCAACAATA 1093
Qy 962 CAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCTG 1021
Db 1094 AAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGCGGGAACAGTTCTG 1153
Qy 1022 ATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTATG 1081
Db 1154 ATGCTGGGCAATGCCCAGAGGGATTCCAGTGCATGAAAGCAGGAAGGAACCCCAACTACG 1213
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Db 1394 TGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAGGCAGAGCAAAAAG 1453
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Qy 1382 CAGCAACGGCAACTGCCTC----------AGAACATTCCAGAGAGCCCAGTGC 1424
Db 1514 CTGCAATGGCCACCTCAGCGGGCACTGTCTCGGAAGACGCCATTGAAGAAGAAGGGGAAG 1573
Qy 1425 AGCAGGCAGGCTCTCAGA-CAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTA 1483
Db 1574 ATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAGTTCCAAGAGCGCGA 1633
Qy 1484 AGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGA 1543
Db 1634 AGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTCTGAAGGCGAGGAGA 1693
Qy 1544 AAGATGA---GGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTT 1600
Db 1694 AAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAAGACGGTATGAGAAGGAAGGCCT 1753
Qy 1601 TTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACC 1660
Db 1754 TCCGGCTGCCAGACAACAGGATAGGG----------AGGAAGTTTTCCATCATGAATC 1801
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Db 1802 AGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAACAGCAAAAGCAGCA 1861
Qy 1721 TTTTCAGCTTTAG------AGGGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAG 1774
Db 1862 TCTTCAGCTTCCGGGGACCCGGTCGGTTCCGGGACCCCGGCTCTGAGAATGAGTTCGCAG 1921
Qy 1775 ATGATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCC 1834
Db 1922 ACGATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTCGCTCTTCATCCCGA 1981
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Db 1982 TCCGCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTACAGCCAGTGCAGCC 2041
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Db 2042 GCTCGTCGCGTGAAAATAGATAAGGCAGCTACGGACAGCGCATCTTCCCCAGCCTGCGGC 2101
Qy 1953 TTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGT 2012
Db 2102 GCAGCGTGAAGCGCAACAGCACGGTGGACTGCAACGGCGTAGTGTCACTCATCGGGCCCG 2161
Qy 2013 GATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATGAGAAA 2072
Db 2162 GCTCACACATCGGGCGGCTCCTG-----CCTGAGGCAACGACTGAGGTGGAAATTAAGAA 2216
Qy 2073 GAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAAAGGCA 2132
Db 2217 GAAAGGCCCTGGATCTCTTTTAGTTTCTATGGACCAACTCGCCTCCTACGGACGGAAGGA 2276
Qy 2133 ACGAGCAATGAGTATAGCCAGCATTCTAACAAATAC---AGTAGAAGAACTTGAAGAATC 2189
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Db    5376 AGGGAGTGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTCTTCTTTGTGAG 5435

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Qy    5424 CTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATT 5483

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Qy    5484 ATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCA 5543

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Qy    5604 ATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACA 5663

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Qy    5724 TACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACG 5783

Db    5856 CACTCTGCGGCGCAAGCAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGTGCCTACAGGGG 5915

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; Sequence 1, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-1

  Query Match             45.4%;  Score 2738.8;  DB 3;  Length 5977;
  Best Local Similarity   69.5%;  Pred. No. 0;
  Matches 4063;  Conservative    3;  Mismatches 1590;  Indels  192;  Gaps   18;

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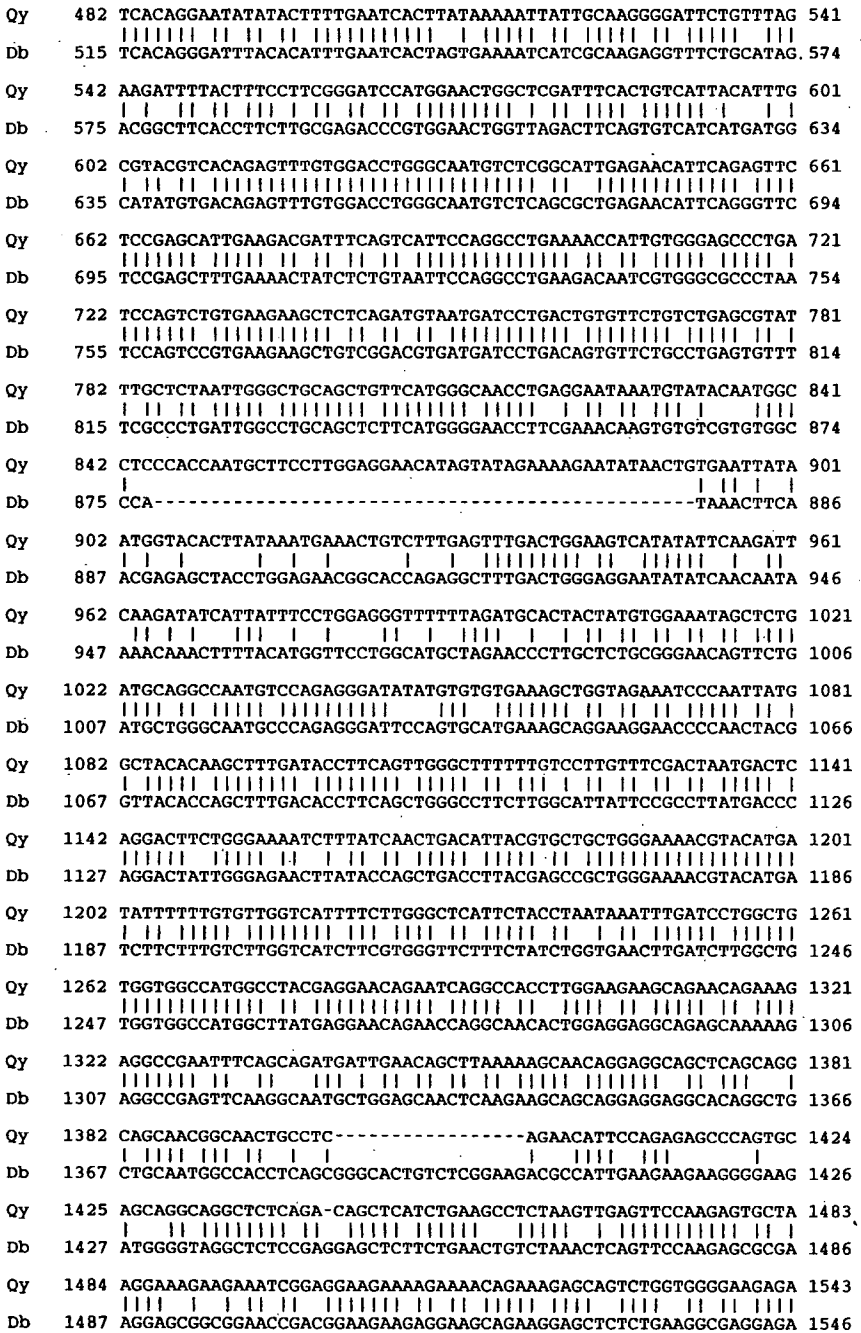
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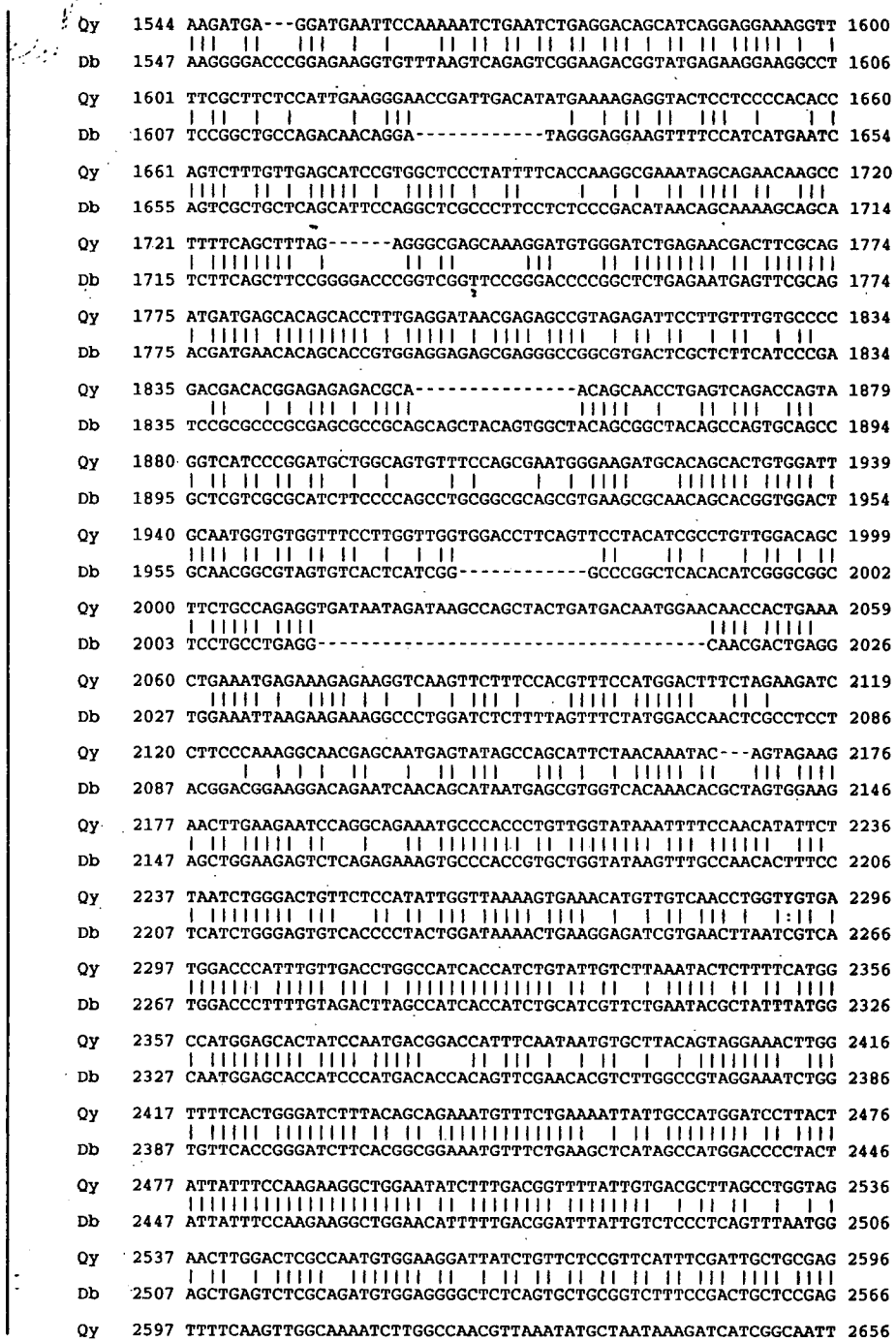
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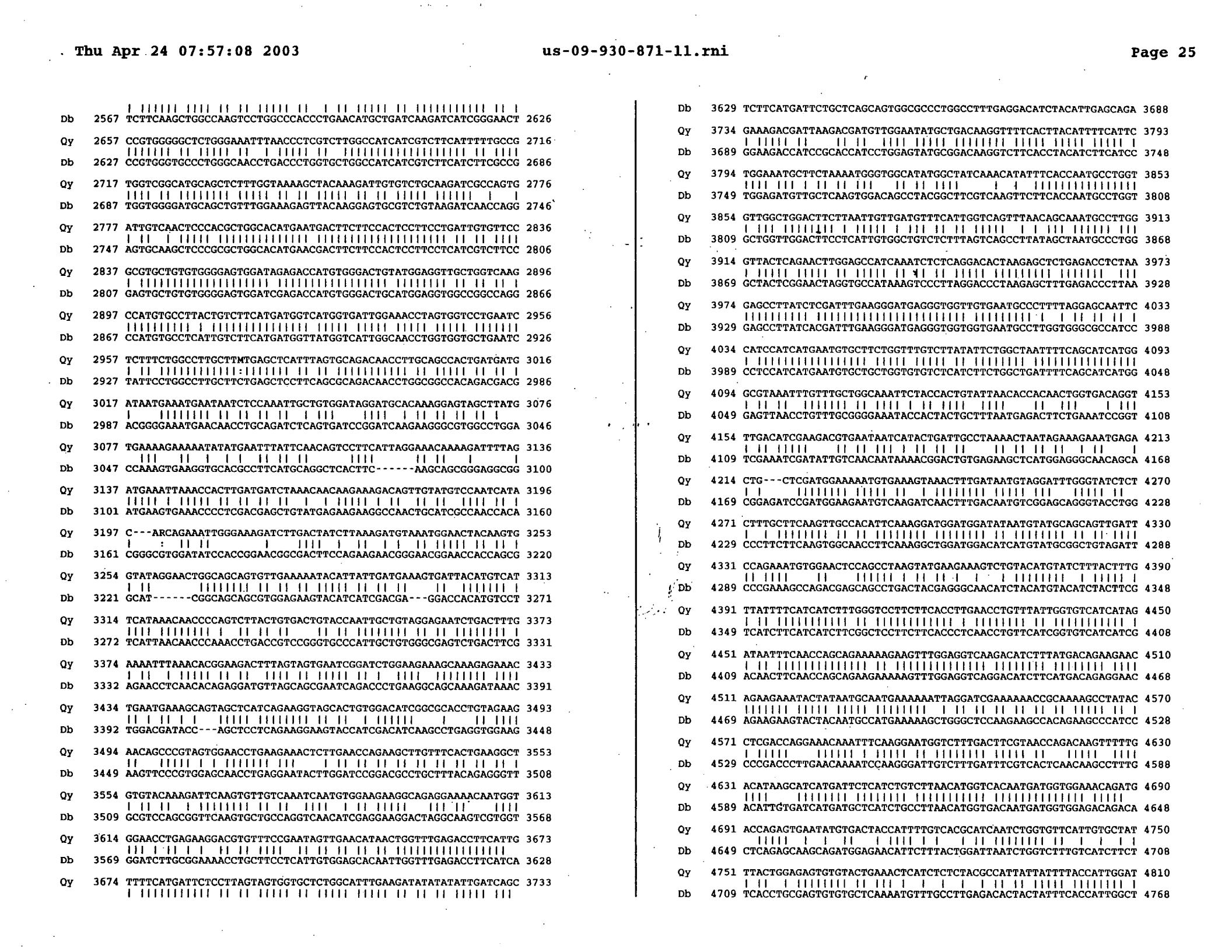
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RESULT 9
US-09-425-043-1
; Sequence 1, Application US/09425043
;
; Patent No. 6335172
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/425,043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/024,020
;      FILING DATE:  16-FEB-1998
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5977 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-1

  Query Match             45.4%;  Score 2738.8;  DB 4;  Length 5977;
  Best Local Similarity   69.5%;  Pred. No. 0;
  Matches 4063;  Conservative    3;  Mismatches 1590;  Indels  192;  Gaps   18;

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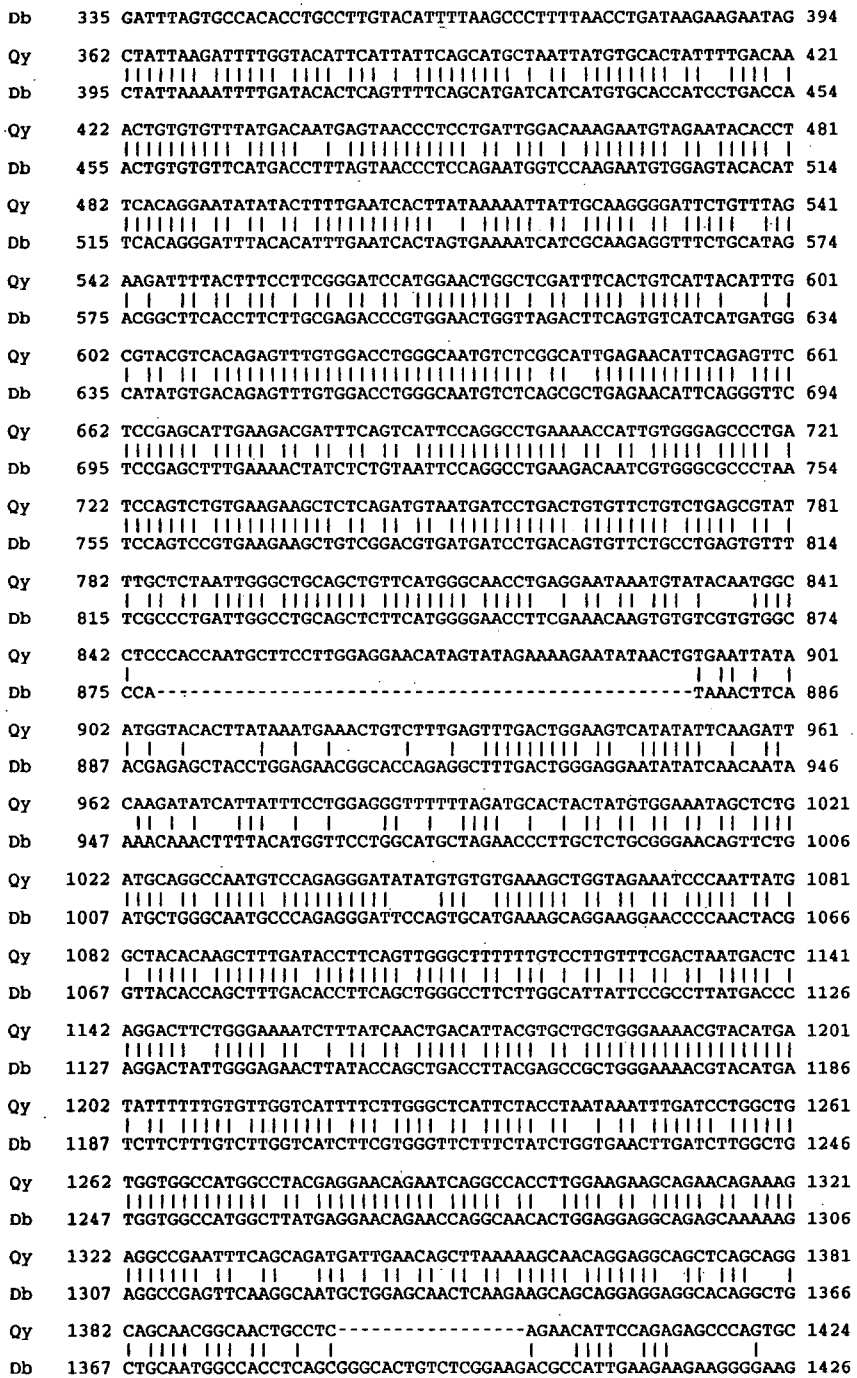
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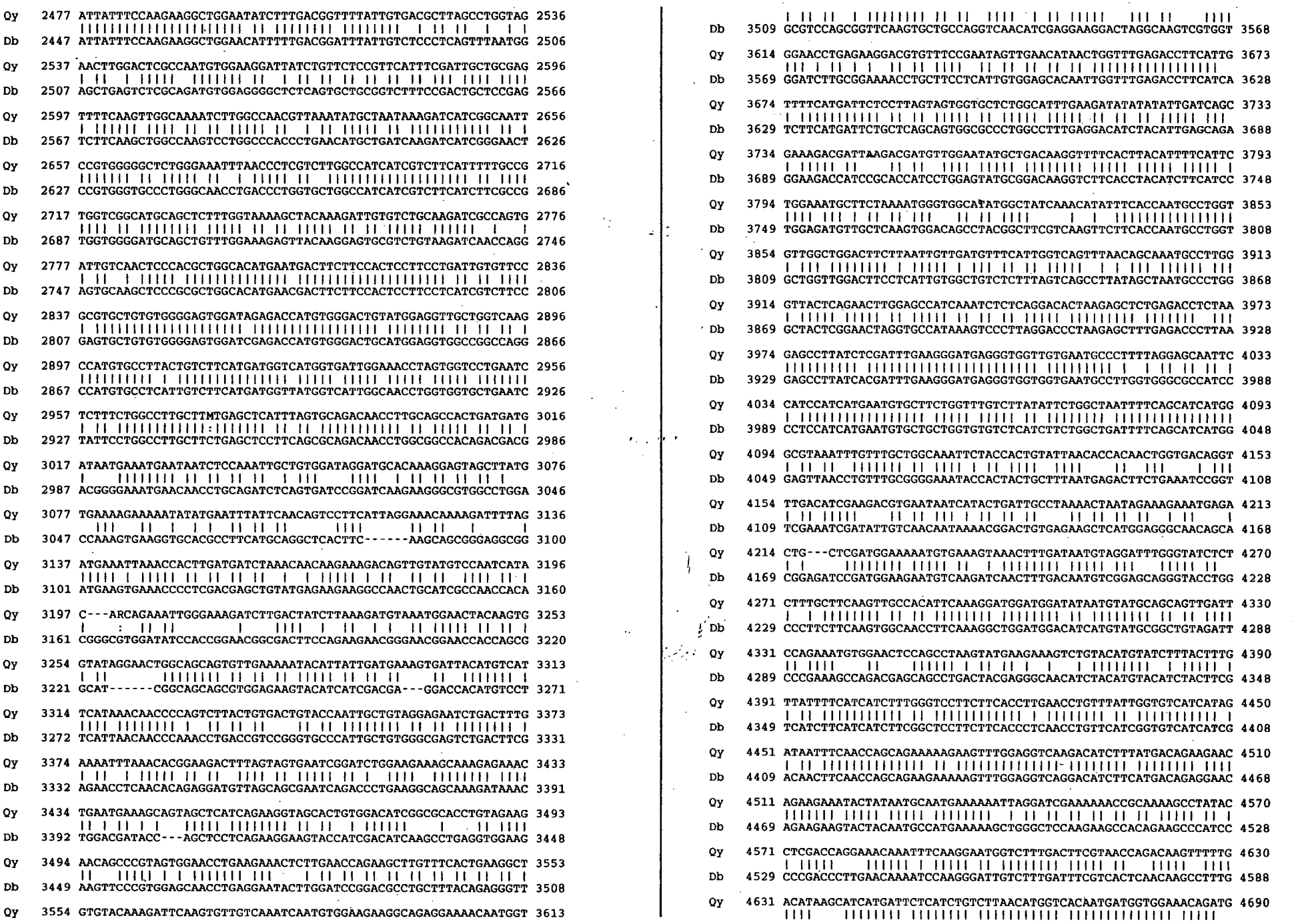
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Qy 2357 CCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGG 2416
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Qy    4691 ACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATTGTGCTAT 4750

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RESULT 10
US-09-024-020B-7
; Sequence 7, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6556 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-7

  Query Match             45.4%;  Score 2738.8;  DB 3;  Length 6556;
  Best Local Similarity   69.5%;  Pred. No. 0;
  Matches 4063;  Conservative    3;  Mismatches 1590;  Indels  192;  Gaps   18;

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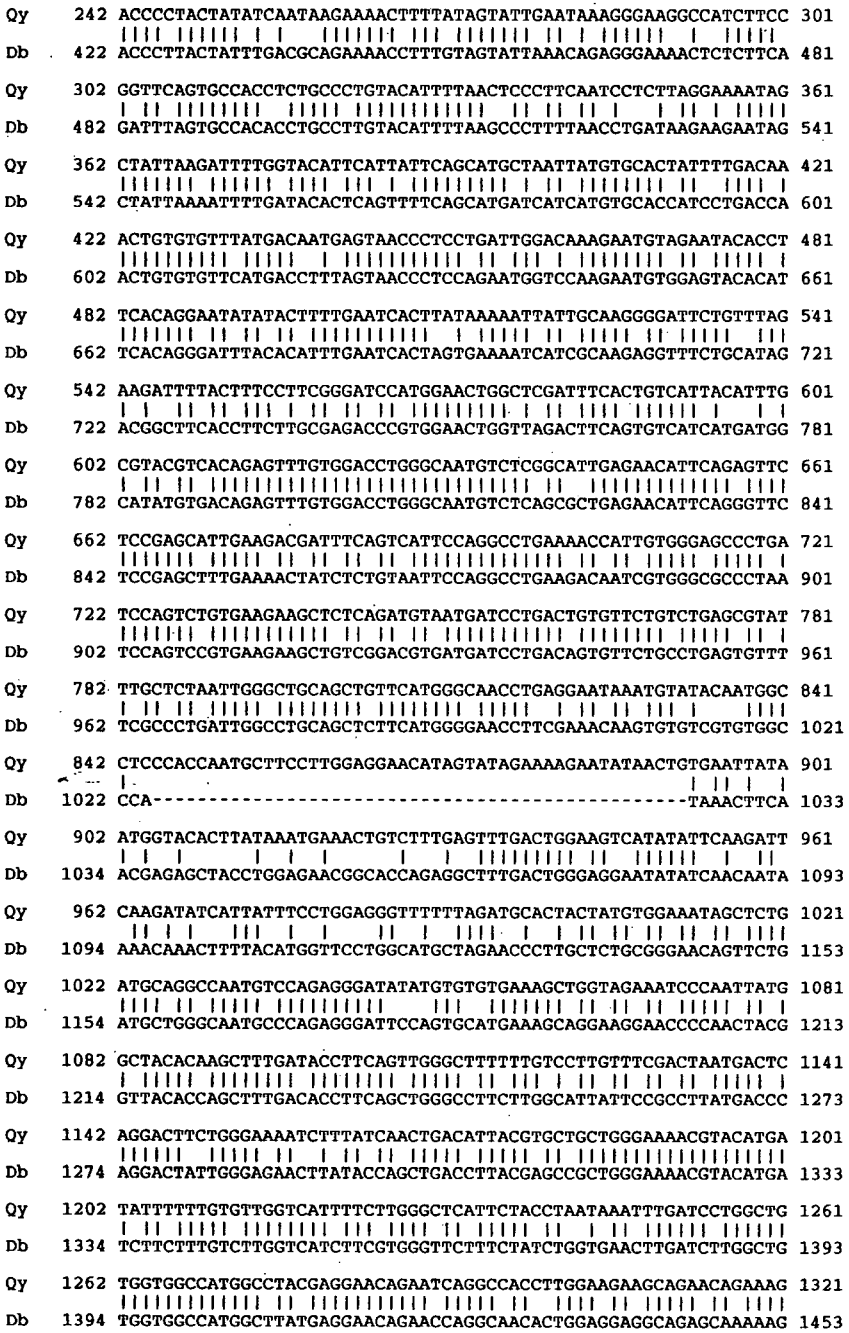
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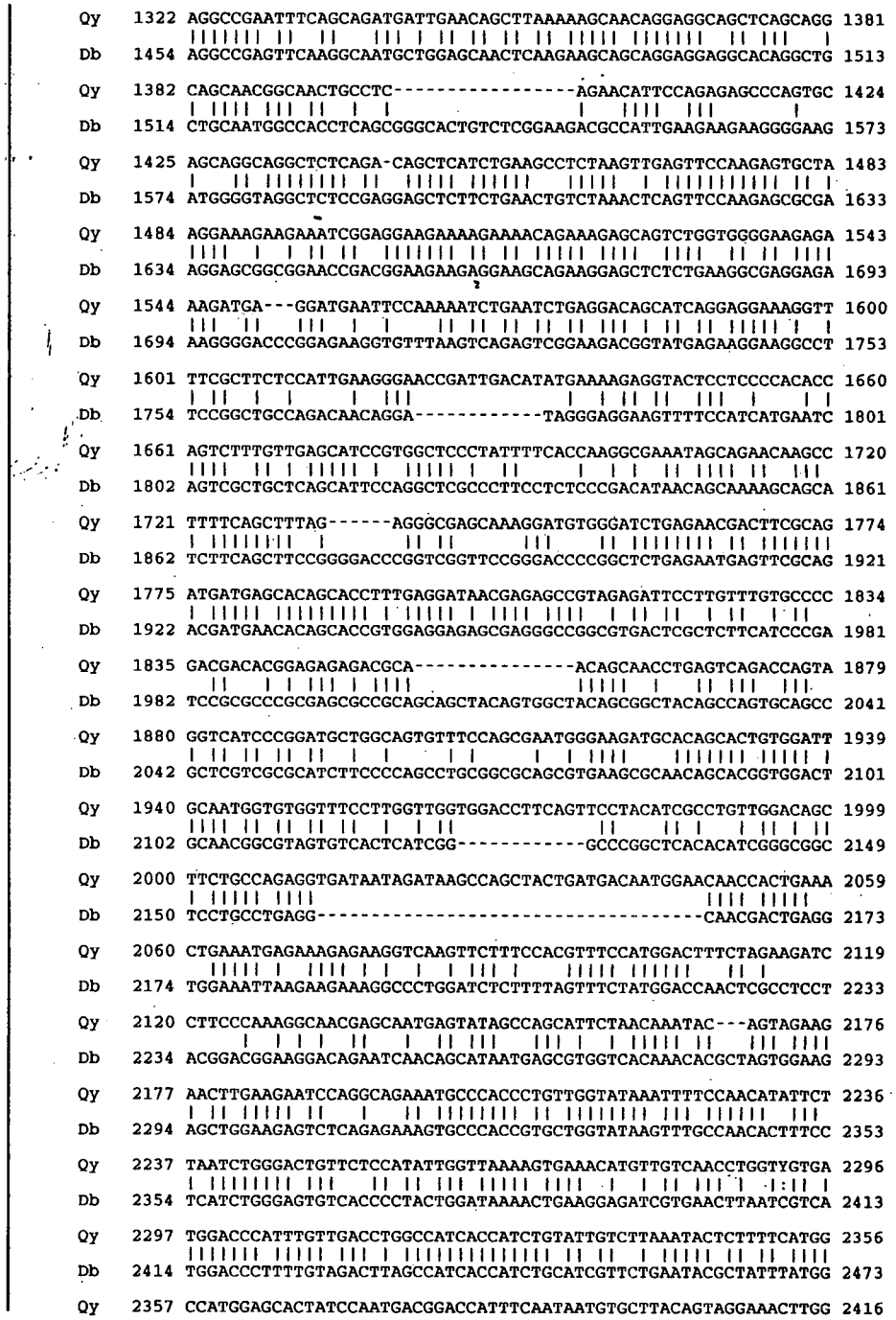
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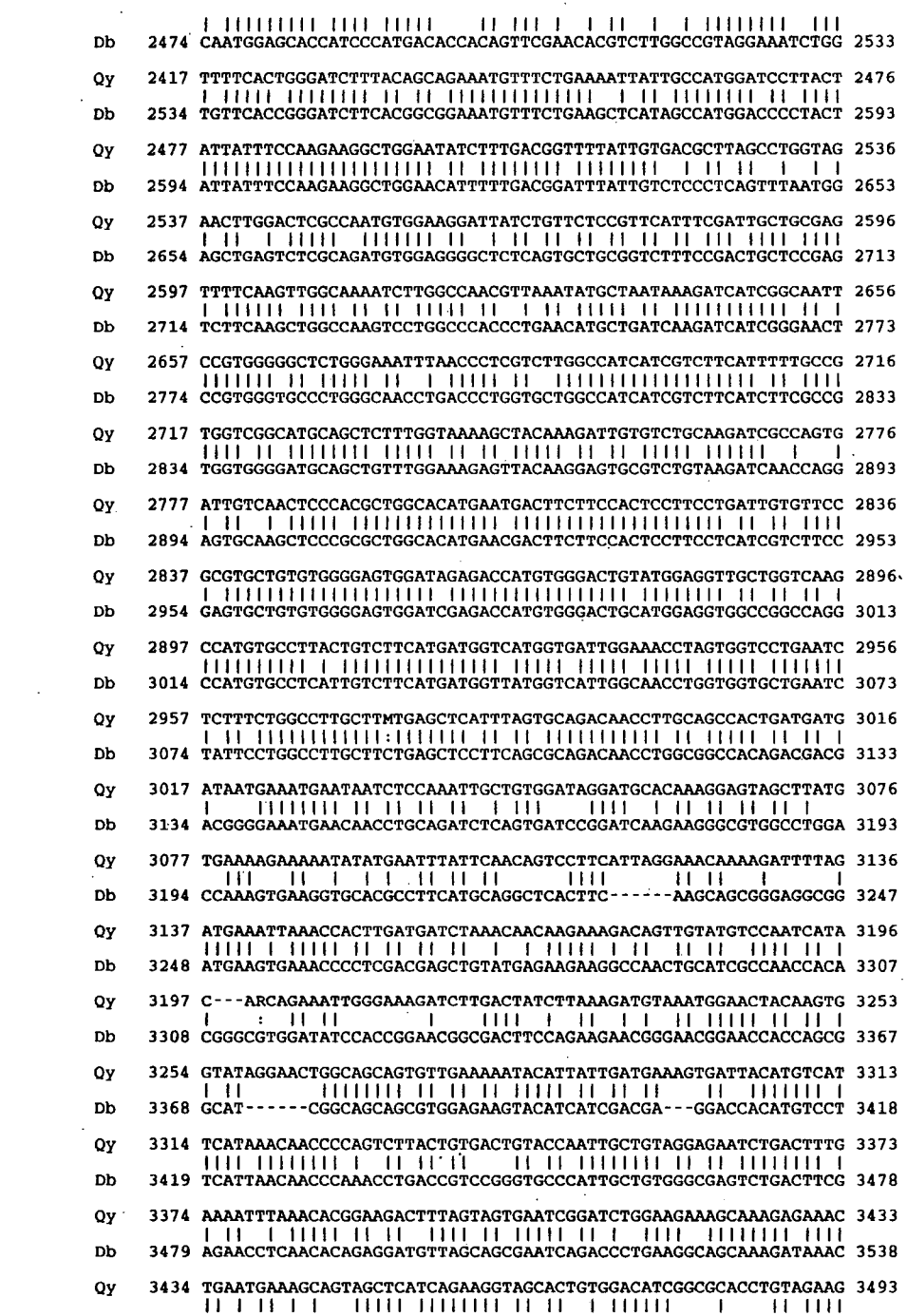
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Db     362 TGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTTG 421
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Db 2474 CAATGGAGCACCATCCCATGACACCACAGTTCGAACACGTCTTGGCCGTAGGAAATCTGG 2533
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Db 2594 ATTATTTCCAAGAAGGCTGGAACATTTTTGACGGATTTATTGTCTCCCTCAGTTTAATGG 2653
Qy 2537 AACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAG 2596
Db 2654 AGCTGAGTCTCGCAGATGTGGAGGGGCTCTCAGTGCTGCGGTCTTTCCGACTGCTCCGAG 2713
Qy 2597 TTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATT 2656
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Qy 2657 CCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCG 2716
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Qy 3314 TCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTG 3373
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Qy 3374 AAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGCAAAGAGAAAC 3433
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Qy 3554 GTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAACAATGGT 3613
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Qy 3674 TTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATATATTGATCAGC 3733
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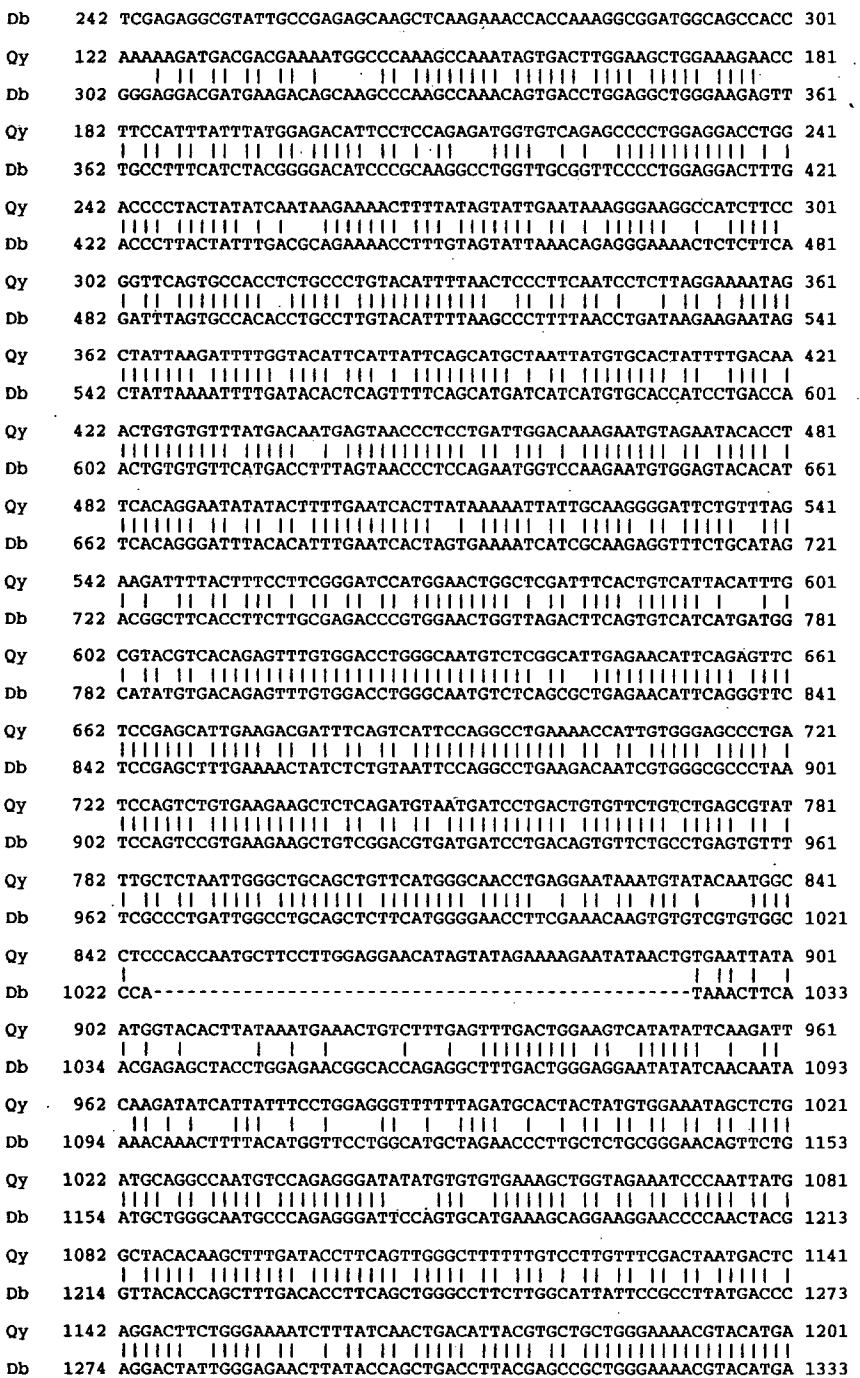
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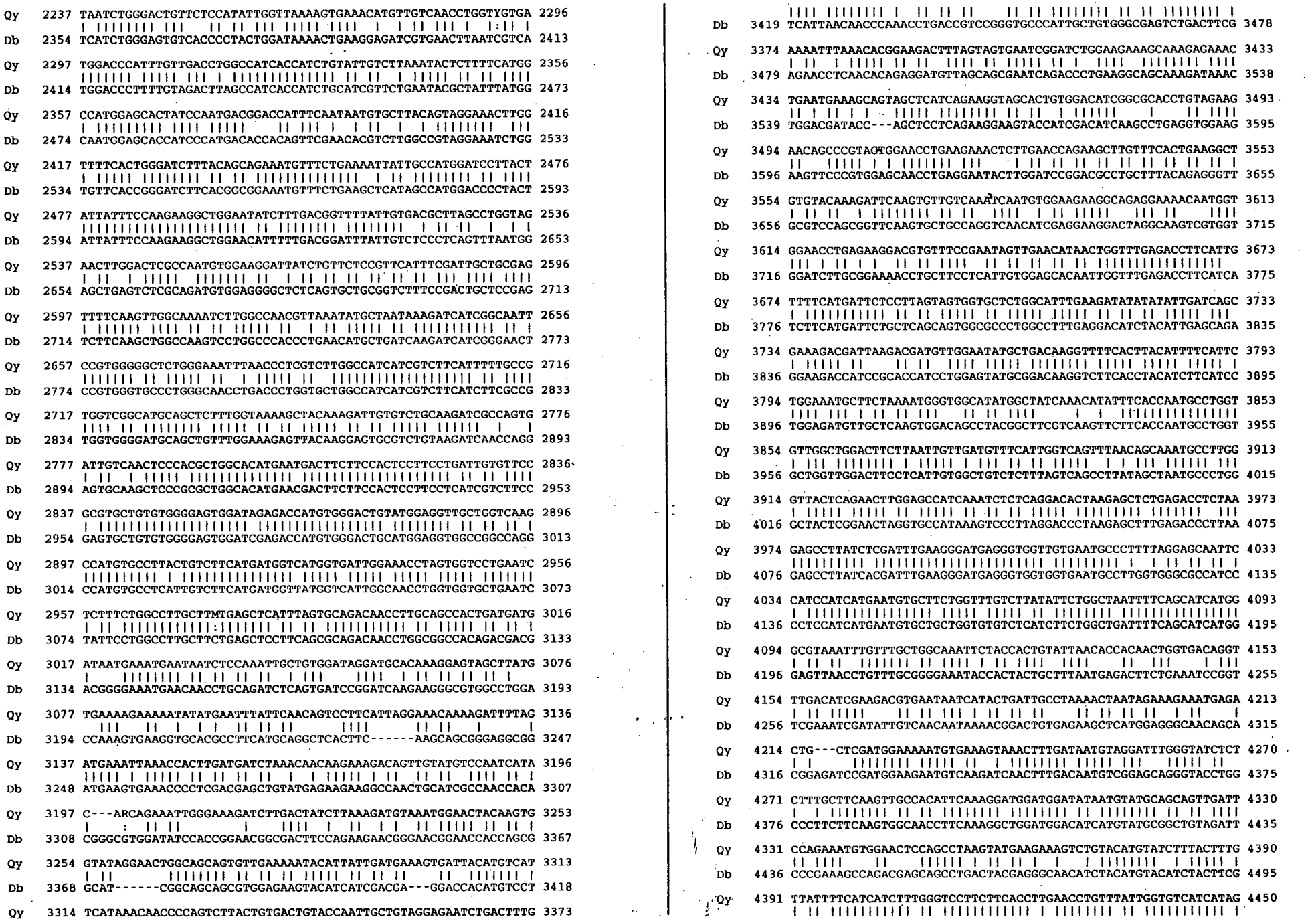
RESULT 11
US-09-425-043-7
; Sequence 7, Application US/09425043
; Patent No. 6335172
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/425,043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/024,020
; FILING DATE: 16-FEB-1998
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6556 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-425-043-7

Query Match 45.4%; Score 2738.8; DB 4; Length 6556;
Best Local Similarity 69.5%; Pred. No. 0;
Matches 4063; Conservative 3; Mismatches 1590; Indels 192; Gaps 18;

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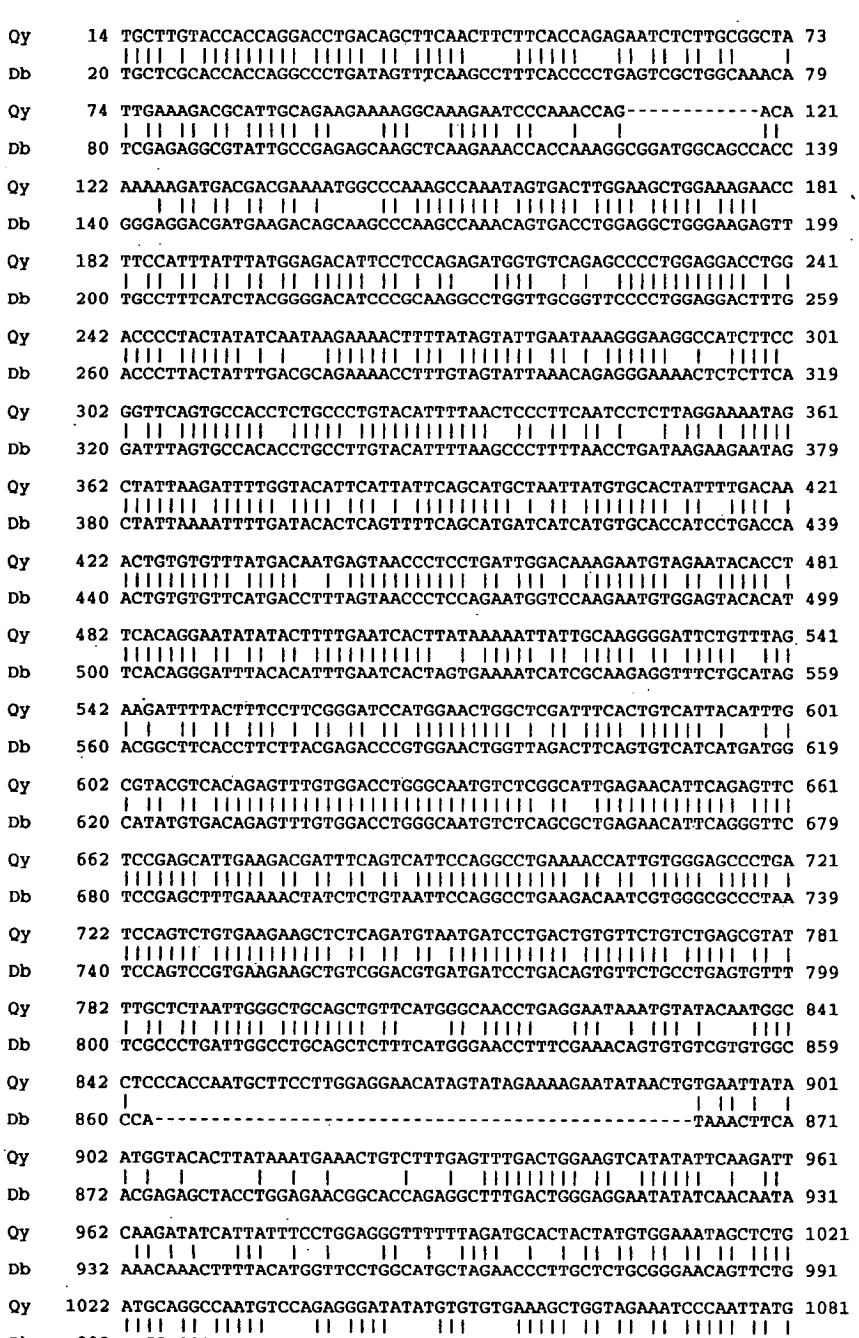
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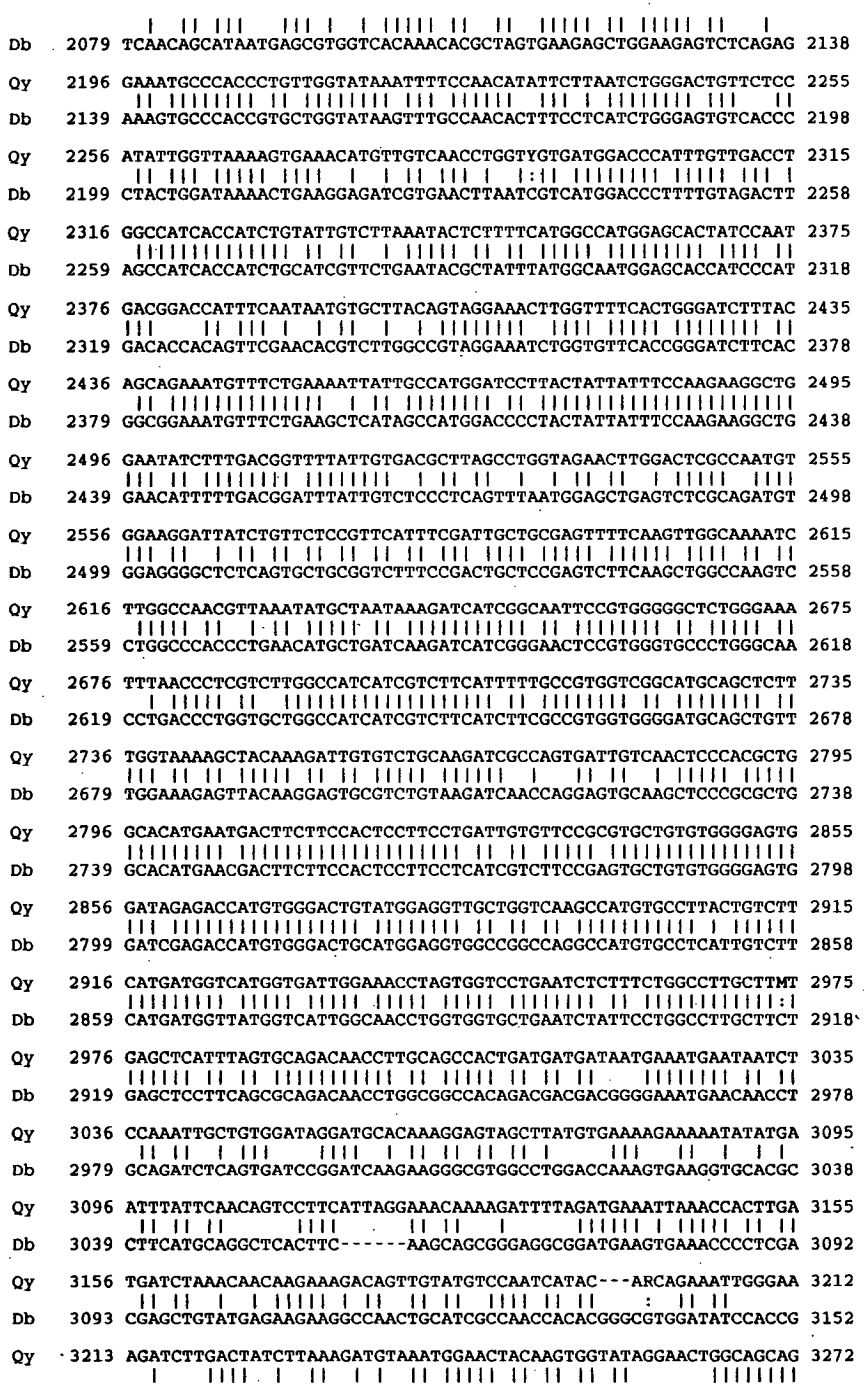
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RESULT 12
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; Sequence 8, Application US/09024020B
; Patent No. 6030810
;  GENERAL INFORMATION:
;    APPLICANT:  DELGADO, STEPHEN G.
;    APPLICANT:  DIETRICH, PAUL S.
;    APPLICANT:  FISH, LINDA M.
;    APPLICANT:  HERMAN, RONALD C.
;    APPLICANT:  SANGAMESWARAN, LAKSHMI
;    TITLE OF INVENTION:  NOVEL CLONED TETRODOTOXIN-SENSITIVE
;    TITLE OF INVENTION:  SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  JANET PAULINE CLARK
;      STREET:  3401 HILLVIEW AVENUE, MS A2-250
;      CITY:  PALO ALTO
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  94304-1397
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,020B
;      FILING DATE:  16-FEB-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/039,447
;      FILING DATE:  26-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CLARK, JANET P.
;      REGISTRATION NUMBER:  34,799
;      REFERENCE/DOCKET NUMBER:  R0020B-REG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 852-3097
;      TELEFAX:  (650) 855-5322
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6826 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-024-020B-8

  Query Match           44.3%;  Score 2674.2;  DB 3;  Length 6826;
  Best Local Similarity  68.8%;  Pred. No. 0;
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Db 1409 ATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAGTTCCAAGAGCGCGA 1468
Qy 1484 AGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGA 1543
Db 1469 AGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTCTGAAGGCGAGGAGA 1528
Qy 1544 AAGATGA---GGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTT 1600
Db 1529 AAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAATACGGTATGAGAAGGAAGGCCT 1588
Qy 1601 TTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACC 1660
Db 1589 TCCGGCTGCCAGACAACAGGATAGGG----------AGGAAGTTTTCCATCATGAATC 1636
Qy 1661 AGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCC 1720
Db 1637 AGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAACAGCAAAAGCAGCA 1696
Qy 1721 TTTTCAGCTTTAGAG---GGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATG 1777
Db 1697 TCTTCAGCTTCGGGGACCCGTCGGTTCGGGACCCCGGCTCTGAGAATGAGTTCGCAGACG 1756
Qy 1778 ATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGAC 1837
Db 1757 ATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTCGCTCTTCATCCCGATCC 1816
Qy 1838 GACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGG 1897
Db 1817 GCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTACAGCCAGTGCAGCCGCT 1876
Qy 1898 CAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCT 1957
Db 1877 CGTCGCGCATCTCCCCAGCCTGCGCGCAGCGTGAAGCCAACAGCACGGTGGACTGCAACG 1936
Qy 1958 TGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAA 2017
Db 1937 GCGTAGTGTCACTCATCGGGCCCGGCTCACACATCGGGCGGCTCCTGC---------- 1984
Qy 2018 TAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATGAGAAAGAGAA 2077
Db 1985 ----------TGAGGCAACGACTGAGGTGGAAATTAAGAAGA-AA 2018
Qy 2078 GGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAG 2137
Db 2019 GGCCCTGGACTCTTTTAGTTTCTATGGACCAACTCGCCTCCTACGGACGGAAGGACAGAA 2078
Qy 2138 CAATGAGTATAGCCAGCATTCTAACAAATACAGTA--GAAGAACTTGAAGAATCCAGGCA 2195


Db 2079 TCAACAGCATAATGAGCGTGGTCACAAACACGCTAGTGAAGAGCTGGAAGAGTCTCAGAG 2138
Qy 2196 GAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGACTGTTCTCC 2255
Db 2139 AAAGTGCCCACCGTGCTGGTATAAGTTTGCCAACACTTTCCTCATCTGGGAGTGTCACCC 2198
Qy 2256 ATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTYGTGATGGACCCATTTGTTGACCT 2315
Db 2199 CTACTGGATAAAACTGAAGGAGATCGTGAACTTAATCGTCATGGACCCTTTTGTAGACTT 2258
Qy 2316 GGCCATCACCATCTGTATTGTCTTAAATACTCTTTTCATGGCCATGGAGCACTATCCAAT 2375
Db 2259 AGCCATCACCATCTGCATCGTTCTGAATACGCTATTTATGGCAATGGAGCACCATCCCAT 2318
Qy 2376 GACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGGATCTTTAC 2435
Db 2319 GACACCACAGTTCGAACACGTCTTGGCCGTAGGAAATCTGGTGTTCACCGGGATCTTCAC 2378
Qy 2436 AGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAAGAAGGCTG 2495
Db 2379 GGCGGAAATGTTTCTGAAGCTCATAGCCATGGACCCCTACTATTATTTCCAAGAAGGCTG 2438
Qy 2496 GAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGT 2555
Db 2439 GAACATTTTTGACGGATTTATTGTCTCCCTCAGTTTAATGGAGCTGAGTCTCGCAGATGT 2498
Qy 2556 GGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATC 2615
Db 2499 GGAGGGGCTCTCAGTGCTGCGGTCTTTCCGACTGCTCCGAGTCTTCAAGCTGGCCAAGTC 2558
Qy 2616 TTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAA 2675
Db 2559 CTGGCCCACCCTGAACATGCTGATCAAGATCATCGGGAACTCCGTGGGTGCCCTGGGCAA 2618
Qy 2676 TTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTT 2735
Db 2619 CCTGACCCTGGTGCTGGCCATCATCGTCTTCATCTTCGCCGTGGTGGGGATGCAGCTGTT 2678
Qy 2736 TGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTCCCACGCTG 2795
Db 2679 TGGAAAGAGTTACAAGGAGTGCGTCTGTAAGATCAACCAGGAGTGCAAGCTCCCGCGCTG 2738
Qy 2796 GCACATGAATGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTG 2855
Db 2739 GCACATGAACGACTTCTTCCACTCCTTCCTCATCGTCTTCCGAGTGCTGTGTGGGGAGTG 2798
Qy 2856 GATAGAGACCATGTGGGACTGTATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTT 2915
Db 2799 GATCGAGACCATGTGGGACTGCATGGAGGTGGCCGGCCAGGCCATGTGCCTCATTGTCTT 2858
Qy 2916 CATGATGGTCATGGTGATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMT 2975
Db 2859 CATGATGGTTATGGTCATTGGCAACCTGGTGGTGCTGAATCTATTCCTGGCCTTGCTTCT 2918
Qy 2976 GAGCTCATTTAGTGCAGACAACCTTGCAGCCACTGATGATGATAATGAAATGAATAATCT 3035
Db 2919 GAGCTCCTTCAGCGCAGACAACCTGGCGGCCACAGACGACGACGGGGAAATGAACAACCT 2978
Qy 3036 CCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAAATATATGA 3095
Db 2979 GCAGATCTCAGTGATCCGGATCAAGAAGGGCGTGGCCTGGACCAAAGTGAAGGTGCACGC 3038
Qy 3096 ATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGA 3155
Db 3039 CTTCATGCAGGCTCACTTC------AAGCAGCGGGAGGCGGATGAAGTGAAACCCCTCGA 3092
Qy 3156 TGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATAC---ARCAGAAATTGGGAA 3212
Db 3093 CGAGCTGTATGAGAAGAAGGCCAACTGCATCGCCAACCACACGGGCGTGGATATCCACCG 3152
Qy 3213 AGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAG 3272
Db 3153 GAACGGCGACTTCCAGAAGAACGGGAACGGAACCACCAGCGGCAT------CGGCAGCAG 3206
Qy 3273 TGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAACCCCAGTCT 3332
Db 3207 CGTGGAGAAGTACATCATCGACGA---GGACCACATGTCCTTCATTAACAACCCAAACCT 3263
Qy 3333 TACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGA 3392
Db 3264 GACCGTCCGGGTGCCCATTGCTGTGGGCGAGTCTGACTTCGAGAACCTCAACACAGAGGA 3323
Qy 3393 CTTTAGTAGTGAATCGGATCTGGAAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTC 3452
Db 3324 TGTTAGCAGCGAATCAGACCCTGAAGGCAGCAAAGATAAACTGGACGATACC---AGCTC 3380
Qy 3453 ATCAGAAGGTAGCACTGTGGACATCGGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACC 3512
Db 3381 CTCAGAAGGAAGTACCATCGACATCAAGCCTGAGGTGGAAGAAGTTCCCGTGGAGCAACC 3440
Qy 3513 TGAAGAAACTCTTGAACCAGAAGCTTGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTG 3572
Db 3441 TGAGGAATACTTGGATCCGGACGCCTGCTTTACAGAGGGTTGCGTCCAGCGGTTCAAGTG 3500
Qy 3573 TTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAACAATGGTGGAACCTGAGAAGGACGTG 3632
Db 3501 CTGCCAGGTCAACATCGAGGAAGGACTAGGCAAGTCGTGGTGGATCTTGCGGAAAACCTG 3560
Qy 3633 TTTCCGAATAGTTGAACATAACTGGTTTGAGACCTTCATTGTTTTCATGATTCTCCTTAG 3692
Db 3561 CTTCCTCATTGTGGAGCACAATTGGTTTGAGACCTTCATCATCTTCATGATTCTGCTCAG 3620
Qy 3693 TAGTGGTGCTCTGGCATTTGAAGATATATATATTGATCAGCGAAAGACGATTAAGACGAT 3752
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Qy 3753 GTTGGAATATGCTGACAAGGTTTTCACTTACATTTTCATTCTGGAAATGCTTCTAAAATG 3812
Db 3681 CCTGGAGTATGCGGACAAGGTCTTCACCTACATCTTCATCCTGGAGATGTTGCTCAAGTG 3740
Qy 3813 GGTGGCATATGGCTATCAAACATATTTCACCAATGCCTGGTGTTGGCTGGACTTCTTAAT 3872
Db 3741 GACCACGTACGGCTTCGTCAAGTTCTTCACCAATGCCTGGTGCTGGTTGGACTTCCTCAT 3800
Qy 3873 TGTTGATGTTTCATTGGTCAGTTTAACAGCAAATGCCTTGGGTTACTCAGAACTTGGAGC 3932
Db 3801 TGTGGCTGTCTCTTTAGTCAGCCTTATAGCTAATGCCCTGGGCTACTCGGAACTAGGTGC 3860
Qy 3933 CATCAAATCTCTCAGGACACTAAGAGCTCTGAGACCTCTAAGAGCCTTATCTCGATTTGA 3992
Db 3861 CATAAAGTCCCTTAGGACCCTAAGAGCTTTGAGACCCTTAAGAGCCTTATCACGATTTGA 3920
Qy 3993 AGGGATGAGGGTGGTTGTGAATGCCCTTTTAGGAGCAATTCCATCCATCATGAATGTGCT 4052
Db 3921 AGGGATGAGGGTGGTGGTGAATGCCTTGGTGGGTGCCATCCCCTCCATCATGAATGTGCT 3980
Qy 4053 TCTGGTTTGTCTTATATTCTGGCTAATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGG 4112
Db 3981 GCTGGTGTGTCTCATCTTCTGGCTGATTTTCAGCATCATGGGAGTTAACCTGTTTGCGGG 4040
Qy 4113 CAAATTCTACCACTGTATTAACACCACAACTGGTGACAGGTTTGACATCGAAGACGTGAA 4172
Db 4041 GAAATACCACTACTGCTTTAATGAGACTTCTGAAATCCGGTTCGAAATCGATATTGTCAA 4100
Qy 4173 TAATCATACTGATTGCCTAAAACTAATAGAAAGAAATGAGACTG---CTCGATGGAAAAA 4229
Db 4101 CAATAAAACGGACTGTGAGAAGCTCATGGAGGGCAACAGCACGGAGATCCGATGGAAGAA 4160
Qy 4230 TGTGAAAGTAAACTTTGATAATGTAGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCCAC 4289
Db 4161 TGTCAAGATCAACTTTGACAATGTCGGAGCAGGGTACCTGGCCCTTCTTCAAGTGGCAAC 4220
Qy 4290 ATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTGGAACTCCA 4349
Db 4221 CTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCCCGAAAGCCAGACGAGCA 4280

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Qy   4350 GCCTAAGTATGAAGAAAGTCTGTACATGTATCTTTACTTTGTTATTTTCATCATCTTTGG 4409
Db   4281 GCCTGACTACGAGGGCAACATCTACATGTACATCTACTTCGTCATCTTCATCATCTTCGG 4340

Qy   4410 GTCCTTCTTCACCTTGAACCTGTTTATTGGTGTCATCATAGATAATTTCAACCAGCAGAA 4469
Db   4341 CTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCATCATCGACAACTTCAACCAGCAGAA 4400

Qy   4470 AAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTATAATGC 4529
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Qy   4530 AATGAAAAAATTAGGATCGAAAAAACCGCAAAAGCCTATACCTCGACCAGGAAACAAATT 4589
Db   4461 CATGAAAAAGCTGGGCTCCAAGAAGCCACAGAAGCCCATCCCCCGACCCTTGAACAAAAT 4520

Qy   4590 TCAAGGAATGGTCTTTGACTTCGTAACCAGACAAGTTTTTGACATAAGCATCATGATTCT 4649
Db   4521 CCAAGGGATTGTCTTTGATTTCGTCACTCAACAAGCCTTTGACATTGTGATCATGATGCT 4580

Qy   4650 CATCTGTCTTAACATGGTCACAATGATGGTGGAAACAGATGACCAGAGTGAATATGTGAC 4709
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Qy   4710 TACCATTTTGTCACGCATCAATCTGGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACT 4769
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Qy   4770 GAAACTCATCTCTCTACGCCATTATTATTTTACCATTGGATGGAATATTTTTGATTTTGT 4829
Db   4701 CAAAATGTTTGCCTTGAGACACTACTACTTCACCATTGGCTGGAACATCTTTGACTTTGT 4760

Qy   4830 GGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGT 4889
Db   4761 GGTGGTCATCCTCTCCATTGTGGGAATGTTCCTGGCTGATATCATTGAGAAGTACTTCGT 4820

Qy   4890 GTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGAT 4949
Db   4821 CTCCCCAACCCTATTCCGAGTTATCCGATTGGCCCGTATTGGGCGCATCTTGCGTCTGAT 4880

Qy   4950 CAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTT 5009
Db   4881 CAAGGGCGCCAAAGGGATCCGCACTCTGCTCTTTGCTCTGATGATGTCGCTGCCCGCCCT 4940

Qy   5010 GTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTC 5069
Db   4941 GTTCAACATCGGCCTCCTGCTCTTCCTCGTCATGTTCATCTTCTCCATTTTTGGCATGTC 5000

Qy   5070 CAACTTTGCCTATGTTAAGAGGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTT 5129
Db   5001 CAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATGTTCAACTTCGAGACATT 5060

Qy   5130 TGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCT 5189
Db   5061 TGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCTGGCTGGGATGGCCTGCT 5120

Qy   5190 AGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAG 5249
Db   5121 GCTGCCAATCCTGAACCG---CCCCCCTGACTGCAGCTTGGACAAAGAGCACCCAGGGAG 5177

Qy   5250 CTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACAT 5309
Db   5178 TGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTCTTCTTTGTGAGCTACAT 5237

Qy   5310 CATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAG 5369
Db   5238 CATCATCTCCTTCCTGATTGTGGTGAACATGTGCATCGCCATCATCCTGGAGAACTTCAG 5297

Qy   5370 TGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGA 5429
Db   5298 CGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGACTTCGAGACTTTCTATGA 5357

Qy   5430 GGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCA 5489
Db   5358 GATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAGTACTGTAAGCTGGCAGA 5417

Qy   5490 GTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCAT 5549
Db   5418 CTTTGCCGACGCCCTGGAGCACCCGCTCCGAGTACCCAAGCCCAACACCATCGAGCTCAT 5477

Qy   5550 TGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGC 5609
Db   5478 CGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGCTTGGACATCCTTTTCGC 5537

Qy   5610 TTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGA 5669
Db   5538 CTTCACCAAGGCAGTCCTGGGAGACAGTGGGGAGTTGGACATCCTGCGGCAGCAGATGGA 5597

Qy   5670 AGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTT 5729
Db   5598 GGAGCGGTTCGTGGCATCCAATCCTTCCAAAGTGTCTTACGAAGCCTATCACACCACTCT 5657

Qy   5730 AAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCT 5789
Db   5658 GCGGCGCAACGAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGTGCCTACAGGGGACACTT 5717

Qy   5790 TTTAAAGCG 5798
Db   5718 GGCTAGGCG 5726
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RESULT 13
US-09-425-043-8
; Sequence 8, Application US/09425043
; Patent No. 6335172
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: FISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/425,043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/024,020
; FILING DATE: 16-FEB-1998
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6826 base pairs

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-425-043-8

  Query Match             44.3%;  Score 2674.2;  DB 4;  Length 6826;
  Best Local Similarity   68.8%;  Pred. No. 0;
  Matches 4009;  Conservative    3;  Mismatches 1651;  Indels  166;  Gaps   18;

Qy      14 TGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAATCTCTTGGGGCTA 73
           |||| | |||||||||| ||||| || |||||    ||||||   || || || ||    |
Db      20 TGCTCGCACCACCAGGCCCTGATAGTTTCAAGCCTTTCACCCCTGAGTCGCTGGCAAACA 79

Qy      74 TTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAG------------ACA 121
           | || || || ||||| ||    |||   ||||| ||   |  |             ||
Db      80 TCGAGAGGCGTATTGCCGAGAGCAAGCTCAAGAAACCACCAAAGGCGGATGGCAGCCACC 139

Qy     122 AAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAACC 181
           | || || || || |      || ||||||| |||||| |||| ||||| ||||
Db     140 GGGAGGACGATGAAGACAGCAAGCCCAAGCCAAACAGTGACCTGGAGGCTGGGAAGAGTT 199

Qy     182 TTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTGG 241
           | || || || || ||||| || | ||   |||| | |  ||||||||||| | |
Db     200 TGCCTTTCATCTACGGGGACATCCCGCAAGGCCTGGTTGCGGTTCCCCTGGAGGACTTTG 259

Qy     242 ACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTCC 301
           |||| ||||||  | |   ||||||| ||| ||||||| || | ||||||  |  |||||
Db     260 ACCCTTACTATTTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGGAAAACTCTCTTCA 319

Qy     302 GGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATAG 361
           | || ||||||||  ||||| ||||||||||||  || || || |   | || | |||||
Db     320 GATTTAGTGCCACACCTGCCTTGTACATTTTAAGCCCTTTTAACCTGATAAGAAGAATAG 379

Qy     362 CTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACAA 421
           ||||||| |||||| |||| ||| | |||||||||| | || |||||||| ||  |||| |
Db     380 CTATTAAAATTTTGATACACTCAGTTTTCAGCATGATCATCATGTGCACCATCCTGACCA 439

Qy     422 ACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACCT 481
           |||||||||| |||||  | |||||||||||| || ||| | |||||||| || ||||| |
Db     440 ACTGTGTGTTCATGACCTTTAGTAACCCTCCAGAATGGTCCAAGAATGTGGAGTACACAT 499

Qy     482 TCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTAG 541
           ||||||| || || || ||||||||||  | ||||| || ||||| || |||||  |||
Db     500 TCACAGGGATTTACACATTTGAATCACTAGTGAAAATCATCGCAAGAGGTTTCTGCATAG 559

Qy     542 AAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTTG 601
           | |  || || ||| | || || || |||||||| | || |||| |||||| |   | |
Db     560 ACGGCTTCACCTTCTTACGAGACCCGTGGAACTGGTTAGACTTCAGTGTCATCATGATGG 619

Qy     602 CGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTTC 661
           | || || ||||||||||||||||||||||||||||| ||  ||||||||||||| ||||
Db     620 CATATGTGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGCTGAGAACATTCAGGGTTC 679

Qy     662 TCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGA 721
           ||||||| ||||| || || || || |||||||||||||| || || ||||| ||||| |
Db     680 TCCGAGCTTTGAAAACTATCTCTGTAATTCCAGGCCTGAAGACAATCGTGGGCGCCCTAA 739

Qy     722 TCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTAT 781
           ||||||| |||||||||| || || || |||||||||||| |||||||| ||||| || |
Db     740 TCCAGTCCGTGAAGAAGCTGTCGGACGTGATGATCCTGACAGTGTTCTGCCTGAGTGTTT 799

Qy     782 TTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGGC 841
           | || || ||||| |||||||| ||    || |||||   |||  | ||| |    ||||
Db     800 TCGCCCTGATTGGCCTGCAGCTCTTTCATGGGAACCTTTCGAAACAGTGTGTCGTGTGGC 859

Qy     842 CTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTATA 901
           |                                                | || |  |
Db     860 CCA-----------------------------------------------TAAACTTCA 871

Qy     902 ATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGATT 961
           | |  |      |  | |      |   |  |||||||| ||  ||||||  |  ||
Db     872 ACGAGAGCTACCTGGAGAACGGCACCAGAGGCTTTGACTGGGAGGAATATATCAACAATA 931

Qy     962 CAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCTG 1021
           || | |   |||  |  |    ||  |  ||||  |  | || || || || || ||||
Db     932 AAACAAACTTTTACATGGTTCCTGGCATGCTAGAACCCTTGCTCTGCGGGAACAGTTCTG 991

Qy    1022 ATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTATG 1081
           |||| || |||||    || ||||   |||    ||||| || || || ||||| || |
Db     992 ATGCTGGGCAATG---CGAAGGATTCCAGTGCAGTAAAGCAGGAAGGAACCCCAACTACG 1048

Qy    1082 GCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACTC 1141
           | ||||| |||||||| |||||||| ||||| || ||| | || || || || ||||| |
Db    1049 GTTACACCAGCTTTGACACCTTCAGCTGGGCCTTCTTGGCATTATTCCGCCTTATGACCC 1108

Qy    1142 AGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATGA 1201
           ||||||  ||||| ||  | || || ||||| ||||| || ||||||||||||||||||
Db    1109 AGGACTATTGGGAGAACTTATACCAGCTGACCTTACGAGCCGCTGGGAAAACGTACATGA 1168

Qy    1202 TATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCTG 1261
           | || ||||| |||||||| ||| |||| || ||||| |   | || |||||| ||||||
Db    1169 TCTTCTTTGTCTTGGTCATCTTCGTGGGTTCTTTCTATCCGGTGAACTTGATCTTGGCTG 1228

Qy    1262 TGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAAG 1321
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Db    1229 TGGTGGCCATGGCTTATGAGGAACAGAACCAGGCAACACTGGAGGAGGCAGAGCAAAAAG 1288

Qy    1322 AGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGG 1381
           |||||||  ||  ||| | || || || || ||||| |||||||  || |||   |
Db    1289 AGGCCGAGTTCAAGGCAATGCTGGAGCAACTCAAGAAGCAGCAGGAGGAGGCACAGGCTG 1348

Qy    1382 CAGCAACGGCAACTGCCTC----------------AGAACATTCCAGAGAGCCCAGTGC 1424
           | |||| ||| ||  |  |                |  ||||  |||       |
Db    1349 CTGCAATGGCCACCTCAGCGGGCACTGTCTCGGAAGACGCCATTGAAGAAGAAGGGGAAG 1408

Qy    1425 AGCAGGCAGGCTCTCAGA-CAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTA 1483
           |   || |||||||| ||  ||||| ||||||   |||||  | ||||||||||| || |
Db    1409 ATGGGGTAGGCTCTCCGAGGAGCTCTTCTGAACTGTCTAAACTCAGTTCCAAGAGCGCGA 1468

Qy    1484 AGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGA 1543
           ||||  |  | || ||  ||||||| || |||| ||||  |||  || || ||||
Db    1469 AGGAGCGGCGGAACCGACGGAAGAAGAGGAAGCAGAAGGAGCTCTCTGAAGGCGAGGAGA 1528

Qy    1544 AAGATGA---GGATGAATTCCAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTT 1600
           |||  ||   |||  |  |    || || || || ||  || | || || ||||| |  |
Db    1529 AAGGGGACCCGGAGAAGGTGTTTAAGTCAGAGTCGGAATACGGTATGAGAAGGAAGGCCT 1588

Qy    1601 TTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACC 1660
           | || |  |     |  |||  |                | || ||  |||  |    | |
Db    1589 TCCGGCTGCCAGACAACAGGATAGGG------------AGGAAGTTTTCCATCATGAATC 1636

Qy    1661 AGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCC 1720
           ||||  || | ||||| |  ||||| |  ||      |  | |  || |||| ||  |||
Db    1637 AGTCGCTGCTCAGCATTCCAGGCTCGCCCTTCCTCTCCCGACATAACAGCAAAAGCAGCA 1696

Qy    1721 TTTTCAGCTTTAGAG---GGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATG 1777
           | ||||||||  | |   |  |   |||    || |||||||| || |||||||| |
Db    1697 TCTTCAGCTTCGGGGACCCGTCGGTTCGGGACCCCGGCTCTGAGAATGAGTTCGCAGACG 1756

Qy    1778 ATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGAC 1837
           |||| |||||||||  | ||||| | |||| ||||  | || ||  | ||  | ||    |
Db    1757 ATGAACACAGCACCGTGGAGGAGAGCGAGGGCCGGCGTGACTCGCTCTTCATCCCGATCC 1816

Qy    1838 GACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGG 1897
           |   | | ||| | |||| |||| ||   |  | | | |           | | |
Db    1817 GCGCCCGCGAGCGCCGCAGCAGCTACAGTGGCTACAGCGGCTACAGCCAGTGCAGCCGCT 1876

Qy    1898 CAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCT 1957
           |   |       |   |       |||  |   |  | |||  |  |       |
Db    1877 CGTCGCGCATCTCCCCAGCCTGCGCGCAGCGTGAAGCCAACAGCACGGTGGACTGCAACG 1936

Qy    1958 TGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAA 2017
           || |   ||     | ||    || |   | || | ||| ||||
Db    1937 GCGTAGTGTCACTCATCGGGCCCGGCTCACACATCGGGCGGCTCCTGC------------ 1984
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Db   4101 CAATAAAACGGACTGTGAGAAGCTCATGGAGGGCAACAGCACGGAGATCCGATGGAAGAA 4160

Qy   4230 TGTGAAAGTAAACTTTGATAATGTAGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCCAC 4289

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Qy   4290 ATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTGGAACTCCA 4349

Db   4221 CTTCAAAGGCTGGATGGACATCATGTATGCGGCTGTAGATTCCCGAAAGCCAGACGAGCA 4280

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Db   4281 GCCTGACTACGAGGGCAACATCTACATGTACATCTACTTCGTCATCTTCATCATCTTCGG 4340

Qy   4410 GTCCTTCTTCACCTTGAACCTGTTTATTGGTGTCATCATAGATAATTTCAACCAGCAGAA 4469

Db   4341 CTCCTTCTTCACCCTCAACCTGTTCATCGGTGTCATCATCGACAACTTCAACCAGCAGAA 4400

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Db   4401 GAAAAAGTTTGGAGGTCAGGACATCTTCATGACAGAGGAACAGAAGAAGTACTATAATGC 4460

Qy   4530 AATGAAAAAATTAGGATCGAAAAAACCGCAAAAGCCTATACCTCGACCAGGAAACAAATT 4589

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Qy   4830 GGTTGTCATTCTCTCCATTGTAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGT 4889

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Qy   5010 GTTTAACATCGGCCTCCTACTCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTC 5069

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Db   5001 CAACTTCGCATACGTGAAGCACGAGGCCGGCATTGACGACATGTTCAACTTCGAGACATT 5060

Qy   5130 TGGCAACAGCATGATCTGCCTATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCT 5189

Db   5061 TGGCAACAGCATGATCTGTTTGTTCCAGATCACAACGTCTGCTGGCTGGGATGGCCTGCT 5120

Qy   5190 AGCACCCATTCTCAACAGTAAGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAG 5249

Db   5121 GCTGCCAATCCTGAACCG---CCCCCCTGACTGCAGCTTGGACAAAGAGCACCCAGGGAG 5177

Qy   5250 CTCAGTTAAGGGAGACTGTGGGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACAT 5309

Db   5178 TGGCTTCAAAGGGGACTGTGGGAACCCCTCGGTGGGCATCTTCTTCTTTGTGAGCTACAT 5237

Qy   5310 CATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAG 5369

Db   5238 CATCATCTCCTTCCTGATTGTGGTGAACATGTGCATCGCCATCATCCTGGAGAACTTCAG 5297

Qy   5370 TGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGA 5429

Db   5298 CGTGGCCACCGAGGAGAGCGCCGACCCTCTGAGTGAGGATGACTTCGAGACTTTCTATGA 5357

Qy   5430 GGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCA 5489

Db   5358 GATCTGGGAGAAGTTTGACCCAGACGCCACCCAGTTCATCGAGTACTGTAAGCTGGCAGA 5417

Qy   5490 GTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCAT 5549

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Qy   5550 TGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGC 5609

Db   5478 CGCCATGGACCTGCCCATGGTGAGCGGAGATCGCATCCACTGCTTGGACATCCTTTTCGC 5537

Qy   5610 TTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGA 5669

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Qy   5670 AGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTT 5729

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Qy   5730 AAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCT 5789

Db   5658 GCGGCGCAACGAGGAGGAGGTGTCTGCAGTGGTCCTGCAGCGTGCCTACAGGGGACACTT 5717

Qy   5790 TTTAAAGCG 5798

Db   5718 GGCTAGGCG 5726
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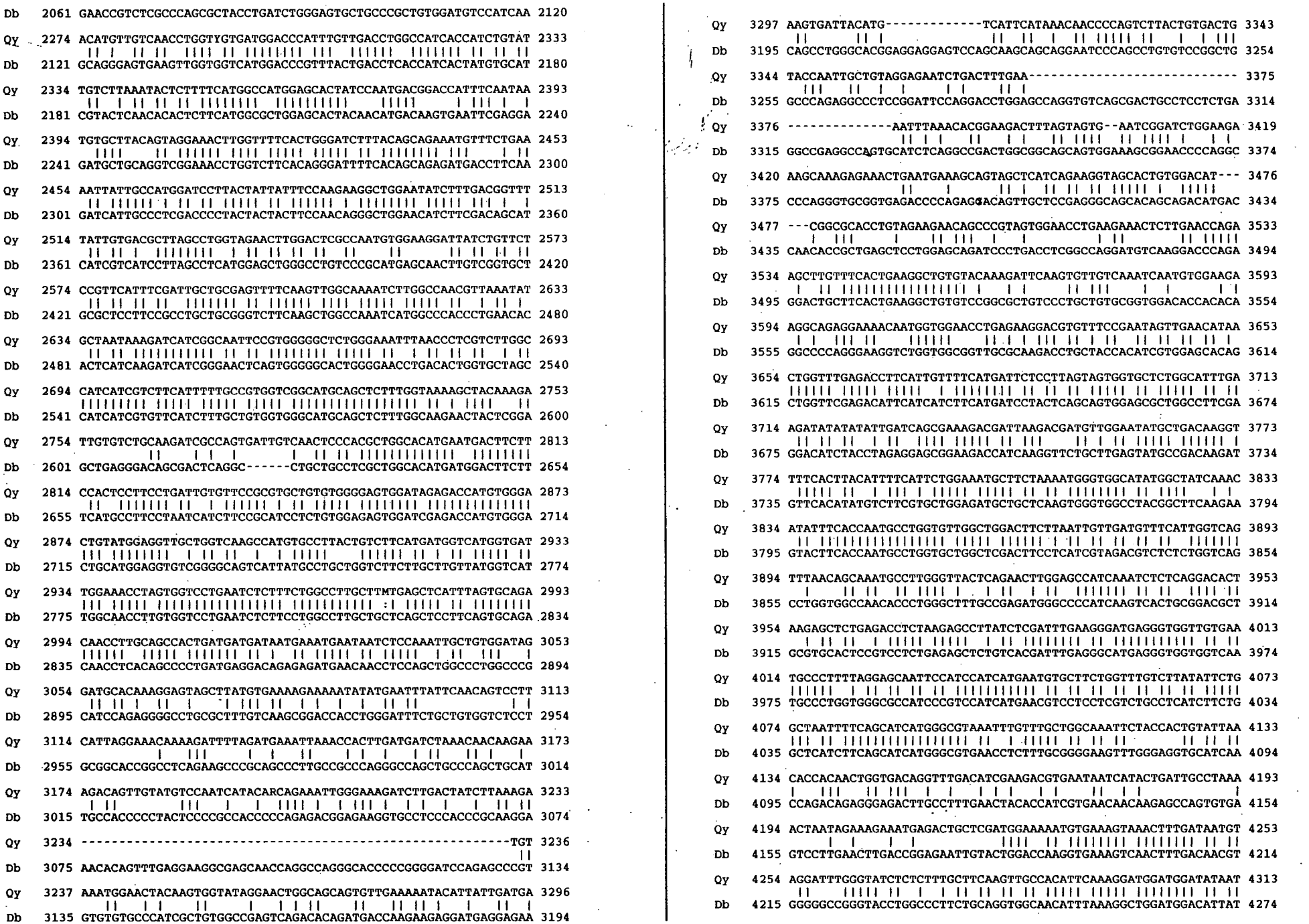
RESULT 14
US-09-634-920-3
; Sequence 3, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/634,920
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/190,057
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6048)
US-09-634-920-3

Query Match 31.6%; Score 1907.2; DB 4; Length 6048;
Best Local Similarity 60.8%; Pred. No. 0;
Matches 3617; Conservative 1; Mismatches 2019; Indels 309; Gaps 19;

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Qy       9 AACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAATCTCTTGC 68

Db       6 AAACTTCCTATTACCTCGGGGCACCAGCAGCTTCCGCAGGTTCACACGGGAGTCCCTGGC 65
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Qy   4314 GTATGCAGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTA 4373
          ||||||||| || || |||||       |||   |||||| |||  ||| | |  || ||
Db   4275 GTATGCAGCTGTGGACTCCAGGGGGTATGAAGAGCAGCCTCAGTGGGAATACAACCTCTA 4334

Qy   4374 CATGTATCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTT 4433
          ||||||  | || ||||| |||||||||||||||||||| |||||||| ||||||| ||
Db   4335 CATGTACATCTATTTTGTCATTTTCATCATCTTTGGGTCTTTCTTCACCCTGAACCTCTT 4394

Qy   4434 TATTGGTGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACAT 4493
          |||||||||||||||| || || |||||||| ||||| || ||||| || || || |||||
Db   4395 TATTGGTGTCATCATTGACAACTTCAACCAACAGAAGAAAAAGTTAGGGGGCCAGGACAT 4454

Qy   4494 CTTTATGACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAA 4553
          ||| |||||||| || |||||||| ||||| ||||| ||||| ||  | || || || ||
Db   4455 CTTCATGACAGAGGAGCAGAAGAAGTACTACAATGCCATGAAGAAGCTGGGCTCCAAGAA 4514

Qy   4554 ACCGCAAAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGT 4613
          || || ||||| || || || ||    ||||| |  || ||  |  | || ||| | ||
Db   4515 GCCCCAGAAGCCCATCCCACGGCCCCTGAACAAGTACCAGGGCTTCATATTCGACATTGT 4574

Qy   4614 AACCAGACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAAT 4673
          ||||  || |  |||||| | | ||||||| |||| |||||  | || ||||| || ||
Db   4575 GACCAAGCAGGCCTTTGACGTCACCATCATGTTTCTGATCTGCTTGAATATGGTGACCAT 4634

Qy   4674 GATGGTGGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCT 4733
          ||||||||| |||||||||| |||    |   | | ||| ||| |    ||||| ||
Db   4635 GATGGTGGAGACAGATGACCAAAGTCCTGAGAAAATCAACATCTTGGCCAAGATCAACCT 4694

Qy   4734 GGTGTTCATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTA 4793
          | | ||  | |   | || || || |||||| |  | || ||    | || ||||| ||
Db   4695 GCTCTTTGTGGCCATCTTCACAGGCGAGTGTATTGTCAAGCTGGCTGCCCTGCGCCACTA 4754

Qy   4794 TTATTTTACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGG 4853
          || || ||||   | |||||||| || || || |||||||||| |||||||| || ||
Db   4755 CTACTTCACCAACAGCTGGAATATCTTCGACTTCGTGGTTGTCATCCTCTCCATCGTGGG 4814

Qy   4854 TATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGAT 4913
          |   | ||  | ||  | ||  | ||||| ||| | ||||| || || |||||||| ||
Db   4815 CACTGTGCTCTCGGACATCATCCAGAAGTACTTCTTCTCCCCGACGCTCTTCCGAGTCAT 4874

Qy   4914 CCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCAC 4973
          ||| || ||  | || |||| |||||  | ||||||  ||| || ||||||||||||||||
Db   4875 CCGCCTGGCCCGAATAGGCCGCATCCTCAGACTGATCCGAGGGGCCAAGGGGATCCGCAC 4934

Qy   4974 GCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTT 5033
          ||||||||||||  | ||||||||||| |||||  | || |||||||| || || |||||
Db   4935 GCTGCTCTTTGCCCTCATGATGTCCCTGCCTGCCCTCTTCAACATCGGGCTGCTGCTCTT 4994

Qy   5034 CCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGA 5093
          ||| |||||||||||||| |||||||||| ||| ||||||| || ||||| ||| ||||
Db   4995 CCTCGTCATGTTCATCTACTCCATCTTTGGCATGGCCAACTTCGCTTATGTCAAGTGGGA 5054

Qy   5094 AGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATT 5153
          | ||| ||||| |||||||||||||  ||||||| | |||||||||| | ||||| ||
Db   5055 GGCTGGCATCGACGACATGTTCAACTTCCAGACCTTCGCCAACAGCATGCTGTGCCTCTT 5114

Qy   5154 CCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCC 5213
          ||| || || || || || |||||||||||  | ||    ||||| |||||||  |  |||
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Qy   5214 ACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAA 5273
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Db   5175 GCCCTACTGCGACCCCACTCTGCCCAACAGCAATGGCTC---TCGGGGGGACTGCGGGAG 5231

Qy   5274 CCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGT 5333
          |||| | || || ||  |||| ||   ||  |||||||||| ||||||||  | |||||
Db   5232 CCCAGCCGTGGGCATCCTCTTCTTCACCACCTACATCATCATCTCCTTCCTCATCGTGGT 5291

Qy   5334 GAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGA 5393
          |||||||||| ||  |||||||||||||||||| || || || || || ||  | ||
Db   5292 CAACATGTACATTGCCATCATCCTGGAGAACTTCAGCGTGGCCACGGAGGAGAGCACCGA 5351

Qy   5394 GCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGA 5453
          ||| |||||||||| ||||| || |||||||||||  | |||||||| ||||| || ||
Db   5352 GCCCCTGAGTGAGGACGACTTCGATATGTTCTATGAGATCTGGGAGAAATTTGACCCAGA 5411

Qy   5454 TGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCC 5513
          || |||||||| || || | |       | ||| | ||||| |  || ||      |||
Db   5412 GGCCACTCAGTTTATTGAGTATTCGGTCCTGTCTGACTTTGCCGACGCCCTGTCTGAGCC 5471

Qy   5514 TCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAG 5573
          |||  | |  |  | || ||| |  |    |||||   ||||||  ||||||||||||
Db   5472 ACTCCGTATCGCCAAGCCCAACCAGATAAGCCTCATCAACATGGACCTGCCCATGGTGAG 5531

Qy   5574 TGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGA 5633
          |||  |||||  ||||| ||  | || ||  | |||||  || || ||  |||| || || ||
Db   5532 TGGGGACCGCATCCATTGCATGGACATTCTCTTTGCCTTCACCAAAAGGGTCCTGGGGGA 5591

Qy   5634 GAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCC 5693
          |  ||| |||||||| || ||    || |||||||| |||   ||||||||  |||| ||
Db   5592 GTCTGGGGAGATGGACGCCCTGAAGATCCAGATGGAGGAGAAGTTCATGGCAGCCAACCC 5651

Qy   5694 TTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATC 5753
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Db   5652 ATCCAAGATCTCCTACGAGCCCATCACCACCACACTCCGGCGCAAGCACGAAGAGGTGTC 5711

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RESULT 15
US-08-836-325-1
; Sequence 1, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Us
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.

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;       REGISTRATION NUMBER:  36,203
;       REFERENCE/DOCKET NUMBER:  0917.0240002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-371-2600
;       TELEFAX:  202-371-2540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3033 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..3033
US-08-836-325-1

  Query Match             29.7%;  Score 1789.8;  DB 3;  Length 3033;
  Best Local Similarity   75.2%;  Pred. No. 0;
  Matches 2287;  Conservative    1;  Mismatches  738;  Indels   15;  Gaps    4;

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Qy   3116 TTAGGAAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAG 3175
            |  || | ||||   |   | || |  |||| |  |  |||| ||||||||||||||
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Db    242 AAAACTATATTTCAAACCGTACCCTTGCGGAGATGAGCAAGGATCACAATTTCCTCAAAG 301

Qy   3236 TAAATGGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATG 3295
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Qy   3356 TAGGAGAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGG 3415
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Qy   3416 AAGAAAGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACA 3475
          |  | ||||||||||||| |||   |  ||   ||| || ||  | |||||||| ||||
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Qy   3476 TCGGCGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAG 3535
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Qy   3536 CTTGTTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAG 3595
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OM nucleic - nucleic search, using sw model

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Searched: 709820 seqs, 544064369 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	5915.8	98.1	5922	10	US-09-930-871-13	Sequence 13, Appl
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ALIGNMENTS

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; Sequence 11, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polyn
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6030
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-11

Query Match 100.0%; Score 6028.8; DB 10; Length 6030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Db  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Qy  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Qy  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Db  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Qy  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Db  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Qy  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Qy  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Db  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Qy  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Db  4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Qy  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Db  4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Qy  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Db  4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Qy  4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Db  4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Qy  4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Db  4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Qy  4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Db  4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Qy  4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Db  4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Qy  4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Db  4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
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Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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RESULT 2
US-09-930-871-1
; Sequence 1, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucl
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5997
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-1

Query Match 98.7%; Score 5952.8; DB 10; Length 5997;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 5997; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487
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Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4288 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4347

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4348 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4407

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4468 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4527

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4528 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4587

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4888 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4947

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4948 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5007

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5008 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5067

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5188 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5247

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5248 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5307

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
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Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db   5788 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5847

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5907

Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5908 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 5967

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db   5968 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 5997


RESULT 3
US-09-930-871-13
; Sequence 13, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynu
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 5922
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-13

  Query Match            98.1%;  Score 5915.8;  DB 10;  Length 5922;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
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Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917


RESULT 4
US-09-930-871-3
; Sequence 3, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polynuc
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 5889
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-3

  Query Match             96.8%;  Score 5839.8;  DB 10;  Length 5889;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 5884;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010
Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127
Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187
Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247
Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307
Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367
Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427
Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607
Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Db   2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Db   3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Db   3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db   3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db   4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

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Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
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Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
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Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Db   4408 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4467

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
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Db   4588 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4647

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4648 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4707

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Db   4708 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4767

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Db   4768 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4827

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
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Db   4828 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4887

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Db   5068 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5127

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Db   5128 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5187

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Db   5308 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5367

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
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Db   5368 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5427

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5428 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5487

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db   5488 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5547

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Db   5548 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5607

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Db   5608 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5667

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5668 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5727

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Db   5728 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5787

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db   5848 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5884


RESULT 5
US-09-930-871-15
; Sequence 15, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 4362
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-15

  Query Match             71.9%;  Score 4336.8;  DB 10;  Length 4362;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAAT 4338
          |||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAAT 4338
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RESULT 6
US-09-930-871-5
; Sequence 5, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polyn
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4329
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-5

Query Match 70.7%; Score 4260.8; DB 10; Length 4329;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 4305; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG---------------------------- 2010

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db   2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db   2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db   2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db   2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db    2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy    2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy    2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy    2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy    2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy    2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy    2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy    3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy    3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy    3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy    3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy    3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy    3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy    3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy    3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy    3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy    3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy    3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy    3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy    3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy    3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy    3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy    3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy    3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy    4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy    4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107

Qy    4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4108 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4167

Qy    4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4168 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4227

Qy    4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4228 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4287

Qy    4321 GCAGTTGATTCCAGAAAT 4338
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Db    4288 GCAGTTGATTCCAGAAAT 4305
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RESULT 7
US-09-930-871-17
; Sequence 17, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780Alel Human Ion Channel Proteins and Polyn
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,989
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4179
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-871-17

Query Match 68.8%; Score 4150.8; DB 10; Length 4179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db    2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db    2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy    2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGG 4152
          ||||||||||||
Db   4141 ACTGGTGACAGG 4152
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RESULT 8
US-09-930-871-7
; Sequence 7, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polyn
; TITLE OF INVENTION: Same

```
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 4146
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-7

  Query Match             67.6%;  Score 4074.8;  DB 10;  Length 4146;
  Best Local Similarity   99.2%;  Pred. No. 0;
  Matches 4119;  Conservative    0;  Mismatches    0;  Indels   33;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Db  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
         ||||||||||||||||||||||||||||||
Db  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAG------------------------------ 2010

Qy  2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2011 ---GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2067

Qy  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db  2068 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2127

Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2128 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2187

Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Db  2188 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2247

Qy  2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
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Db  2248 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2307

Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2308 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2367

Qy  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Db  2368 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2427

Qy  2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2428 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2487

Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Db  2488 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2547

Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db  2548 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2607

Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
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Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667

Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Db  2668 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2727

Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Db  2728 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2787

Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Db  2788 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2847

Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db  2848 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2907

Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Db  2908 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 2967

Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Db  2968 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3027

Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db  3028 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3087

Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db  3088 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3147

Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db  3148 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3207

Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Db  3208 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3267

Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Db  3268 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3327

Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Db  3328 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3387

Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db  3388 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3447

Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Db  3448 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3507

Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3508 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3567

Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db  3568 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3627

Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db  3628 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3687

Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db  3688 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3747

Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3748 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3807

Qy  3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3808 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3867

Qy  3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3868 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3927

Qy  3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3928 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 3987

Qy  4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3988 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4047

Qy  4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4048 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4107
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Qy   4141 ACTGGTGACAGG 4152
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Db   4108 ACTGGTGACAGG 4119


RESULT 9
US-09-930-871-19
; Sequence 19, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 4197
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-19

  Query Match             67.3%;  Score 4057.8;  DB 10;  Length 4197;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 4133;  Conservative    0;  Mismatches    0;  Indels   64;  Gaps    1;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
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Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGA---------------------- 4000
          |||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGATAATCTTGCTCCAACT 4020

Qy   4001 ------------------------------------------GGGTGGTTGTGAATGC 4016
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Db   4021 TGGATGGGGTGGAGCGCTGGTTCCTCCCCTGAGCCCTTTATTATGGGTGGTTGTGAATGC 4080

Qy   4017 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4076
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 CCTTTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCT 4140

Qy   4077 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAA 4133
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 AATTTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAA 4197


RESULT 10
US-09-930-871-9
; Sequence 9, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Daniel
;  APPLICANT:  Mathur, Brian
;  TITLE OF INVENTION: No. US20020076780A1el Human Ion Channel Proteins and Polynucleoti
;  TITLE OF INVENTION:  Same
;  FILE REFERENCE: LEX-0216-USA
;  CURRENT APPLICATION NUMBER: US/09/930,871
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/225,989
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 4164
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-930-871-9

  Query Match             66.0%;  Score 3981.8;  DB 10;  Length 4164;
  Best Local Similarity   97.7%;  Pred. No. 0;
  Matches 4100;  Conservative    0;  Mismatches    0;  Indels   97;  Gaps    2;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db  1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Db  2608 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2667
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RESULT 11
US-09-917-800A-1604
; Sequence 1604, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1604
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013119
US-09-917-800A-1604

Query Match 59.1%; Score 3563.8; DB 10; Length 6822;
Best Local Similarity 76.1%; Pred. No. 0;
Matches 4596; Conservative 2; Mismatches 1224; Indels 219; Gaps 8;

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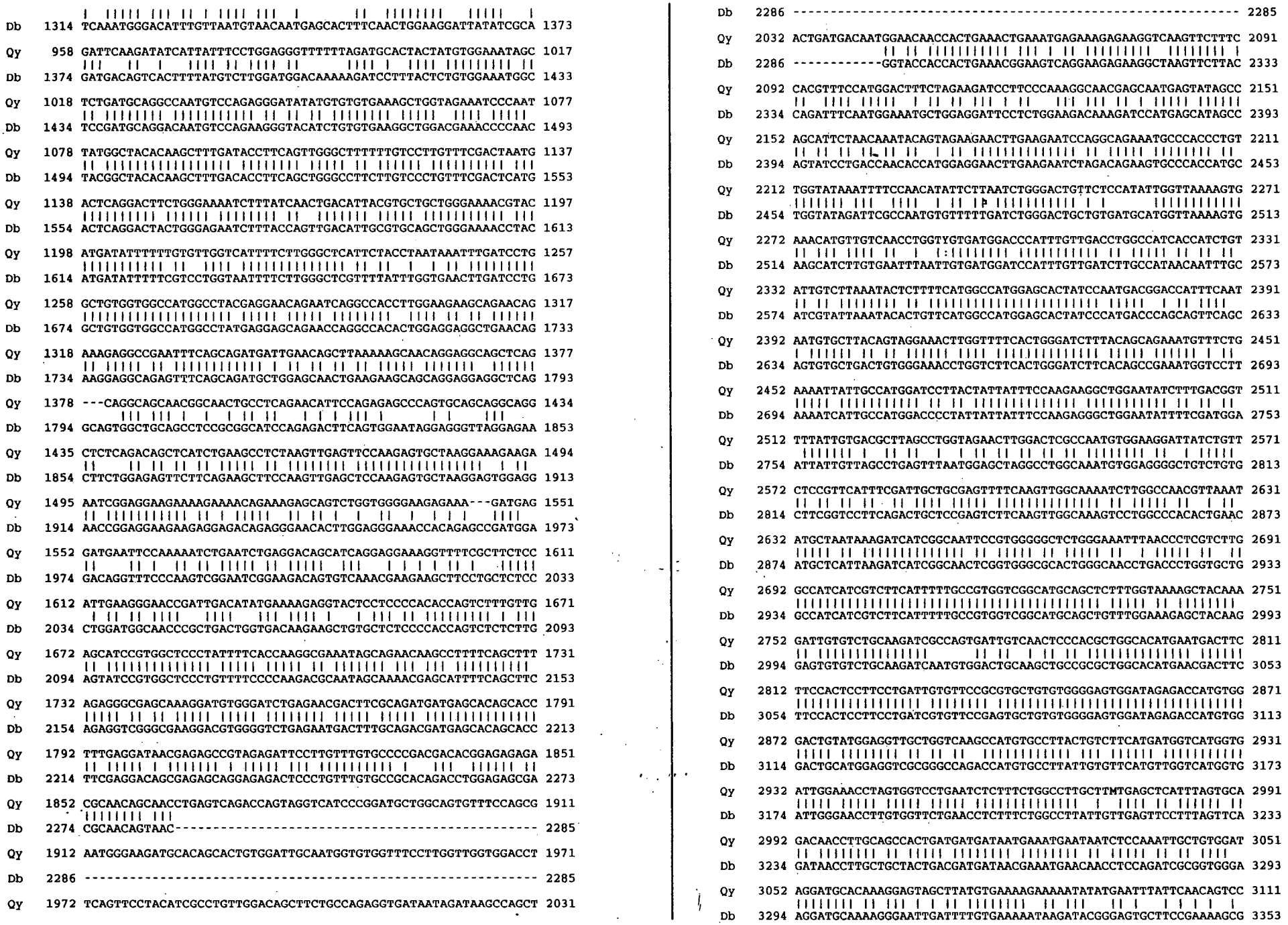
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Db   1074 CTCCGAGCATTGAAAACAATATCAGTCATTCCAGGTTTAAAGACCATCGTGGGGGCCCTG 1133

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Db   1134 ATCCAGTCCGTGAAGAAGCTGTCCGACGTCATGATCCTCACCGTGTTCTGTCTCAGTGTC 1193

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db   1254 CCCCCGAGCGATTCGGCTTTTGAAACCAACACTACTTCCTACTTCAATGGCACAATGGAT 1313

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RESULT 12
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; Sequence 1, Application US/09896994
; Publication No. US20030074024A1
;  GENERAL INFORMATION:
;       APPLICANT: Ken Stokes
;                  Jos e Morissette
;       TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                           SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1ris
;            STREET: One Liberty Place - 46th Floor
;            CITY: Philadelphia
;            STATE: PA
;            COUNTRY: U.S.A.
;            ZIP: 19103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WordPerfect 6.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/896,994
;            FILING DATE: 02-Jul-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/514,907
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Paul K. Legaard
;            REGISTRATION NUMBER: 38,534
;            REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (215) 568-3100
;            TELEFAX: (215) 568-3439
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 6048 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
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US-09-896-994-1

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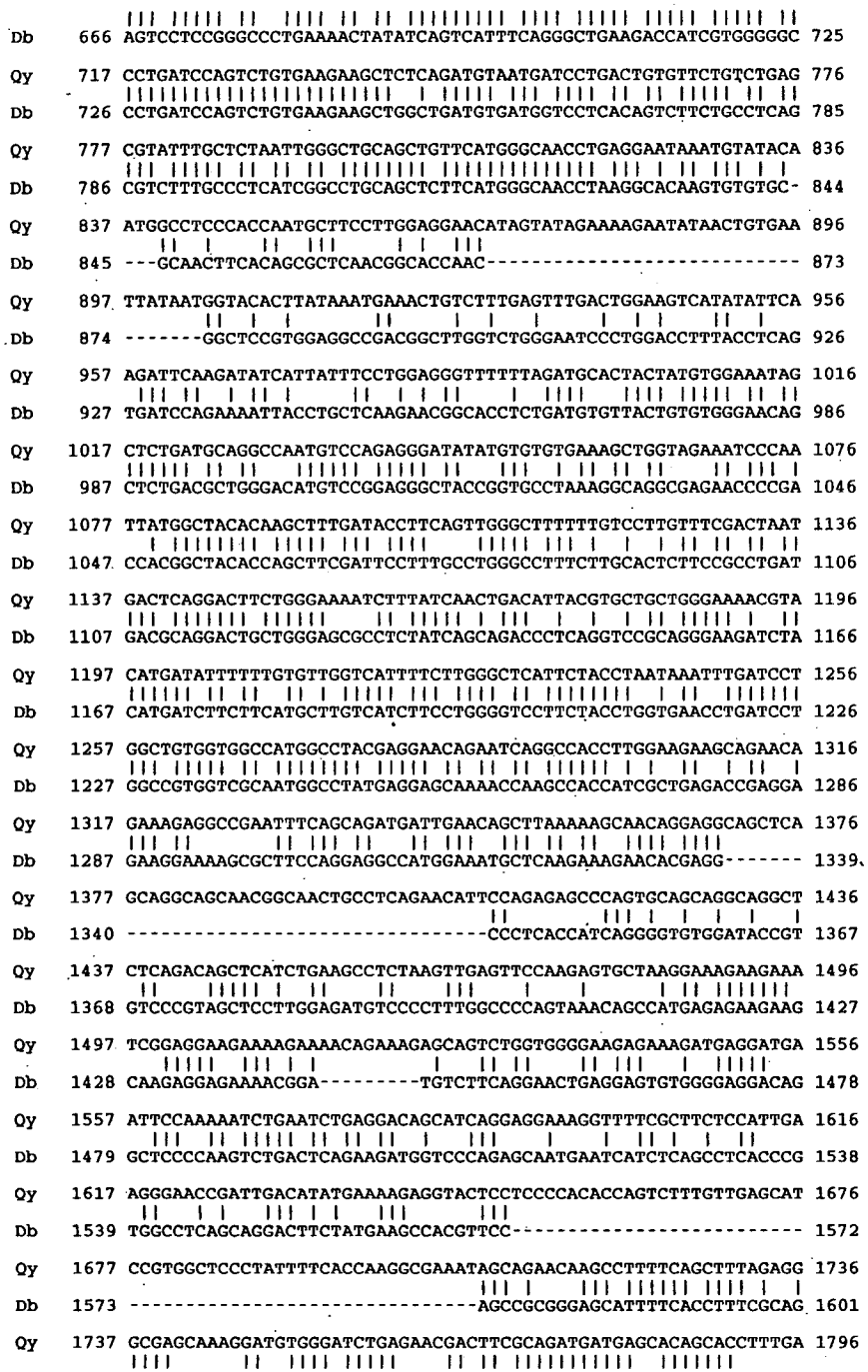
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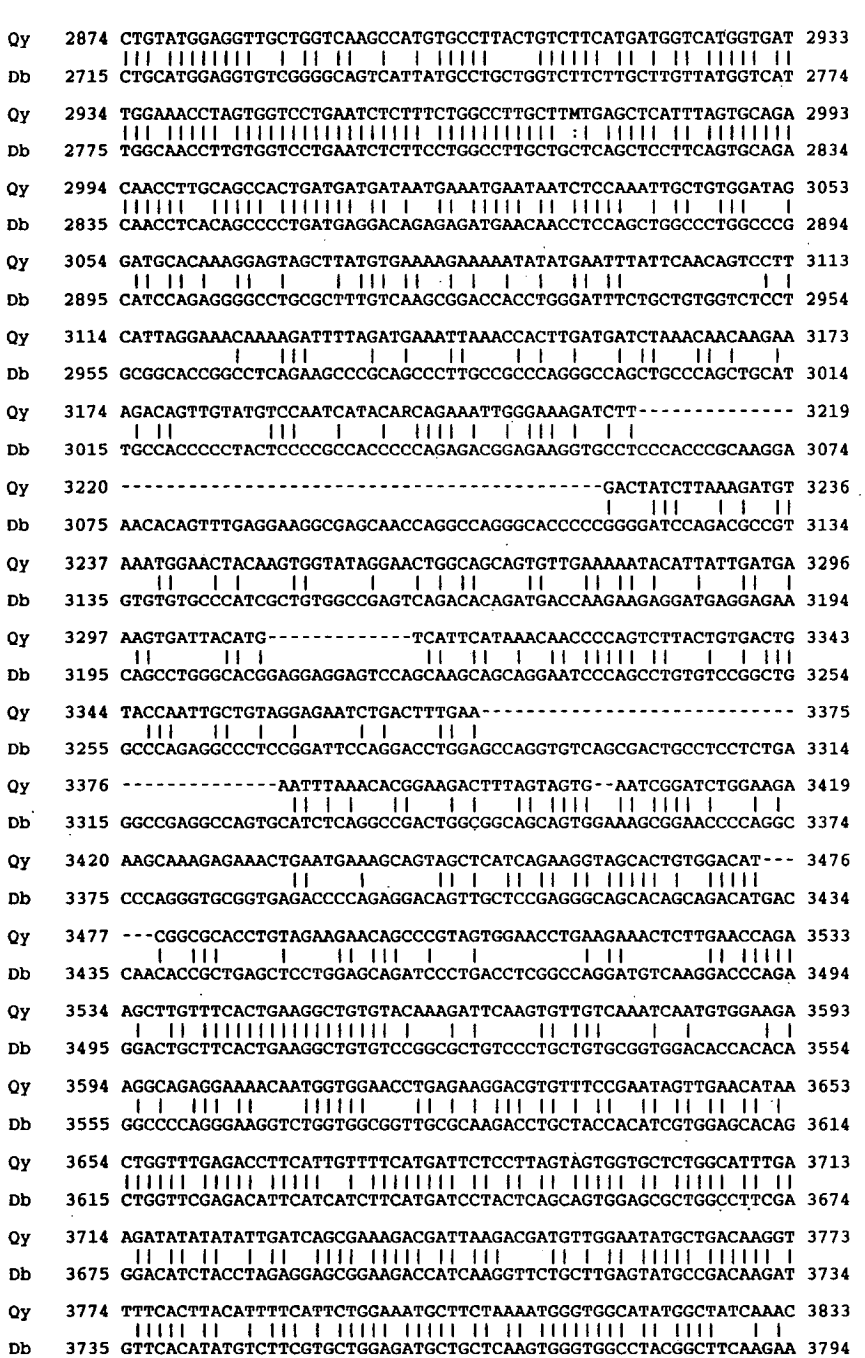
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RESULT 13
US-09-840-125-3
; Sequence 3, Application US/09840125
; Patent No. US20020061524A1
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE: 2323-155
;  CURRENT APPLICATION NUMBER: US/09/840,125
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: 09/634,920
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,488
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;  LENGTH: 6048
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(6048)
US-09-840-125-3

  Query Match           31.6%;  Score 1907.2;  DB 10;  Length 6048;
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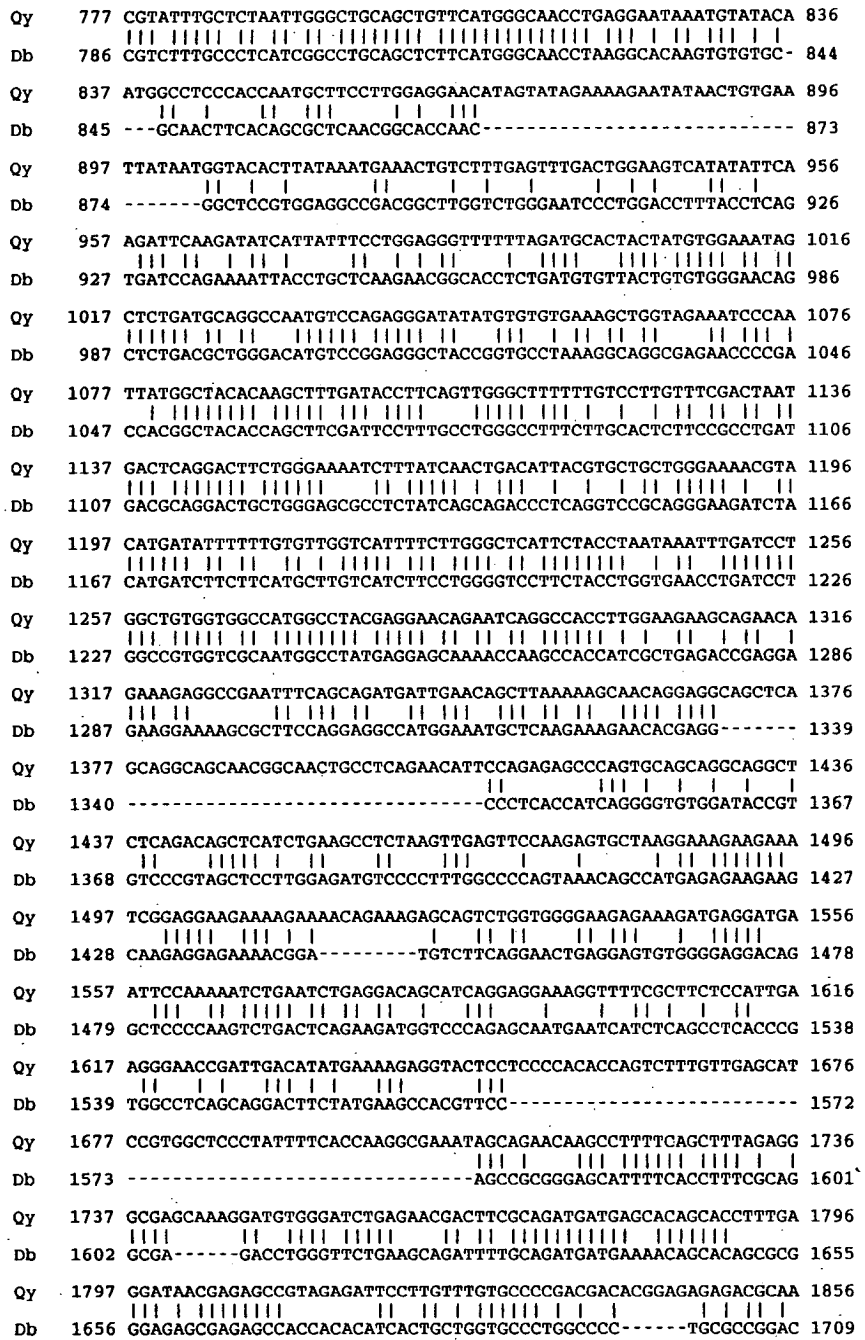
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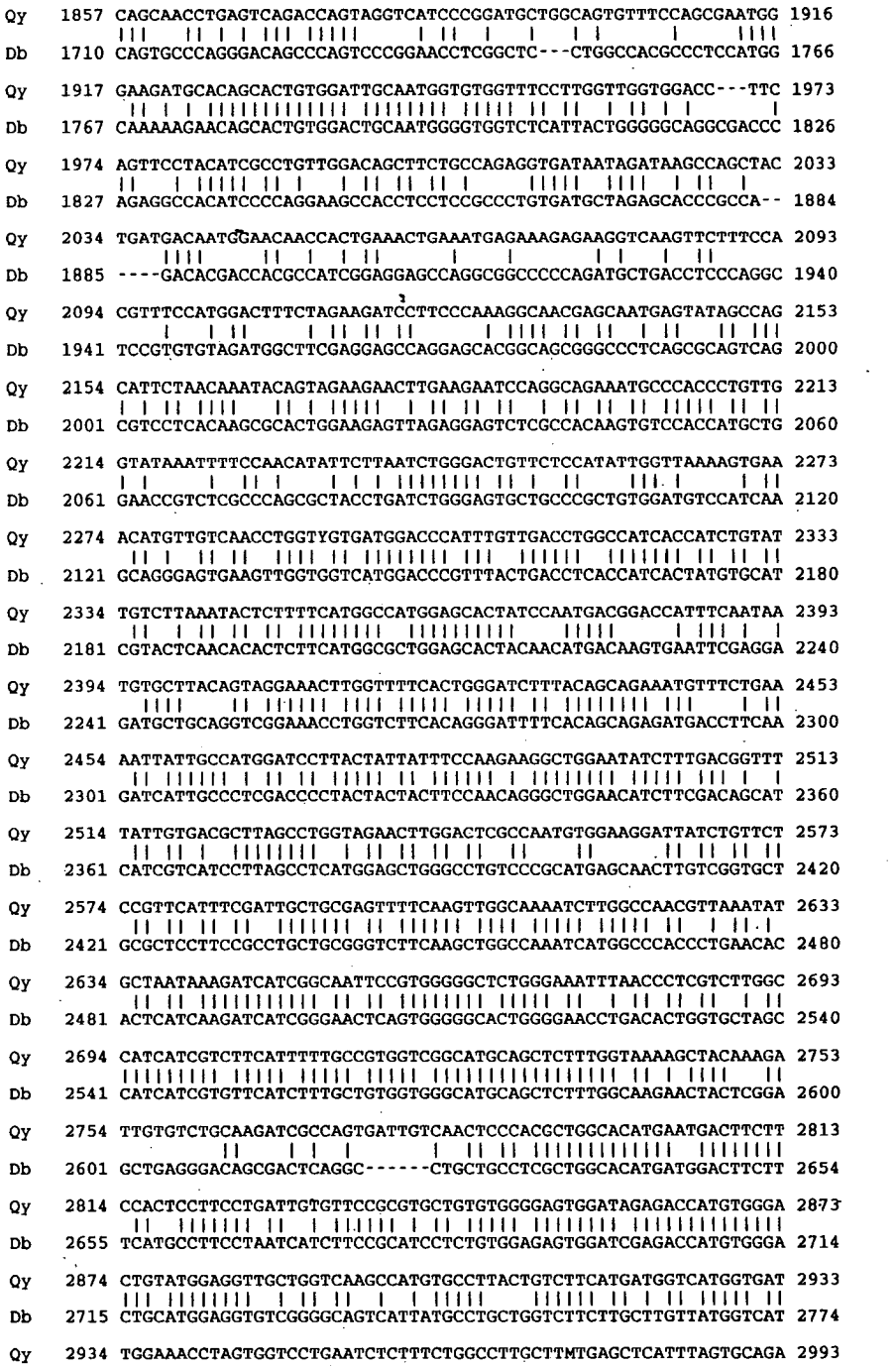
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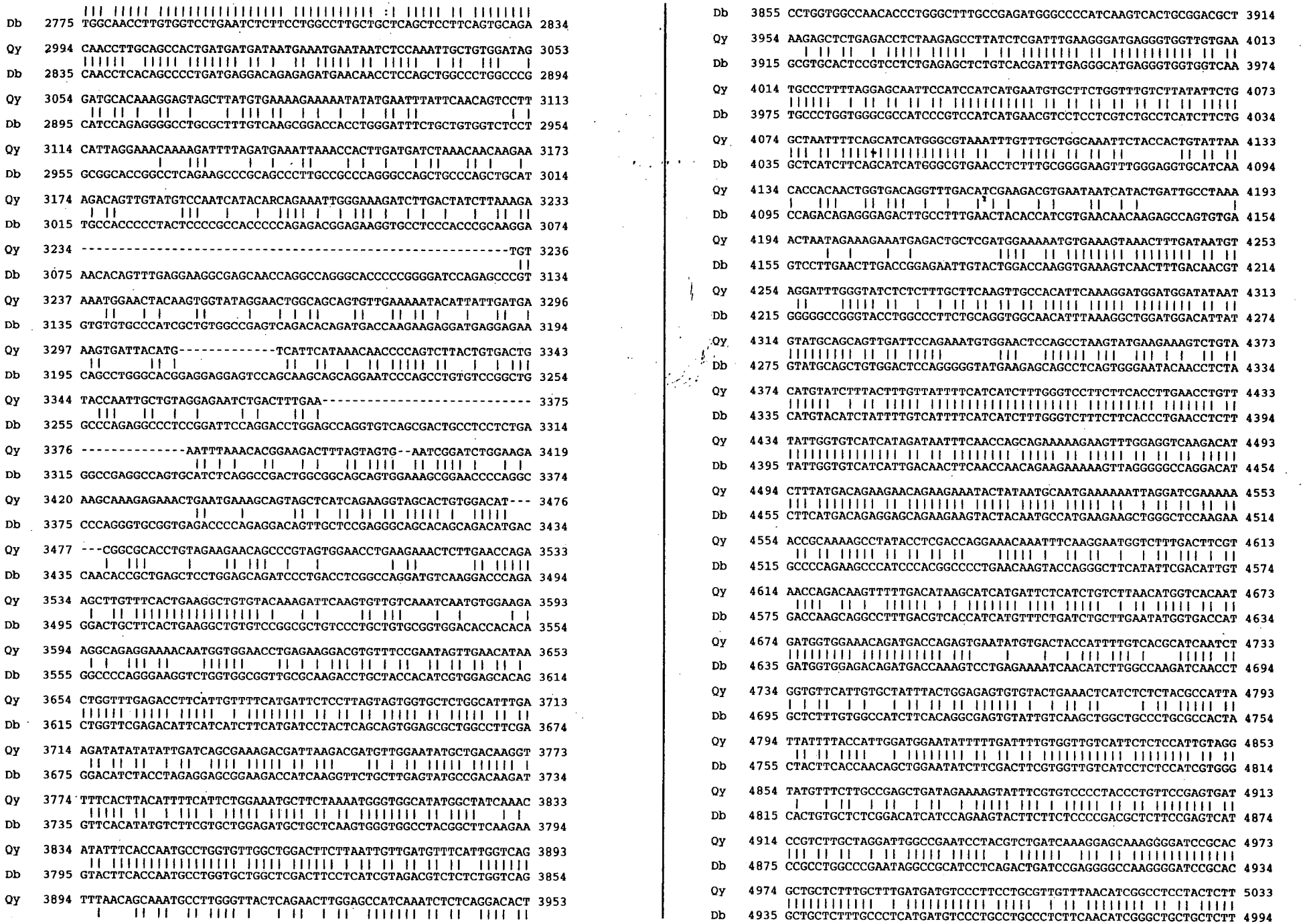
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Db   5712 GGCCATGGTTATCCAGAGAGCCTTCCGCAGGCACCTGCTGCAACGCTCTTTGAAGCATGC 5771

Qy   5814 TTCCTT 5819
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Db   5772 CTCCTT 5777


RESULT 14
US-09-864-761-10189/c
; Sequence 10189, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10189
;   LENGTH: 1992
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010127.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
US-09-864-761-10189

  Query Match             19.6%;  Score 1181;  DB 10;  Length 1992;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-298;
  Matches 1181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4850 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 4909
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Db   1447 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 1388

Qy   4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 1328

Qy   4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 1268

Qy   5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 1208

Qy   5090 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 5149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 1148

Qy   5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
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Db    1147 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 1088

Qy    5210 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 5269
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 1028

Qy    5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1027 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 968

Qy    5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     967 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 908

Qy    5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
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Db     907 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 848

Qy    5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 788

Qy    5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
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Db     787 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 728

Qy    5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 668

Qy    5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 608

Qy    5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 548

Qy    5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
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Db     547 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 488

Qy    5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 428

Qy    5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
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Db     427 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 368

Qy    5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 308

Qy    5990 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db     307 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 267


RESULT 15
US-09-864-761-18334/c
; Sequence 18334, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
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;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18334
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;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: MAP TO AC010127.2
;  OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
;  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.87
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;  OTHER INFORMATION: NT HIT: M91803.1, EVALUE 0.00e+00
;  OTHER INFORMATION: SWISSPROT HIT: P04774, EVALUE 0.00e+00
;  OTHER INFORMATION: EST_HUMAN HIT: AL120392.1, EVALUE 1.00e-129
US-09-864-761-18334

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  Matches 1157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
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Qy    5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
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Qy    5090 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 5149
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Db     917 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 858

Qy    5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
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Db     797 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 738

Qy    5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
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Db     737 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 678

Qy    5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
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Db     677 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 618

Qy    5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
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Qy    5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
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Db     557 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 498

Qy    5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
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Db     377 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 318

Qy    5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
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Db     317 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 258

Qy    5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
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Db     257 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 198

Qy    5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
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Db     197 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 138

Qy    5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
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Db     137 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 78

Qy    5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
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Db      77 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 18

Qy    5990 ATGAGCAAGAAGGCAAA 6006
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Job time : 441 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 11:26:44 ; Search time 9987 Seconds
(without alignments)
17571.835 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	5705	94.6	8378	6	AX164171	AX164171 Sequence
4	4897	81.2	8378	6	AX164172	AX164172 Sequence
5	4338	71.9	4362	6	AX391144	AX391144 Sequence
6	4152	68.9	4179	6	AX391146	AX391146 Sequence
7	4003	66.4	4197	6	AX391148	AX391148 Sequence
8	3987	66.1	5997	6	AX391130	AX391130 Sequence
9	3874	64.2	5889	6	AX391132	AX391132 Sequence
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13	2109	35.0	4146	6	AX391136	AX391136 Sequence
14	2011	33.3	4164	6	AX391138	AX391138 Sequence
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17	1109	18.4	1269	9	HSSCN1A	X65362 Homo sapien
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19	1060	17.6	3403	6	AX164202	AX164202 Sequence
20	404	6.7	163106	2	AP002375	AP002375 Homo sapi
c 21	384	6.4	163106	2	AP002375	AP002375 Homo sapi
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25	333	5.5	965	6	AX164187	AX164187 Sequence
c 26	309	5.1	54810	2	AC068732	AC068732 Homo sapi
27	284	4.7	677	6	AX164197	AX164197 Sequence
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29	274	4.5	409	6	AX164182	AX164182 Sequence
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31	245	4.1	829	6	AX164191	AX164191 Sequence
32	218	3.6	845	6	AX164186	AX164186 Sequence
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ALIGNMENTS

RESULT 1
AX391140
LOCUS AX391140 6030 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 11 from Patent WO0214498.
ACCESSION AX391140
VERSION AX391140.1 GI:19584237
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same

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  JOURNAL   Patent: WO 0214498-A 11 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT     1786 a   1190 c   1345 g   1706 t      3 others
ORIGIN

  Query Match           100.0%;  Score 6030;  DB 6;  Length 6030;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 6030;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

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Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

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Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

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Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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RESULT 2
AX391142
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DEFINITION  Sequence 13 from Patent WO0214498.
ACCESSION   AX391142
VERSION     AX391142.1  GI:19584238
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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  JOURNAL   Patent: WO 0214498-A 13 21-FEB-2002;
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
BASE COUNT     1746 a    1166 c    1320 g    1687 t      3 others
ORIGIN

  Query Match             98.1%;  Score 5917;  DB 6;  Length 5922;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

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Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
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Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
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Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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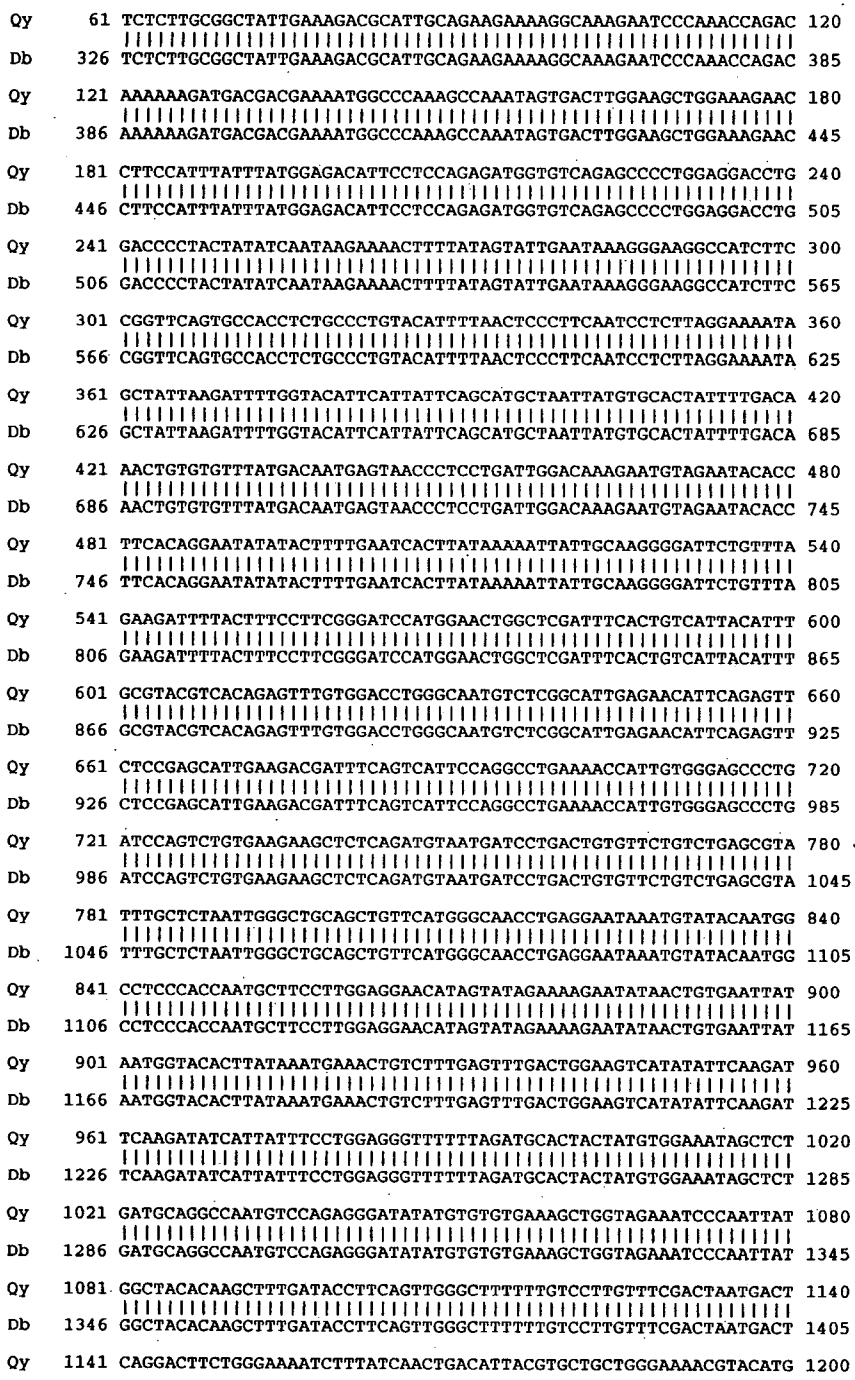
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RESULT 3
AX164171
LOCUS       AX164171               8378 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0138564.
ACCESSION   AX164171
VERSION     AX164171.1  GI:14545110
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 1 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
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BASE COUNT     2496 a   1575 c   1782 g   2525 t
ORIGIN

  Query Match           94.6%;  Score 5705;  DB 6;  Length 8378;
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  Matches 6025;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
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Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325
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Qy 301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
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Qy 361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db 626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685
Qy 421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Qy 961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db   2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

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Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3926 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTC-GGCATTTGAAGATATA 3984

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Db   4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 4104

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Db   4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Db   4165 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4224

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4225 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4284

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Db   4285 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4344

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Db   4345 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4404

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db   4405 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4464

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db   4465 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4524

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
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Db   4525 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4584

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4585 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4644

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704
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Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
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Db   4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
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Db   4765 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4824

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
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Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
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Db   4885 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4944

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
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Db   4945 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5004

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
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Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
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Db   5125 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 5184

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
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Db   5185 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 5244

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
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Db   5245 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5304

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Db   5425 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5484

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db   5485 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5544

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
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Db   5545 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5604

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
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Db   5605 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5664

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
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Db   5665 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5724

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db   5725 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5784

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db   5785 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5844

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Db   5845 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5904

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Db   5905 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5964

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5965 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 6024

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
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Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Db   6145 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6204

Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
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Db   6205 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6264

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
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Db   6265 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6294
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RESULT 4
AX164172
LOCUS       AX164172               8378 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138564.
ACCESSION   AX164172
VERSION     AX164172.1  GI:14545111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8378)
  AUTHORS   Rouleau,G.A., Lafreniere,R.G., Rochefort,D., Cossette,P. and
            Ragsdale,D.
  TITLE     Loci for idiopathic generalized epilepsy, mutations thereof and
            method using same to assess, diagnose, prognose or treat epilepsy
  JOURNAL   Patent: WO 0138564-A 2 31-MAY-2001;
            McGill University (CA)
FEATURES             Location/Qualifiers
     source          1. .8378
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2498 a   1571 c   1775 g   2534 t
ORIGIN

  Query Match           81.2%;  Score 4897;  DB 6;  Length 8378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5337;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy     688 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 1012

Qy     748 GTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAATTGGGCTGCAGCTGTTC 807
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 GTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAATTGGGCTGCAGCTGTTC 1072
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Qy    808 ATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCAATGCTTCCTTGGAGGAA 867
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Db   1073 ATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCAATGCTTCCTTGGAGGAA 1132

Qy    868 CATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACACTTATAAATGAAACTGTC 927
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Db   1133 CATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACACTTATAAATGAAACTGTC 1192

Qy    928 TTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATCATTATTTCCTGGAGGGT 987
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Db   1193 TTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATCATTATTTCCTGGAGGGT 1252

Qy    988 TTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCCAATGTCCAGAGGGATAT 1047
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Db   1253 TTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCCAATGTCCAGAGGGATAT 1312

Qy   1048 ATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAAGCTTTGATACCTTCAGT 1107
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Db   1313 ATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAAGCTTTGATACCTTCAGT 1372

Qy   1108 TGGGCTTTTTTGTCCTTGTTTCGACTAATGACTCAGGACTTCTGGGAAAATCTTTATCAA 1167
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Db   1373 TGGGCTTTTTTGTCCTTGTTTCGACTAATGACTCAGGACTTCTGGGAAAATCTTTATCAA 1432

Qy   1168 CTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTGTGTTGGTCATTTTCTTG 1227
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Db   1433 CTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTGTATTGGTCATTTTCTTG 1492

Qy   1228 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1287
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Db   1493 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1552

Qy   1288 AATCAGGCCACCTTGGAAGAAGCAGAACAGAAAGAGGCCGAATTTCAGCAGATGATTGAA 1347
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Db   1553 AATCAGGCCACCTTGGAAGAAGCAGAACAGAAAGAGGCCGAATTTCAGCAGATGATTGAA 1612

Qy   1348 CAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGGCAACTGCCTCAGAACAT 1407
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Db   1613 CAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGGCAACTGCCTCAGAACAT 1672

Qy   1408 TCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTG 1467
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Qy   1468 AGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAG 1527
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Db   1733 AGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAG 1792

Qy   1528 TCTGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATC 1587
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 TCTGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATC 1852

Qy   1588 AGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTAC 1647
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Db   1853 AGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTAC 1912

Qy   1648 TCCTCCCCACACCAGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAAT 1707
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Db   1913 TCCTCCCCACACCAGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAAT 1972

Qy   1708 AGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGAC 1767
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Db   1973 AGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGAC 2032

Qy   1768 TTCGCAGATGATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTT 1827
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Db   2033 TTCGCAGATGATGAGC-CAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTT 2091

Qy   1828 GTGCCCCGACGACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCC 1887
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Db   2092 GTGCCCCGACGACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCC 2151

Qy   1888 CGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGT 1947
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Db   2152 CGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGT 2211

Qy   1948 GTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCA 2007
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Db   2212 GTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCA 2271

Qy   2008 GAGGTGATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATG 2067
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Db   2272 GAGGTGATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATG 2331

Qy   2068 AGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAA 2127
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Db   2332 AGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAA 2391

Qy   2128 AGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAA 2187
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Db   2392 AGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAA 2451

Qy   2188 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2247
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Db   2452 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2511

Qy   2248 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTGYGTGATGGACCCATTT 2307
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Db   2512 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTTGTGATGGACCCATTT 2571

Qy   2308 GTTGACCTGGCCATCACCATCTGTATTGTCTTAAATACTCTTTTCATGGCCATGGAGCAC 2367
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Db   2572 GTTGACCTGGCCATCACCATCTGTATTGTCTTAAATACTCTTTTCATGGCCATGGAGCAC 2631

Qy   2368 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2427
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Db   2632 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2691

Qy   2428 ATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAA 2487
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Qy   2488 GAAGGCTGGAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTC 2547
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Qy   2548 GCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTG 2607
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Qy   2608 GCAAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCT 2667
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Db   2932 CTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATG 2991

Qy   2728 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 2787
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Qy   2788 CCACGCTGGCACATGAATGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGT 2847
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Qy   2848 GGGGAGTGGATAGAGACCATGTGGGACTGTATGGAGGTTGCTGGTCAAGCCATGTGCCTT 2907
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Qy   2968 TTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCAGCCACTGATGATGATAATGAAATG 3027
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Qy   3328 AGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAAATTTAAACACG 3387
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Qy   3388 GAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGCAAAGAGAAACTGAATGAAAGCAGT 3447
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Qy   3568 AAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAACAATGGTGGAACCTGAGAAGG 3627
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Qy   4348 CAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTTTACTTTGTTATTTTCATCATCTTT 4407
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RESULT 5
AX391144
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DEFINITION  Sequence 15 from Patent WO0214498.
ACCESSION   AX391144
VERSION     AX391144.1  GI:19584239
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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  JOURNAL   Patent: WO 0214498-A 15 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
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BASE COUNT     1300 a    845 c    995 g   1219 t      3 others
ORIGIN
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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 4338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
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RESULT 6
AX391146
LOCUS AX391146 4179 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 17 from Patent WO0214498.
ACCESSION AX391146
VERSION AX391146.1 GI:19584240
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0214498-A 17 21-FEB-2002;
Lexicon Genetics Incorporated (US)
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/db_xref="taxon:9606"
BASE COUNT 1239 a 815 c 958 g 1164 t 3 others
ORIGIN

Query Match 68.9%; Score 4152; DB 6; Length 4179;
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Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
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Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

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Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

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Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

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Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
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Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
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Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
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Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
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Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
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Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGG 4152
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Db   4141 ACTGGTGACAGG 4152
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RESULT 7
AX391148

LOCUS	AX391148	4197 bp	DNA	linear	PAT	19-MAR-2002
DEFINITION	Sequence 19 from Patent WO0214498.					
ACCESSION	AX391148					
VERSION	AX391148.1 GI:19584241					
KEYWORDS	.					
SOURCE	human.					
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Turner,C.A., Mathur,B. and Mathur,D.					
TITLE	Novel human ion channel proteins and polynucleotides encoding the same					
JOURNAL	Patent: WO 0214498-A 19 21-FEB-2002; Lexicon Genetics Incorporated (US)					
FEATURES	Location/Qualifiers					
source	1. .4197 /organism="Homo sapiens" /db_xref="taxon:9606"					
BASE COUNT	1232 a	821 c	965 g	1176 t	3 others	
ORIGIN						

Query Match 66.4%; Score 4003; DB 6; Length 4197;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
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Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
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Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
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Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

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Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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RESULT 8
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LOCUS AX391130 5997 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 1 from Patent WO0214498.
ACCESSION AX391130
VERSION AX391130.1 GI:19584232
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0214498-A 1 21-FEB-2002;
Lexicon Genetics Incorporated (US)
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BASE COUNT 1773 a 1185 c 1338 g 1698 t 3 others
ORIGIN

Query Match 66.1%; Score 3987; DB 6; Length 5997;
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Matches 3987; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
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RESULT 9
AX391132

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VERSION     AX391132.1  GI:19584233
KEYWORDS    .
SOURCE      human.
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REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
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BASE COUNT     1733 a   1161 c   1313 g   1679 t      3 others
ORIGIN
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Query Match 64.2%; Score 3874; DB 6; Length 5889;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3874; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
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Qy   5584 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5643
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Db   5611 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5670

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RESULT 10
AY043484
LOCUS       AY043484               6046 bp    mRNA    linear   PRI 24-APR-2002
DEFINITION  Homo sapiens voltage-gated sodium channel type I mRNA, complete
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ACCESSION   AY043484
VERSION     AY043484.1  GI:15421161
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki-Miyazaki,E., Fukushima,K., Shimomura,J.,
            Fujiwara,T., Hamano,S., Inoue,Y. and Yamakawa,K.
  TITLE     Frequent mutations of SCN1A in severe myoclonic epilepsy in infancy
  JOURNAL   Neurology 58 (7), 1122-1124 (2002)
  MEDLINE   21938587
   PUBMED   11940708
REFERENCE   2  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
            mRNA
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6046)
  AUTHORS   Sugawara,T., Mazaki,E.M. and Yamakawa,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-2001) Neurogenetics, BSI, RIKEN, 2-1 Hirosawa,
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FEATURES             Location/Qualifiers
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BASE COUNT     1808 a    1188 c    1345 g    1704 t       1 others
ORIGIN

  Query Match           60.2%;  Score 3628;  DB 9;  Length 6046;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3978;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
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Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
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Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
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Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
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Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
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Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
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Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
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Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
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Qy  4144 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4203
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Qy  5404 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5463
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Qy  5464 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5523
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Qy  5524 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5583
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Qy  5584 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5643
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Db  5551 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5610
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Qy    5644 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5703
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Qy    5704 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5763
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Qy    5764 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5823
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Qy    5944 TGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGC 6003
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Db    5971 AAAGATGAAAAAGCCAAAGGGAAAT 5995
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RESULT 11
AF225985
LOCUS       AF225985               8131 bp    mRNA    linear   PRI 01-FEB-2001
DEFINITION  Homo sapiens voltage-gated sodium channel alpha subunit SCN1A
            (SCN1A) mRNA, complete cds.
ACCESSION   AF225985
VERSION     AF225985.1  GI:12642269
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Cloning of cDNA for human voltage-gated sodium channel alpha
            subunit, SCN1A
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 8131)
  AUTHORS   Jeong,S.-Y., Goto,J. and Kanazawa,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2000) Department of Neurology, University of
            Tokyo, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo
            113-8655, Japan
FEATURES             Location/Qualifiers
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                     FTGIYTFESLIKIIARGFCLEDFTFLRDPWNWLDFTVITFAYVTEFVDLGNVSALRTF
                     RVLRALKTISVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALIGLQLFMGNLRNK
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BASE COUNT     2453 a   1530 c   1719 g   2422 t      7 others
ORIGIN
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  Query Match             54.8%;  Score 3302;  DB 9;  Length 8131;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3982;  Conservative    0;  Mismatches    4;  Indels    5;  Gaps    3;

Qy    2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
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Db    2029 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2088

Qy    2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2089 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2148

Qy    2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
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Db    2269 AACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2328

Qy    2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
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Db    2329 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2388

Qy    2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
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Qy    2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
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Db    2449 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2508

Qy    2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
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Db    2509 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2568

Qy    2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Db   2569 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2628

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
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Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
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Qy   2764 AAGATCGCCAGTGATTGTCAACTCCC---ACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db   2749 AAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCACTCC 2808

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
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Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
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Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
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Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
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Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
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Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGT-GGACATCGG 3479
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Qy   3480 CGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTG 3539
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Qy   3540 TTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAG 3599
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Qy   4140 AACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAAT 4199
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Db   4128 AACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAAT 4187

Qy   4200 AGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATT 4259
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Qy   4260 TGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGC 4319
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Qy   4320 AGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTA 4379
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Qy   4380 TCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGG 4439
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Qy   4500 GACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCA 4559
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Db   4488 GACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCA 4547

Qy   4560 AAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAG 4619
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Db   4548 AAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAG 4607

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Db   4608 ACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGT 4667

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Db   4668 GGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTT 4727

Qy   4740 CATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT 4799
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Db   4728 CATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT 4787
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Qy   4800 TACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTT 4859
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Db   4788 TACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTT 4847

Qy   4860 TCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCT 4919
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Qy   4920 TGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCT 4979
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Qy   4980 CTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGT 5039
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Qy   5160 TACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGA 5219
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Qy   5220 CTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATC 5279
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Qy   5640 AGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAA 5699
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Qy   5880 AATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGC 5939
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RESULT 12
AX391134
LOCUS AX391134 4329 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 5 from Patent WO0214498.
ACCESSION AX391134
VERSION AX391134.1 GI:19584234
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Turner,C.A., Mathur,B. and Mathur,D.
TITLE Novel human ion channel proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0214498-A 5 21-FEB-2002;
Lexicon Genetics Incorporated (US)
FEATURES Location/Qualifiers
source 1. .4329
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1287 a 840 c 988 g 1211 t 3 others
ORIGIN

Query Match 38.1%; Score 2295; DB 6; Length 4329;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Qy   2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
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RESULT 13
AX391136
LOCUS       AX391136               4146 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 7 from Patent WO0214498.
ACCESSION   AX391136
VERSION     AX391136.1  GI:19584235
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 7 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 35.0%; Score 2109; DB 6; Length 4146;
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Matches 2109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850

Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910

Qy   2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970

Qy   3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
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Db   2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030

Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
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Db   3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090

Qy   3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
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Db   3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150

Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
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Db   3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210

Qy   3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
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Db   3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270

Qy   3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
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Db   3271 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3330

Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
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Db   3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390

Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
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Db   3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450

Qy   3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
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Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
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Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

Qy   3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
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Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
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Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
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Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
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Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
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Db   3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870

Qy   3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
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Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
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Qy   4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
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Db   3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy   4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
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Db   4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110
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Qy   4144 GGTGACAGG 4152
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Db   4111 GGTGACAGG 4119


RESULT 14
AX391138
LOCUS       AX391138               4164 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 9 from Patent WO0214498.
ACCESSION   AX391138
VERSION     AX391138.1  GI:19584236
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Turner,C.A., Mathur,B. and Mathur,D.
  TITLE     Novel human ion channel proteins and polynucleotides encoding the
            same
  JOURNAL   Patent: WO 0214498-A 9 21-FEB-2002;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .4164
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     1219 a    816 c    958 g   1168 t      3 others
ORIGIN

  Query Match             33.3%;  Score 2011;  DB 6;  Length 4164;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2011;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
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Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
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Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
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Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
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Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGG 2011
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RESULT 15
AC010127/c
LOCUS       AC010127               190066 bp    DNA     linear   PRI 09-MAY-2001
DEFINITION  Homo sapiens BAC clone RP11-2I8 from 2, complete sequence.
ACCESSION   AC010127
VERSION     AC010127.12  GI:11597116
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 190066)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 190066)
  AUTHORS   Goyea,E., Abbott,A. and MacDonald,J.
  TITLE     The sequence of Homo sapiens BAC clone RP11-2I8
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 190066)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 190066)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 190066)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 190066)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2001) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Dec 7, 2000 this sequence version replaced gi:10765079.
            ---------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            ---------- Summary Statistics
                Center project name: H_NH0002I08
            ----------

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO.  For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries.  Genomics 51:1-8.  The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu)
            VECTOR:  pBACe3.6
            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-467P13; the clone sequenced
            to the right is AP001199.  Actual start of this clone is at base
            position 1 of RP11-2I8; actual end is at base position 190066 of
            RP11-2I8.

            The sequence RP11-2I8 between bases 157391 to 157436 was derived
            from a single plasmid subclone sequenced only on one strand.
FEATURES             Location/Qualifiers
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                     /clone_lib="RPCI-11"
     repeat_region   457. .706
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     repeat_region   707. .1017
                     /rpt_family="Alu"
     repeat_region   1018. .1135
                     /rpt_family="MER1_type"
     repeat_region   1144. .1195
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     repeat_region   1219. .1483
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     misc_feature    2551. .2631
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     repeat_region   3384. .3515
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     misc_feature    3774. .4167
                     /note="similar to  EST AV711245 (NID:g10730551)"
     misc_feature    4258. .4387
                     /note="similar to  EST AV711245 (NID:g10730551)"
     repeat_region   5279. .5567
                     /rpt_family="Alu"
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repeat_region   5974. .6047
                /rpt_family="MIR"
repeat_region   6317. .6487
                /rpt_family="L2"
repeat_region   6810. .7116
                /rpt_family="MER1_type"
repeat_region   7406. .7609
                /rpt_family="L2"
misc_feature    7586. .7935
                /note="similar to  EST H67583 (NID:g1026323) yr61c05.r1"
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repeat_region   10548. .10904
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Matches 1181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   4850 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 4909
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Qy   4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
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Qy   4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
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Job time : 10789 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 11:23:44 ; Search time 768 Seconds
(without alignments)
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Perfect score: 6030
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1.	6030	100.0	6030	24	AAD32844	Human ion channel
2	5917	98.1	5922	24	AAD32845	Human ion channel
3	5705	94.6	8378	22	AAH55763	Human adult form o
4	5262	87.3	6027	24	AAD27266	Human transporter
5	4897	81.2	8378	22	AAH55764	Human neonatal for
6	4338	71.9	4362	24	AAD32846	Human ion channel
7	4152	68.9	4179	24	AAD32847	Human ion channel
8	4003	66.4	4197	24	AAD32848	Human ion channel
9	3987	66.1	5997	24	AAD32839	Human ion channel
10	3874	64.2	5889	24	AAD32840	Human ion channel
11	3302	54.8	8131	24	ABL39689	Human sodium chann
12	2295	38.1	4329	24	AAD32841	Human ion channel
13	2109	35.0	4146	24	AAD32842	Human ion channel
14	2011	33.3	4164	24	AAD32843	Human ion channel
c 15	1181	19.6	1992	22	AAK02861	Human brain expres
c 16	1181	19.6	1992	22	AAI02784	Probe #2775 used t
c 17	1157	19.2	1194	22	ABA48040	Human breast cell
c 18	1157	19.2	1194	22	ABA65925	Human foetal liver
c 19	1157	19.2	1194	22	ABA33014	Probe #11480 for g
c 20	1157	19.2	1194	22	AAK14344	Human brain expres
c 21	1157	19.2	1194	22	AAK40073	Human bone marrow
c 22	1157	19.2	1194	22	AAI20854	Probe #10787 for g
c 23	1157	19.2	1194	22	AAI46090	Probe #14776 used
c 24	1157	19.2	1194	22	AAI06565	Probe #6556 used t
c 25	1157	19.2	1194	24	ABS14151	Human genome-deriv
c 26	1141	18.9	1178	22	AAK15629	Human brain expres
c 27	1141	18.9	1178	22	AAI07805	Probe #7796 used t
28	1060	17.6	3403	22	AAH55792	Human SCN1A genomi
c 29	969	16.1	969	22	ABA42912	Human breast cell
c 30	969	16.1	969	22	ABA53333	Human foetal liver
c 31	969	16.1	969	22	ABA23110	Probe #1576 for ge
c 32	969	16.1	969	22	AAK01598	Human brain expres
c 33	969	16.1	969	22	AAK27041	Human bone marrow
c 34	969	16.1	969	22	AAI11641	Probe #1574 for ge
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c 36	969	16.1	969	22	AAI01568	Probe #1559 used t
c 37	969	16.1	969	24	ABS01620	Human genome-deriv
38	832	13.8	1456	22	ABA08320	Human Na channel p
39	358	5.9	1425	23	AAS84262	DNA encoding novel
40	353	5.9	909	22	AAH55782	Human SCN1A genomi
41	333	5.5	965	22	AAH55777	Human SCN1A genomi
42	284	4.7	606	23	ABV58235	Human prostate exp
43	284	4.7	677	22	AAH55787	Human SCN1A genomi
44	274	4.5	409	22	AAH55772	Human SCN1A genomi
45	274	4.5	539	22	AAH55791	Human SCN1A genomi

ALIGNMENTS

RESULT 1
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ID AAD32844 standard; cDNA; 6030 BP.
XX
AC AAD32844;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #6.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..6030
FT /*tag= a
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FT /transl_except= (pos:3199..3201, aa:Xaa)
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PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX

PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20515.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 2; Page 55-57; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 6030 BP; 1786 A; 1190 C; 1345 G; 1706 T; 3 other;

Query Match 100.0%; Score 6030; DB 24; Length 6030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
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Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCCTGGAGGACCTG 240
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Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
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Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
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Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Db    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy    6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
          ||||||||||||||||||||||||||||||
Db    6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030


RESULT 2
AAD32845
ID   AAD32845 standard; cDNA; 5922 BP.
XX
AC   AAD32845;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #7.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5922
FT                   /*tag= a
FT                   /product= "Human ion channel protein #7"
FT                   /transl_except= (pos:2974..2976, aa:Xaa)
FT                   /transl_except= (pos:3199..3201, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20516.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 62-64; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5922 BP; 1746 A; 1166 C; 1320 G; 1687 T; 3 other;

  Query Match          98.1%;  Score 5917;  DB 24;  Length 5922;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 5917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

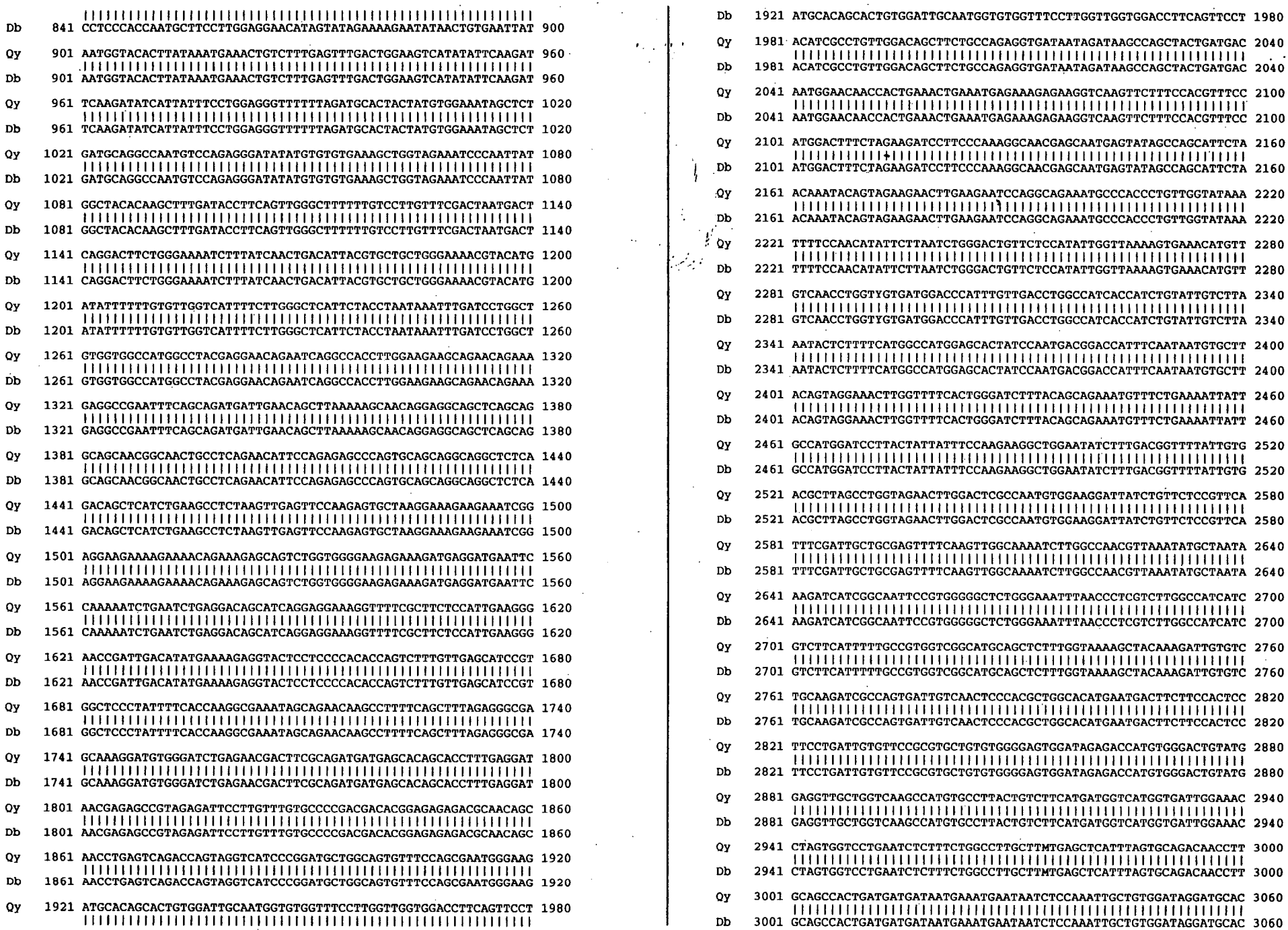
Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Db 841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Qy 901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db 901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Qy 961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db 961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Qy 1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db 1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Qy 1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db 1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Qy 1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db 1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Qy 1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db 1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Qy 1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db 1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Qy 1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db 1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Qy 1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db 1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Qy 1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy 1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db 1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Db 1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Qy 1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db 1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Qy 1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db 1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Qy 1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db 1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy 1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db 1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Qy 1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db 1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Qy 1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db 1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy 1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy 2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db 2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Qy 2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Qy 2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db 2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Qy 2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db 2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Qy 2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db 2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Qy 2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db 2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Qy 2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db 2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Qy 2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
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Db 2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy 2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db 2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Qy 2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db 2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy 2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db 2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Qy 2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db 2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy 2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db 2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy 2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db 2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy 2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db 2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy 3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db 3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

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Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
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Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
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Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db    5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy    5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
Db    5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy    5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
Db    5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy    5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
Db    5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy    5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
Db    5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
Db    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
Db    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
Db    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
Db    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
Db    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
Db    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
Db    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917


RESULT 3
AAH55763
ID   AAH55763 standard; cDNA; 8378 BP.
XX
AC   AAH55763;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human adult form of SCN1A nucleotide sequence SEQ ID NO:1.
XX
KW   Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW   diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW   anticonvulsant; neuroprotective; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138564-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-CA01404.
XX
PR   26-NOV-1999;   99US-0167623.
XX
PA   (UYMC-) UNIV MCGILL.
XX
PI   Rouleau GA,  LaFreniere RG,  Rochefort D,  Cossette P,  Ragsdale D;
XX
DR   WPI; 2001-355945/37.
DR   P-PSDB; AAB99674.
XX
PT   Determining a predisposition to epilepsy and/or development of epilepsy
PT   comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT   DNA variant, equivalent, or mutation which shows a linkage
PT   disequilibrium -
XX
PS   Disclosure; Page 90-93; 268pp; English.
XX
CC   The present invention describes a method (M1) of determining an
CC   individual's predisposition to epilepsy and/or development of epilepsy,
CC   as well as predicting the individual's response to medication. The
CC   method comprises determining the genotype of at least one gene selected
CC   from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC   which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC   sodium channel genes located on chromosome 2. The idiopathic generalised
CC   epilepsy (IGE) gene is more specifically localised on chromosome
CC   2q23-q31. Compounds identified as modulators of the biological activity
CC   of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC   epilepsy or other neurological disorders. They have anticonvulsant and
CC   neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC   AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC   primers, oligonucleotides and proteins given in the exemplification of
CC   the present invention.
XX
SQ   Sequence 8378 BP; 2496 A; 1575 C; 1782 G; 2525 T; 0 other;

  Query Match             94.6%;  Score 5705;  DB 22;  Length 8378;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 6025;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
Db     266 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 325

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
Db     326 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 385

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
Db     386 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 445

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
Db     446 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 505

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
Db     506 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 565

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
Db     566 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 625

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
Db     626 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 685

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Db     686 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 745

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db     746 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 805

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
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Db    806 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 865

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    866 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 925

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    926 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 985

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    986 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 1045

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1046 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 1105

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1106 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 1165

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1166 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 1225

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1226 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1285

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1286 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1345

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1346 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1405

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1406 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1465

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1466 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1525

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1526 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1585

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1586 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1645

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1646 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1705

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1706 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1765

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1766 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1825

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1826 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1885

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1886 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1945

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1946 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 2005

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2006 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 2065

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2066 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 2125

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2126 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 2185

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2186 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 2245

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2246 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2305

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2306 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2365

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2366 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2425

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2426 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2485

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2486 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2545

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2546 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2605

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2606 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2665

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2666 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2725

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2726 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2785

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2786 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2845

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2846 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2905

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2906 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2965

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2966 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 3025
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Qy 2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db 3026 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 3085
Qy 2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db 3086 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 3145
Qy 2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db 3146 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 3205
Qy 2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db 3206 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3265
Qy 3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db 3266 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3325
Qy 3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db 3326 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3385
Qy 3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db 3386 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3445
Qy 3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db 3446 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3505
Qy 3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db 3506 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3565
Qy 3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db 3566 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3625
Qy 3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db 3626 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3685
Qy 3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db 3686 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3745
Qy 3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db 3746 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3805
Qy 3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db 3806 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3865
Qy 3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db 3866 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3925
Qy 3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db 3926 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTC-GGCATTTGAAGATATA 3984
Qy 3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db 3985 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 4044
Qy 3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db 4045 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 4104
Qy 3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
Db 4105 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 4164
Qy 3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
Db 4165 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 4224
Qy 3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
Db 4225 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4284
Qy 4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
Db 4285 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4344
Qy 4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
Db 4345 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4404
Qy 4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
Db 4405 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4464
Qy 4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
Db 4465 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4524
Qy 4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
Db 4525 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4584
Qy 4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
Db 4585 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4644
Qy 4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
Db 4645 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4704
Qy 4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
Db 4705 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4764
Qy 4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
Db 4765 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4824
Qy 4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
Db 4825 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4884
Qy 4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
Db 4885 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4944
Qy 4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
Db 4945 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 5004
Qy 4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
Db 5005 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 5064
Qy 4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
Db 5065 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 5124
Qy 4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
Db 5125 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 5184
Qy 4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

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Db    5185 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 5244

Qy    4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5245 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5304

Qy    5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
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Db    5305 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5364

Qy    5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
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Db    5365 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5424

Qy    5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
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Db    5425 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5484

Qy    5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
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Db    5485 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5544

Qy    5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5545 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5604

Qy    5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5605 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5664

Qy    5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
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Db    5665 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5724

Qy    5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
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Db    5725 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5784

Qy    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
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Db    5785 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5844

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
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Db    5845 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5904

Qy    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
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Db    5905 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5964

Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
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Db    5965 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 6024

Qy    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
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Db    6025 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 6084

Qy    5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
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Db    6085 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 6144

Qy    5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
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Db    6145 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 6204

Qy    5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6205 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6264

Qy    6001 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
           ||||||||||||||||||||||||||||||
Db    6265 GGCAAAGATGAAAAAGCCAAAGGGAAATAA 6294
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RESULT 4
AAD27266
ID   AAD27266 standard; cDNA; 6027 BP.
XX
AC   AAD27266;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human transporter and ion channel-13 (TRICH-13) cDNA.
XX
KW   Human; transporter and ion channel-13; TRICH-13; neuroprotective; asthma;
KW   nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW   antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW   Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW   amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW   Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW   cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW   bradyarrythmia; gene expression; drug screening; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..6027
FT                   /*tag= a
FT                   /product= "Human TRICH-13 protein"
FT                   /note= "CDS does not include stop codon"
FT                   /partial
XX
PN   WO200192304-A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US17065.
XX
PR   26-MAY-2000; 2000US-208424P.
PR   01-JUN-2000; 2000US-209001P.
PR   08-JUN-2000; 2000US-210588P.
PR   16-JUN-2000; 2000US-212335P.
PR   22-JUN-2000; 2000US-213747P.
PR   29-JUN-2000; 2000US-215391P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Thornton M,  Walia NK,  Yue H,  Nguyen DB,  Lai P,  Gandhi AR;
PI   Tribouley CM,  Yao MG,  Ramkumar J,  Au-Young J,  Lu Y,  Tang YT;
PI   Azimzai Y,  Bruns CM,  Griffin JA,  Yang J,  Sanjanwala MS;
PI   Raumann BE,  Lee EA,  Hafalia A,  Baughn MR,  Green BD,  Khan FA;
PI   Kearney L,  Elliot VS,  Seilhamer JJ,  Policky JL,  Borowsky ML;
PI   Burford N,  Ding L,  Lu DAM,  Hillman JL;
XX
DR   WPI; 2002-122055/16.
DR   P-PSDB; AAE16776.
XX
PT   New human transporters and ion channels (TRICH) polypeptides useful for
PT   diagnosing, treating or preventing disorders associated with aberrant
PT   expression of TRICH -
XX
PS   Claim 11; Page 196-197; 210pp; English.
XX
CC   The invention relates to human transporters and ion channels (TRICH)
CC   polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC   sequences are useful in the diagnosis, treatment, and prevention of
CC   disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC   palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC   amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC   muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC   asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC   cardiac disease (angina, hypertension, or bradyarrythmia) and in the
CC   assessment of the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of transporters and ion channels.
CC   The polynucleotides may be used to detect and quantify gene expression
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CC   in biopsied tissues in which TRICH expression may be correlated with a
CC   disease, to generate hybridization probes for mapping naturally occurring
CC   genomic sequence, and in drug screening. The present sequence is human
CC   TRICH-13 cDNA.
XX
SQ   Sequence 6027 BP; 1785 A; 1189 C; 1348 G; 1705 T; 0 other;

  Query Match            87.3%;  Score 5262;  DB 24;  Length 6027;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 6012;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
           |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGCAGACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAGTACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAGGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGGCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
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Db    1201 ATATTTTTTGTATTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
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Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
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Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
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Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

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Qy    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db    1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
          |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GTCAACCTGGTTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
          ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   2401 ACAGTAGGAAACTTGGTATTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGGGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||  ||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   2941 CTAGTGGTACTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
          ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTCACTGAAGGTTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTAGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db   4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy   4321 GCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   4321 GCAGTTGATTCCAGAAATGTAGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTAT 4380

Qy   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGT 4440

Qy   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 GTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATG 4500

Qy   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 ACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAA 4560

Qy   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 AAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGA 4620

Qy   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 CAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTG 4680

Qy   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTC 4740

Qy   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTT 4800

Qy   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 ACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTT 4860

Qy   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTT 4920

Qy   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 GCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTC 4980

Qy   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 TTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTC 5040

Qy   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGG 5100

Qy   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATT 5160

Qy   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 ACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGAC 5220

Qy   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCT 5280

Qy   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340

Qy   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400

Qy   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460

Qy   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
          ||||||||||||H||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520

Qy   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580

Qy   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640

Qy   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700

Qy   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760

Qy   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820

Qy   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 ACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATA 5880

Qy   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 ATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCA 5940

Qy   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 GCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAA 6000

Qy   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
          |||||||||||||||||||||||||||
Db   6001 GGCAAAGATGAAAAAGCCAAAGGGAAA 6027
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RESULT 5
AAH55764
ID AAH55764 standard; cDNA; 8378 BP.
XX
AC AAH55764;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human neonatal form of SCN1A nucleotide sequence SEQ ID NO:2.
XX
KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective; ss.
XX
OS Homo sapiens.
XX
PN WO200138564-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-CA01404.
XX

PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99675.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 93-96; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Query Match 81.2%; Score 4897; DB 22; Length 8378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5337; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Qy    688 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 747
Db    953 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 1012

Qy    748 GTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAATTGGGCTGCAGCTGTTC 807
Db   1013 GTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAATTGGGCTGCAGCTGTTC 1072

Qy    808 ATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCAATGCTTCCTTGGAGGAA 867
Db   1073 ATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCAATGCTTCCTTGGAGGAA 1132

Qy    868 CATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACACTTATAAATGAAACTGTC 927
Db   1133 CATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACACTTATAAATGAAACTGTC 1192

Qy    928 TTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATCATTATTTCCTGGAGGGT 987
Db   1193 TTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATCATTATTTCCTGGAGGGT 1252

Qy    988 TTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCCAATGTCCAGAGGGATAT 1047
Db   1253 TTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCCAATGTCCAGAGGGATAT 1312

Qy   1048 ATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAAGCTTTGATACCTTCAGT 1107
Db   1313 ATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAAGCTTTGATACCTTCAGT 1372

Qy   1108 TGGGCTTTTTTGTCCTTGTTTCGACTAATGACTCAGGACTTCTGGGAAAATCTTTATCAA 1167
Db   1373 TGGGCTTTTTTGTCCTTGTTTCGACTAATGACTCAGGACTTCTGGGAAAATCTTTATCAA 1432

Qy   1168 CTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTGTGTTGGTCATTTTCTTG 1227
Db   1433 CTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTGTATTGGTCATTTTCTTG 1492

Qy   1228 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1287
Db   1493 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1552

Qy   1288 AATCAGGCCACCTTGGAAGAAGCAGAACAGAAAGAGGCCGAATTTCAGCAGATGATTGAA 1347
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Qy   1348 CAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGGCAACTGCCTCAGAACAT 1407
Db   1613 CAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGGCAACTGCCTCAGAACAT 1672

Qy   1408 TCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTG 1467
Db   1673 TCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTG 1732

Qy   1468 AGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAG 1527
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Qy   1528 TCTGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATC 1587
Db   1793 TCTGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATC 1852

Qy   1588 AGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTAC 1647
Db   1853 AGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGGAACCGATTGACATATGAAAAGAGGTAC 1912

Qy   1648 TCCTCCCCACACCAGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAAT 1707
Db   1913 TCCTCCCCACACCAGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAAT 1972

Qy   1708 AGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGAC 1767
Db   1973 AGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGAC 2032

Qy   1768 TTCGCAGATGATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTT 1827
Db   2033 TTCGCAGATGATGAGC-CAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTT 2091

Qy   1828 GTGCCCCGACGACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCC 1887
Db   2092 GTGCCCCGACGACACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCATCC 2151

Qy   1888 CGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGT 1947
Db   2152 CGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGT 2211

Qy   1948 GTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCA 2007
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Qy   2008 GAGGTGATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATG 2067
Db   2272 GAGGTGATAATAGATAAGCCAGCTACTGATGACAATGGAACAACCACTGAAACTGAAATG 2331

Qy   2068 AGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAA 2127
Db   2332 AGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATGGACTTTCTAGAAGATCCTTCCCAA 2391

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Db   2392 AGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAA 2451

Qy   2188 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2247
Db   2452 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2511

Qy   2248 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTYGTGATGGACCCATTT 2307
Db   2512 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTTGTGATGGACCCATTT 2571
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Qy 2308 GTTGACCTGGCCATCACCATCTGTATTGTCTTAAATACTCTTTTCATGGCCATGGAGCAC 2367
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Qy 2368 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2427
Db 2632 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2691
Qy 2428 ATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAA 2487
Db 2692 ATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCCATGGATCCTTACTATTATTTCCAA 2751
Qy 2488 GAAGGCTGGAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTC 2547
Db 2752 GAAGGCTGGAATATCTTTGACGGTTTTATTGTGACGCTTAGCCTGGTAGAACTTGGACTC 2811
Qy 2548 GCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTG 2607
Db 2812 GCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTTCGATTGCTGCGAGTTTTCAAGTTG 2871
Qy 2608 GCAAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCT 2667
Db 2872 GCAAAATCTTGGCCAACGTTAAATATGCTAATAAAGATCATCGGCAATTCCGTGGGGGCT 2931
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Db 2932 CTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTCTTCATTTTTGCCGTGGTCGGCATG 2991
Qy 2728 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 2787
Db 2992 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 3051
Qy 2788 CCACGCTGGCACATGAATGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGT 2847
Db 3052 CCACGCTGGCACATGAATGACTTCTTCCACTCCTTCCTGATTGTGTTCCGCGTGCTGTGT 3111
Qy 2848 GGGGAGTGGATAGAGACCATGTGGGACTGTATGGAGGTTGCTGGTCAAGCCATGTGCCTT 2907
Db 3112 GGGGAGTGGATAGAGACCATGTGGGACTGTATGGAGGTTGCTGGTCAAGCCATGTGCCTT 3171
Qy 2908 ACTGTCTTCATGATGGTCATGGTGATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCC 2967
Db 3172 ACTGTCTTCATGATGGTCATGGTGATTGGAAACCTAGTGGTCCTGAATCTCTTTCTGGCC 3231
Qy 2968 TTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCAGCCACTGATGATGATAATGAAATG 3027
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Qy 3028 AATAATCTCCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAA 3087
Db 3292 AATAATCTCCAAATTGCTGTGGATAGGATGCACAAAGGAGTAGCTTATGTGAAAAGAAAA 3351
Qy 3088 ATATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAA 3147
Db 3352 ATATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAGATGAAATTAAA 3411
Qy 3148 CCACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATACARCAGAAATT 3207
Db 3412 CCACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATACAGCAGAAATT 3471
Qy 3208 GGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTATAGGAACTGGC 3267
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Qy 3268 AGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAACCCC 3327
Db 3532 AGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAAACAACCCC 3591
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Db 3592 AGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAAATTTAAACACG 3651
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Db 3772 GAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTCACTGAAGGCTGTGTACAAAGATTC 3831
Qy 3568 AAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAACAATGGTGGAACCTGAGAAGG 3627
Db 3832 AAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGAAAACAATGGTGGAACCTGAGAAGG 3891
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Qy 3808 AAATGGGTGGCATATGGCTATCAAACATATTTCACCAATGCCTGGTGTTGGCTGGACTTC 3867
Db 4072 AAATGGGTGGCATATGGCTATCAAA-ATATTTCACCAATGCCTGGTGTTGGCTGGACTTC 4130
Qy 3868 TTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCAAATGCCTTGGGTTACTCAGAACTT 3927
Db 4131 TTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCAAATGCCTTGGGTTACTCAGAACTT 4190
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Db 4191 GGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTGAGACCTCTAAGAGCCTTATCTCGA 4250
Qy 3988 TTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTAGGAGCAATTCCATCCATCATGAAT 4047
Db 4251 TTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTAGGAGCAATTCCATCCATCATGAAT 4310
Qy 4048 GTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTCAGCATCATGGGCGTAAATTTGTTT 4107
Db 4311 GTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTCAGCATCATGGGCGTAAATTTGTTT 4370
Qy 4108 GCTGGCAAATTCTACCACTGTATTAACACCACAACTGGTGACAGGTTTGACATCGAAGAC 4167
Db 4371 GCTGGCAAATTCTACCACTGTATTAACACCACAACTGGTGACAGGTTTGACATCGAAGAC 4430
Qy 4168 GTGAATAATCATACTGATTGCCTAAAACTAATAGAAAGAAATGAGACTGCTCGATGGAAA 4227
Db 4431 GTGAATAATCATACTGATTGCCTAAAACTAATAGAAAGAAATGAGACTGCTCGATGGAAA 4490
Qy 4228 AATGTGAAAGTAAACTTTGATAATGTAGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCC 4287
Db 4491 AATGTGAAAGTAAACTTTGATAATGTAGGATTTGGGTATCTCTCTTTGCTTCAAGTTGCC 4550
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Db 4551 ACATTCAAAGGATGGATGGATATAATGTATGCAGCAGTTGATTCCAGAAATGTGGAACTC 4610
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Db 4611 CAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTTTACTTTGTTATTTTCATCATCTTT 4670
Qy 4408 GGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTCATCATAGATAATTTCAACCAGCAG 4467
Db 4671 GGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTCATCATAGATAATTTCAACCAGCAG 4730
Qy 4468 AAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTATAAT 4527

PR 26-NOV-1999; 99US-0167623.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Rouleau GA, LaFreniere RG, Rochefort D, Cossette P, Ragsdale D;
XX
DR WPI; 2001-355945/37.
DR P-PSDB; AAB99675.
XX
PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a
PT DNA variant, equivalent, or mutation which shows a linkage
PT disequilibrium -
XX
PS Disclosure; Page 93-96; 268pp; English.
XX
CC The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The
CC method comprises determining the genotype of at least one gene selected
CC from SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation
CC which shows a linkage disequilibrium. SCN1a, SCN2A and SCN3A are all
CC sodium channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome
CC 2q23-q31. Compounds identified as modulators of the biological activity
CC of SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating
CC epilepsy or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to
CC AAB99679 represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR
CC primers, oligonucleotides and proteins given in the exemplification of
CC the present invention.
XX
SQ Sequence 8378 BP; 2498 A; 1571 C; 1775 G; 2534 T; 0 other;

Query Match 81.2%; Score 4897; DB 22; Length 8378;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5337; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Qy    688 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 747
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Db    953 ATTCCAGGCCTGAAAACCATTGTGGGAGCCCTGATCCAGTCTGTGAAGAAGCTCTCAGAT 1012

Qy    748 GTAATGATCCTGACTGTGTTCTGTCTGAGCGTATTTGCTCTAATTGGGCTGCAGCTGTTC 807
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    808 ATGGGCAACCTGAGGAATAAATGTATACAATGGCCTCCCACCAATGCTTCCTTGGAGGAA 867
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    868 CATAGTATAGAAAAGAATATAACTGTGAATTATAATGGTACACTTATAAATGAAACTGTC 927
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Qy    928 TTTGAGTTTGACTGGAAGTCATATATTCAAGATTCAAGATATCATTATTTCCTGGAGGGT 987
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Qy    988 TTTTTAGATGCACTACTATGTGGAAATAGCTCTGATGCAGGCCAATGTCCAGAGGGATAT 1047
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Qy   1048 ATGTGTGTGAAAGCTGGTAGAAATCCCAATTATGGCTACACAAGCTTTGATACCTTCAGT 1107
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1168 CTGACATTACGTGCTGCTGGGAAAACGTACATGATATTTTTTGTGTTGGTCATTTTCTTG 1227
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Qy   1228 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1287
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 GGCTCATTCTACCTAATAAATTTGATCCTGGCTGTGGTGGCCATGGCCTACGAGGAACAG 1552

Qy   1288 AATCAGGCCACCTTGGAAGAAGCAGAACAGAAAGAGGCCGAATTTCAGCAGATGATTGAA 1347
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Qy   1348 CAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAGGCAGCAACGGCAACTGCCTCAGAACAT 1407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1408 TCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCAGACAGCTCATCTGAAGCCTCTAAGTTG 1467
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Qy   1468 AGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGGAGGAAGAAAAGAAAACAGAAAGAGCAG 1527
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Qy   1528 TCTGGTGGGGAAGAGAAAGATGAGGATGAATTCCAAAAATCTGAATCTGAGGACAGCATC 1587
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1768 TTCGCAGATGATGAGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTT 1827
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Qy   1888 CGGATGCTGGCAGTGTTTCCAGCGAATGGGAAGATGCACAGCACTGTGGATTGCAATGGT 1947
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1948 GTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCTACATCGCCTGTTGGACAGCTTCTGCCA 2007
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2128 AGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAA 2187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2392 AGGCAACGAGCAATGAGTATAGCCAGCATTCTAACAAATACAGTAGAAGAACTTGAAGAA 2451

Qy   2188 TCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTTTCCAACATATTCTTAATCTGGGAC 2247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2248 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTYGTGATGGACCCATTT 2307
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Db   2512 TGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTCAACCTGGTTGTGATGGACCCATTT 2571
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Qy 2368 TATCCAATGACGGACCATTTCAATAATGTGCTTACAGTAGGAAACTTGGTTTTCACTGGG 2427
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Qy 2728 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 2787
Db 2992 CAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGCAAGATCGCCAGTGATTGTCAACTC 3051
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Qy 4048 GTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTCAGCATCATGGGCGTAAATTTGTTT 4107
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Qy 4168 GTGAATAATCATACTGATTGCCTAAAACTAATAGAAAGAAATGAGACTGCTCGATGGAAA 4227
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Qy 4468 AAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACAGAAGAACAGAAGAAATACTATAAT 4527

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Qy   6028 TAA 6030
          |||
Db   6291 TAA 6293
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RESULT 6
AAD32846
ID AAD32846 standard; cDNA; 4362 BP.
XX
AC AAD32846;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #8.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..4362
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FT		/product= "Human ion channel protein #8"
FT		/transl_except= (pos:2974..2976, aa:Xaa)
FT		/transl_except= (pos:3199..3201, aa:Xaa)
FT		/note= "Xaa = any amino acid"

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PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20517.
XX

PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 69-70; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4362 BP; 1300 A; 845 C; 995 G; 1219 T; 3 other;

Query Match 71.9%; Score 4338; DB 24; Length 4362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
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Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

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Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
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Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040

Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100

Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160

Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
Db   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220

Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280

Qy   2281 GTCAACCTGGTGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2281 GTCAACCTGTTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340

Qy   2341 AATACTCTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
Db   2341 AATACCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400

Qy   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
Db   2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460

Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520

Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580

Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640

Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

Qy   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db   2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
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Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480

Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600

Qy   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db   3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660

Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Db    3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy    3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy    3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy    3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
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Db    3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy    4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy    4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 TTCATCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy    4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200
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Db    4141 ACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATA 4200

Qy    4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260
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Db    4201 GAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTT 4260

Qy    4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 GGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCA 4320

Qy    4321 GCAGTTGATTCCAGAAAT 4338
           |||||||||||||||||
Db    4321 GCAGTTGATTCCAGAAAT 4338
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RESULT 7
AAD32847
ID AAD32847 standard; cDNA; 4179 BP.
XX
AC AAD32847;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #9.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..4179
FT   /*tag= a
FT   /product= "Human ion channel protein #9"
FT   /transl_except= (pos:2974..2976, aa:Xaa)
FT   /transl_except= (pos:3199..3201, aa:Xaa)
FT   /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20518.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 73-75; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4179 BP; 1239 A; 815 C; 958 G; 1164 T; 3 other;

Query Match 68.9%; Score 4152; DB 24; Length 4179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
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Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
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Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
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Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
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Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
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Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
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Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
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Qy   2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
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Qy   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Db   2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
Qy   2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Db   2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
Qy   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Db   2281 GTCAACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTA 2340
Qy   2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Qy   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Db   2461 GCCATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTG 2520
Qy   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db   2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db   2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
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Qy   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700

Qy   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
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Db   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
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Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
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Qy   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
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Db   3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540

Qy   3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
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Qy   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720

Qy   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780

Qy   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
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Db   3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840

Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTT 4020

Qy   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATT 4080

Qy   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACA 4140

Qy   4141 ACTGGTGACAGG 4152
          ||||||||||||
Db   4141 ACTGGTGACAGG 4152
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RESULT 8
AAD32848
ID AAD32848 standard; cDNA; 4197 BP.
XX
AC AAD32848;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #10.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..4197
FT   /*tag= a
FT   /product= "Human ion channel protein #10"
FT   /transl_except= (pos:2974..2976, aa:Xaa)
FT   /transl_except= (pos:3199..3201, aa:Xaa)
FT   /note= "Xaa = any amino acid"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20519.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug

PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 78-79; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in
CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4197 BP; 1232 A; 821 C; 965 G; 1176 T; 3 other;

Query Match 66.4%; Score 4003; DB 24; Length 4197;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4003; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy    1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
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Db    1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy    1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Qy  1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db  1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Qy  1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db  1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Qy  1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
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Qy  1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
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Qy  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db  1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Qy  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Db  1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGGTGATAATAGATAAGCCAGCTACTGATGAC 2040
Qy  2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Db  2041 AATGGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCC 2100
Qy  2101 ATGGACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTA 2160
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Qy  2161 ACAAATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAA 2220
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Qy  2221 TTTTCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTT 2280
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Qy  2341 AATACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTT 2400
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Qy  2401 ACAGTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATT 2460
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Qy  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Db  2521 ACGCTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCA 2580
Qy  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Db  2581 TTTCGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATA 2640
Qy  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Db  2641 AAGATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATC 2700
Qy  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
Db  2701 GTCTTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTC 2760
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Qy  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Db  2761 TGCAAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCC 2820
Qy  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Db  2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
Qy  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Db  2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
Qy  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Db  2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
Qy  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Db  3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
Qy  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Db  3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
Qy  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Db  3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
Qy  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Db  3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
Qy  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Db  3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
Qy  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Db  3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
Qy  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Db  3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
Qy  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Db  3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGC 3480
Qy  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Db  3481 GCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGT 3540
Qy  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Db  3541 TTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGA 3600
Qy  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Db  3601 GGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTT 3660
Qy  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Db  3661 GAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATA 3720
Qy  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Db  3721 TATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACT 3780
Qy  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
Db  3781 TACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTC 3840
```

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Qy   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACA 3900

Qy   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCT 3960

Qy   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGG 4003
          |||||||||||||||||||||||||||||||||||||||||||
Db   3961 CTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGG 4003


RESULT 9
AAD32839
ID   AAD32839 standard; cDNA; 5997 BP.
XX
AC   AAD32839;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #1.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5997
FT                   /*tag= a
FT                   /product= "Human ion channel protein #1"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20510.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 28-30; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5997 BP; 1773 A; 1185 C; 1338 G; 1698 T; 3 other;

  Query Match             66.1%;  Score 3987;  DB 24;  Length 5997;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2011 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2070

Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2071 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2130

Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2131 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2190

Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430

Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730

Qy   2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790

Qy   2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850
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Qy   2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910

Qy   2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970

Qy   3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030

Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090

Qy   3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150

Qy   3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210

Qy   3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270

Qy   3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3271 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3330

Qy   3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390

Qy   3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450

Qy   3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510

Qy   3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
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Db   3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570

Qy   3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630

Qy   3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690

Qy   3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
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Db   3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750

Qy   3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
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Db   3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810

Qy   3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870

Qy   3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930

Qy   3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990

Qy   4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy   4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110

Qy   4144 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4111 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4170

Qy   4204 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4171 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4230

Qy   4264 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4231 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4290

Qy   4324 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4291 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4350

Qy   4384 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4351 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4410

Qy   4444 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4411 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4470

Qy   4504 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4471 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4530

Qy   4564 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4531 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4590

Qy   4624 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4591 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4650

Qy   4684 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4651 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4710

Qy   4744 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4711 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4770

Qy   4804 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4771 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4830

Qy   4864 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4831 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4890

Qy   4924 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4891 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4950

Qy   4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4951 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5010

Qy   5044 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    5011 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5070

Qy    5104 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5071 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5130

Qy    5164 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5131 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5190

Qy    5224 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5191 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5250

Qy    5284 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5251 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5310

Qy    5344 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5311 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5370

Qy    5404 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5371 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5430

Qy    5464 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5431 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5490

Qy    5524 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5491 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5550

Qy    5584 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5551 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5610

Qy    5644 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5611 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5670

Qy    5704 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5671 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5730

Qy    5764 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5731 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5790

Qy    5824 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5791 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5850

Qy    5884 GACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCT 5943
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5851 GACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCT 5910

Qy    5944 TGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGC 6003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5911 TGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGC 5970

Qy    6004 AAAGATGAAAAAGCCAAAGGGAAATAA 6030
           ||||||||||||||||||||||||||||
Db    5971 AAAGATGAAAAAGCCAAAGGGAAATAA 5997


RESULT 10
AAD32840
ID   AAD32840 standard; cDNA; 5889 BP.
XX
AC   AAD32840;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Human ion channel cDNA #2.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..5889
FT                   /*tag= a
FT                   /product= "Human ion channel protein #2"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA, Mathur B, Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20511.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 35-36; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 5889 BP; 1733 A; 1161 C; 1313 G; 1679 T; 3 other;

  Query Match            64.2%;  Score 3874;  DB 24;  Length 5889;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3874;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2011 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2070
Qy  2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2071 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2130
Qy  2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2131 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2190
Qy  2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2191 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2250
Qy  2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2251 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2310
Qy  2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2311 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2370
Qy  2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2371 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2430
Qy  2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490
Qy  2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2491 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2550
Qy  2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2551 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2610
Qy  2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2611 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2670
Qy  2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2671 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2730
Qy  2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2731 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2790
Qy  2824 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2883
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2791 CTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATGGAG 2850
Qy  2884 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2943
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2851 GTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAACCTA 2910
Qy  2944 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 3003
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2911 GTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTTGCA 2970
Qy  3004 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3063
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2971 GCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCACAAA 3030
Qy  3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3031 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3090
Qy  3124 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3091 CAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGT 3150
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Qy  3184 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3151 ATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGA 3210
Qy  3244 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3211 ACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGAT 3270
Qy  3304 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3363
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3271 TACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAA 3330
Qy  3364 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3331 TCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAAAGC 3390
Qy  3424 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3391 AAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGACATCGGCGCA 3450
Qy  3484 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3543
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3451 CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTGTTTC 3510
Qy  3544 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3603
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3511 ACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAGAGGA 3570
Qy  3604 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3663
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3571 AAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTTTGAG 3630
Qy  3664 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3723
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3631 ACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATATATAT 3690
Qy  3724 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3783
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3691 ATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCACTTAC 3750
Qy  3784 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3843
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3751 ATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTTCACC 3810
Qy  3844 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3903
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3811 AATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAACAGCA 3870
Qy  3904 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3963
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3871 AATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGCTCTG 3930
Qy  3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990
Qy  4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050
Qy  4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110
Qy  4144 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4111 GGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAATAGAA 4170
Qy  4204 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4171 AGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATTTGGG 4230
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Qy   4264 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4231 TATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGCAGCA 4290

Qy   4324 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4291 GTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTATCTT 4350

Qy   4384 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4351 TACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGGTGTC 4410

Qy   4444 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4411 ATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTATGACA 4470

Qy   4504 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4471 GAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAAACCGCAAAAG 4530

Qy   4564 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4531 CCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAGACAA 4590

Qy   4624 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4591 GTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGGTCACAATGATGGTGGAA 4650

Qy   4684 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4651 ACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTTCATT 4710

Qy   4744 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4711 GTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTTTACC 4770

Qy   4804 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4771 ATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTTTCTT 4830

Qy   4864 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4831 GCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCTTGCT 4890

Qy   4924 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4891 AGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCTCTTT 4950

Qy   4984 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4951 GCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGTCATG 5010

Qy   5044 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5011 TTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGGGATC 5070

Qy   5104 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5071 GATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAATTACA 5130

Qy   5164 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5131 ACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGACTGT 5190

Qy   5224 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5191 GACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATCTGTT 5250

Qy   5284 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5251 GGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTAC 5310

Qy   5344 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5311 ATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGT 5370

Qy   5404 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5371 GAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAG 5430

Qy   5464 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5431 TTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTG 5490

Qy   5524 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5491 CCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGG 5550

Qy   5584 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5551 ATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAG 5610

Qy   5644 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5611 ATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTC 5670

Qy   5704 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5671 TCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATT 5730

Qy   5764 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5731 ATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACG 5790

Qy   5824 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5791 TACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATT 5850

Qy   5884 GACAGAATAAATGAAAACTCTATTACAGAAAAAA 5917
          ||||||||||||||||||||||||||||||||||
Db   5851 GACAGAATAAATGAAAACTCTATTACAGAAAAAA 5884
```

RESULT 11
ABL39689
ID ABL39689 standard; cDNA; 8131 BP.
XX
AC ABL39689;
XX
DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN1A encoding cDNA SEQ ID NO:1.
XX
KW Human; sodium channel; SCN1A; chromosome 2q24; gene; ss;
KW familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 15..6018
FT /*tag= a
FT /product= "sodium channel SCN1A"
XX
PN WO200196552-A1.
XX
PD 20-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-JP04956.
XX
PR 13-JUN-2000; 2000JP-0177540.
PR 13-JUN-2000; 2000JP-0177544.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Kanazawa I, Goto J, Jeong S;
XX

DR WPI; 2002-098066/13.
DR P-PSDB; ABB06026.
XX
PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
PT studying physiological mechanism in which excitant cells participate
PT and causes of diseases and developing drugs for motor endplate disease
PT -
XX
PS Claim 5; Page 20-40; 88pp; Japanese.
XX
CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence encodes the human sodium channel SCN1A. SCN1A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful
CC in studying the physiological mechanism in which excitant cells
CC participate and cause human diseases, and in developing remedies for
CC e.g. familial hypercalcaemic periodic paralysis of extremities and
CC motor endplate disease.
XX
SQ Sequence 8131 BP; 2453 A; 1530 C; 1719 G; 2422 T; 7 other;

Query Match 54.8%; Score 3302; DB 24; Length 8131;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3982; Conservative 0; Mismatches 4; Indels 5; Gaps 3;

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Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2088

Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2148

Qy   2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2208

Qy   2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 TCCAACATATTCTCAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2268

Qy   2284 AACCTGGTYGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2343
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2269 AACCTGGTCGTGATGGACCCATTTGTTGACCTGGCCATCACCATCTGTATTGTCTTAAAT 2328

Qy   2344 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2329 ACTCTTTTCATGGCCATGGAGCACTATCCAATGACGGACCATTTCAATAATGTGCTTACA 2388

Qy   2404 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2389 GTAGGAAACTTGGTTTTCACTGGGATCTTTACAGCAGAAATGTTTCTGAAAATTATTGCC 2448

Qy   2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2449 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2508

Qy   2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2509 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2568

Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2569 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2628

Qy   2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2629 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2688

Qy   2704 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2689 TTCATTTTTGCCGTGGTCGGCATGCAGCTCTTTGGTAAAAGCTACAAAGATTGTGTCTGC 2748
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Qy   2764 AAGATCGCCAGTGATTGTCAACTCCC---ACGCTGGCACATGAATGACTTCTTCCACTCC 2820
          |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db   2749 AAGATCGCCAGTGATTGTCAACTCCCACAACGCTGGCACATGAATGACTTCTTCCACTCC 2808

Qy   2821 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2809 TTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGACTGTATG 2868

Qy   2881 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2869 GAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATTGGAAAC 2928

Qy   2941 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTMTGAGCTCATTTAGTGCAGACAACCTT 3000
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2929 CTAGTGGTCCTGAATCTCTTTCTGGCCTTGCTTCTGAGCTCATTTAGTGCAGACAACCTT 2988

Qy   3001 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2989 GCAGCCACTGATGATGATAATGAAATGAATAATCTCCAAATTGCTGTGGATAGGATGCAC 3048

Qy   3061 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3049 AAAGGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGG 3108

Qy   3121 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3109 AAACAAAAGATTTTAGATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGT 3168

Qy   3181 TGTATGTCCAATCATACARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3240
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   3169 TGTATGTCCAATCATACAACAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAAT 3228

Qy   3241 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3229 GGAACTACAAGTGGTATAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGT 3288

Qy   3301 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3289 GATTACATGTCATTCATAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGA 3348

Qy   3361 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3349 GAATCTGACTTTGAAAATTTAAACACGGAAGACTTTAGTAGTGAATCGGATCTGGAAGAA 3408

Qy   3421 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGT-GGACATCGG 3479
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   3409 AGCAAAGAGAAACTGAATGAAAGCAGTAGCTCATCAGAAGGTAGCACTGTGGGACATCGG 3468

Qy   3480 CGCACCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTG 3539
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3469 CGC-CCTGTAGAAGAACAGCCCGTAGTGGAACCTGAAGAAACTCTTGAACCAGAAGCTTG 3527

Qy   3540 TTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAG 3599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3528 TTTCACTGAAGGCTGTGTACAAAGATTCAAGTGTTGTCAAATCAATGTGGAAGAAGGCAG 3587

Qy   3600 AGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTT 3659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3588 AGGAAAACAATGGTGGAACCTGAGAAGGACGTGTTTCCGAATAGTTGAACATAACTGGTT 3647

Qy   3660 TGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATAT 3719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3648 TGAGACCTTCATTGTTTTCATGATTCTCCTTAGTAGTGGTGCTCTGGCATTTGAAGATAT 3707

Qy   3720 ATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCAC 3779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3708 ATATATTGATCAGCGAAAGACGATTAAGACGATGTTGGAATATGCTGACAAGGTTTTCAC 3767

Qy   3780 TTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTT 3839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3768 TTACATTTTCATTCTGGAAATGCTTCTAAAATGGGTGGCATATGGCTATCAAACATATTT 3827

Qy   3840 CACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAAC 3899
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Db   3828 CACCAATGCCTGGTGTTGGCTGGACTTCTTAATTGTTGATGTTTCATTGGTCAGTTTAAC 3887

Qy   3900 AGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGC 3959
Db   3888 AGCAAATGCCTTGGGTTACTCAGAACTTGGAGCCATCAAATCTCTCAGGACACTAAGAGC 3947

Qy   3960 TCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCT 4019
Db   3948 TCTGAGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCT 4007

Qy   4020 TTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAAT 4079
Db   4008 TTTAGGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAAT 4067

Qy   4080 TTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCAC 4139
Db   4068 TTTCAGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCAC 4127

Qy   4140 AACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAAT 4199
Db   4128 AACTGGTGACAGGTTTGACATCGAAGACGTGAATAATCATACTGATTGCCTAAAACTAAT 4187

Qy   4200 AGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGGATT 4259
Db   4188 AGAAAGAAATGAGACTGCTCGATGGAAAAATGTGAAAGTAAACTTTGATAATGTAGCATT 4247

Qy   4260 TGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGC 4319
Db   4248 TGGGTATCTCTCTTTGCTTCAAGTTGCCACATTCAAAGGATGGATGGATATAATGTATGC 4307

Qy   4320 AGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTA 4379
Db   4308 AGCAGTTGATTCCAGAAATGTGGAACTCCAGCCTAAGTATGAAGAAAGTCTGTACATGTA 4367

Qy   4380 TCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGG 4439
Db   4368 TCTTTACTTTGTTATTTTCATCATCTTTGGGTCCTTCTTCACCTTGAACCTGTTTATTGG 4427

Qy   4440 TGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTAT 4499
Db   4428 TGTCATCATAGATAATTTCAACCAGCAGAAAAAGAAGTTTGGAGGTCAAGACATCTTTAT 4487

Qy   4500 GACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAACCGCA 4559
Db   4488 GACAGAAGAACAGAAGAAATACTATAATGCAATGAAAAAATTAGGATCGAAAAACCGCA 4547

Qy   4560 AAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAG 4619
Db   4548 AAAGCCTATACCTCGACCAGGAAACAAATTTCAAGGAATGGTCTTTGACTTCGTAACCAG 4607

Qy   4620 ACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGTCACAATGATGGT 4679
Db   4608 ACAAGTTTTTGACATAAGCATCATGATTCTCATCTGTCTTAACATGTCACAATGATGGT 4667

Qy   4680 GGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTT 4739
Db   4668 GGAAACAGATGACCAGAGTGAATATGTGACTACCATTTTGTCACGCATCAATCTGGTGTT 4727

Qy   4740 CATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT 4799
Db   4728 CATTGTGCTATTTACTGGAGAGTGTGTACTGAAACTCATCTCTCTACGCCATTATTATTT 4787

Qy   4800 TACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTT 4859
Db   4788 TACCATTGGATGGAATATTTTTGATTTTGTGGTTGTCATTCTCTCCATTGTAGGTATGTT 4847

Qy   4860 TCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCT 4919
Db   4848 TCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAGTGATCCGTCT 4907

Qy   4920 TGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCT 4979
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Db   4908 TGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCCGCACGCTGCT 4967

Qy   4980 CTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGT 5039
Db   4968 CTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTACTCTTCCTAGT 5027

Qy   5040 CATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGG 5099
Db   5028 CATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGAGGGAAGTTGG 5087

Qy   5100 GATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAAT 5159
Db   5088 GATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCCTATTCCAAAT 5147

Qy   5160 TACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGA 5219
Db   5148 TACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTAAGCCACCCGA 5207

Qy   5220 CTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATC 5279
Db   5208 CTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTGGGAACCCATC 5267

Qy   5280 TGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACAT 5339
Db   5268 TGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACAT 5327

Qy   5340 GTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCT 5399
Db   5328 GTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCT 5387

Qy   5400 GAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAAC 5459
Db   5388 GAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAAC 5447

Qy   5460 TCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAA 5519
Db   5448 TCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAA 5507

Qy   5520 TCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGA 5579
Db   5508 TCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGA 5567

Qy   5580 CCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGG 5639
Db   5568 CCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGG 5627

Qy   5640 AGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAA 5699
Db   5628 AGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAA 5687

Qy   5700 GGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGT 5759
Db   5688 GGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGT 5747

Qy   5760 CATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTT 5819
Db   5748 CATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTT 5807

Qy   5820 TACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGAT 5879
Db   5808 TACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGAT 5867

Qy   5880 AATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGC 5939
Db   5868 AATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGC 5927

Qy   5940 AGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGA 5999
Db   5928 AGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGA 5987

Qy   6000 AGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
Db   5988 AGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6018
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RESULT 12
AAD32841
ID   AAD32841 standard; cDNA; 4329 BP.
XX
AC   AAD32841;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #3.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4329
FT                   /*tag= a
FT                   /product= "Human ion channel protein #3"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20512.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders -
XX
PS   Claim 1; Page 41-42; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
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SQ   Sequence 4329 BP; 1287 A; 840 C; 988 G; 1211 T; 3 other;

  Query Match             38.1%;  Score 2295;  DB 24;  Length 4329;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2295;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2070

Qy    2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2071 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2130

Qy    2164 AATACAGTAGAAGAACTTGAAGAATCCAGGCAGAAATGCCCACCCTGTTGGTATAAATTT 2223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2224 TCCAACATATTCTTAATCTGGGACTGTTCTCCATATTGGTTAAAAGTGAAACATGTTGTC 2283
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Qy    2464 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2431 ATGGATCCTTACTATTATTTCCAAGAAGGCTGGAATATCTTTGACGGTTTTATTGTGACG 2490

Qy    2524 CTTAGCCTGGTAGAACTTGGACTCGCCAATGTGGAAGGATTATCTGTTCTCCGTTCATTT 2583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Qy    2644 ATCATCGGCAATTCCGTGGGGGCTCTGGGAAATTTAACCCTCGTCTTGGCCATCATCGTC 2703
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Qy    2764 AAGATCGCCAGTGATTGTCAACTCCCACGCTGGCACATGAATGACTTCTTCCACTCCTTC 2823
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Qy   3064 GGAGTAGCTTATGTGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAA 3123
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Qy   4324 GTTGATTCCAGAAAT 4338
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Db   4291 GTTGATTCCAGAAAT 4305
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RESULT 13
AAD32842
ID AAD32842 standard; cDNA; 4146 BP.
XX
AC AAD32842;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel cDNA #4.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW gene; medical disorder; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..4146
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FT		/product= "Human ion channel protein #4"
FT		/transl_except= (pos:2941..2943, aa:Xaa)
FT		/transl_except= (pos:3166..3168, aa:Xaa)
FT		/note= "Xaa = any amino acid"

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PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US25650.
XX
PR 16-AUG-2000; 2000US-225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI; 2002-280757/32.
DR P-PSDB; AAE20513.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders -
XX
PS Claim 1; Page 46-47; 83pp; English.
XX
CC The present sequence is a cDNA encoding novel human protein (NHP), ion
CC channel protein. NHP share structural similarity with mammalian sodium
CC channel proteins particularly voltage-gated sodium channel proteins.
CC NHP oligonucleotides are useful as hybridisation probes for screening
CC libraries and assessing gene expression patterns. Sequences derived
CC from regions adjacent to the intron/exon boundaries of NHP gene can be
CC used to design primers for use in amplification assays to detect
CC mutations within the exons, splice sites, introns that can be used in
CC diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC for drug screening effective in the treatment of symptomatic or
CC phenotypic manifestations of perturbing the normal function of NHP in

CC the body, and nucleotide constructs encoding NHP products are useful to
CC genetically engineer host cells to express NHP products in vivo. These
CC genetically engineered cells function as bioreactors in the body
CC delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC protein to the body. Nucleotide construct encoding NHP products are
CC also useful in gene therapy for modulating NHP expression and to
CC produce genetically engineered host cells to express NHP products in
CC vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC and/or triple helix sequences that are useful for NHP gene regulation.
CC The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases.
XX
SQ Sequence 4146 BP; 1226 A; 810 C; 951 G; 1156 T; 3 other;

Query Match 35.0%; Score 2109; DB 24; Length 4146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2044 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2103
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Db   2011 GGAACAACCACTGAAACTGAAATGAGAAAGAGAAGGTCAAGTTCTTTCCACGTTTCCATG 2070

Qy   2104 GACTTTCTAGAAGATCCTTCCCAAAGGCAACGAGCAATGAGTATAGCCAGCATTCTAACA 2163
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Qy   2584 CGATTGCTGCGAGTTTTCAAGTTGGCAAAATCTTGGCCAACGTTAAATATGCTAATAAAG 2643
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Qy    3964 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 4023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3931 AGACCTCTAAGAGCCTTATCTCGATTTGAAGGGATGAGGGTGGTTGTGAATGCCCTTTTA 3990

Qy    4024 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3991 GGAGCAATTCCATCCATCATGAATGTGCTTCTGGTTTGTCTTATATTCTGGCTAATTTTC 4050

Qy    4084 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4051 AGCATCATGGGCGTAAATTTGTTTGCTGGCAAATTCTACCACTGTATTAACACCACAACT 4110

Qy    4144 GGTGACAGG 4152
          |||||||||
Db    4111 GGTGACAGG 4119


RESULT 14
AAD32843
ID   AAD32843 standard; cDNA; 4164 BP.
XX
AC   AAD32843;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human ion channel cDNA #5.
XX
KW   Human; novel human protein; NHP; voltage-gated sodium channel;
KW   gene therapy; bioreactor; mental disorder; biological disorder;
KW   gene; medical disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4164
FT                   /*tag= a
FT                   /product= "Human ion channel protein #5"
FT                   /transl_except= (pos:2941..2943, aa:Xaa)
FT                   /transl_except= (pos:3166..3168, aa:Xaa)
FT                   /note= "Xaa = any amino acid"
XX
PN   WO200214498-A2.
XX
PD   21-FEB-2002.
XX
PF   15-AUG-2001; 2001WO-US25650.
XX
PR   16-AUG-2000; 2000US-225989P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Turner CA,  Mathur B,  Mathur D;
XX
DR   WPI; 2002-280757/32.
DR   P-PSDB; AAE20514.
XX
PT   Novel polynucleotides encoding human sodium channel proteins,
PT   particularly voltage-gated sodium channel proteins useful for drug
PT   screening, diagnosis and in gene therapy of biological disorders
XX
PS   Claim 1; Page 51-52; 83pp; English.
XX
CC   The present sequence is a cDNA encoding novel human protein (NHP), ion
CC   channel protein. NHP share structural similarity with mammalian sodium
CC   channel proteins particularly voltage-gated sodium channel proteins.
CC   NHP oligonucleotides are useful as hybridisation probes for screening
CC   libraries and assessing gene expression patterns. Sequences derived
CC   from regions adjacent to the intron/exon boundaries of NHP gene can be
CC   used to design primers for use in amplification assays to detect
CC   mutations within the exons, splice sites, introns that can be used in
CC   diagnostics and pharmacogenomics. NHP nucleotide sequences are useful
CC   for drug screening effective in the treatment of symptomatic or
CC   phenotypic manifestations of perturbing the normal function of NHP in
CC   the body, and nucleotide constructs encoding NHP products are useful to
CC   genetically engineer host cells to express NHP products in vivo. These
CC   genetically engineered cells function as bioreactors in the body
CC   delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion
CC   protein to the body. Nucleotide construct encoding NHP products are
CC   also useful in gene therapy for modulating NHP expression and to
CC   produce genetically engineered host cells to express NHP products in
CC   vivo. NHP nucleotide sequences may also be used as part of ribozyme
CC   and/or triple helix sequences that are useful for NHP gene regulation.
CC   The NHP polypeptides are useful for generating antibodies, as
CC   reagents in diagnostic assays, for identifying other cellular gene
CC   products related to NHP and as reagents in assays for screening for
CC   compounds that are useful in the treatment of mental, biological or
CC   medical disorders and diseases.
XX
SQ   Sequence 4164 BP; 1219 A; 816 C; 958 G; 1168 T; 3 other;

  Query Match           33.3%;  Score 2011;  DB 24;  Length 4164;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2011;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240

Qy    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACCCCTACTATATCAATAAGAAAACTTTTATAGTATTGAATAAAGGGAAGGCCATCTTC 300

Qy    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTTCAGTGCCACCTCTGCCCTGTACATTTTAACTCCCTTCAATCCTCTTAGGAAAATA 360

Qy    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTATTAAGATTTTGGTACATTCATTATTCAGCATGCTAATTATGTGCACTATTTTGACA 420

Qy    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AACTGTGTGTTTATGACAATGAGTAACCCTCCTGATTGGACAAAGAATGTAGAATACACC 480

Qy    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTCACAGGAATATATACTTTTGAATCACTTATAAAAATTATTGCAAGGGGATTCTGTTTA 540

Qy    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GAAGATTTTACTTTCCTTCGGGATCCATGGAACTGGCTCGATTTCACTGTCATTACATTT 600

Qy    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCGTACGTCACAGAGTTTGTGGACCTGGGCAATGTCTCGGCATTGAGAACATTCAGAGTT 660

Qy    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTCCGAGCATTGAAGACGATTTCAGTCATTCCAGGCCTGAAAACCATTGTGGGAGCCCTG 720

Qy    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780
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Db    721 ATCCAGTCTGTGAAGAAGCTCTCAGATGTAATGATCCTGACTGTGTTCTGTCTGAGCGTA 780

Qy    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840
Db    781 TTTGCTCTAATTGGGCTGCAGCTGTTCATGGGCAACCTGAGGAATAAATGTATACAATGG 840

Qy    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900
Db    841 CCTCCCACCAATGCTTCCTTGGAGGAACATAGTATAGAAAAGAATATAACTGTGAATTAT 900

Qy    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960
Db    901 AATGGTACACTTATAAATGAAACTGTCTTTGAGTTTGACTGGAAGTCATATATTCAAGAT 960

Qy    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020
Db    961 TCAAGATATCATTATTTCCTGGAGGGTTTTTTAGATGCACTACTATGTGGAAATAGCTCT 1020

Qy   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080
Db   1021 GATGCAGGCCAATGTCCAGAGGGATATATGTGTGTGAAAGCTGGTAGAAATCCCAATTAT 1080

Qy   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140
Db   1081 GGCTACACAAGCTTTGATACCTTCAGTTGGGCTTTTTTGTCCTTGTTTCGACTAATGACT 1140

Qy   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200
Db   1141 CAGGACTTCTGGGAAAATCTTTATCAACTGACATTACGTGCTGCTGGGAAAACGTACATG 1200

Qy   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260
Db   1201 ATATTTTTTGTGTTGGTCATTTTCTTGGGCTCATTCTACCTAATAAATTTGATCCTGGCT 1260

Qy   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320
Db   1261 GTGGTGGCCATGGCCTACGAGGAACAGAATCAGGCCACCTTGGAAGAAGCAGAACAGAAA 1320

Qy   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380
Db   1321 GAGGCCGAATTTCAGCAGATGATTGAACAGCTTAAAAAGCAACAGGAGGCAGCTCAGCAG 1380

Qy   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440
Db   1381 GCAGCAACGGCAACTGCCTCAGAACATTCCAGAGAGCCCAGTGCAGCAGGCAGGCTCTCA 1440

Qy   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500
Db   1441 GACAGCTCATCTGAAGCCTCTAAGTTGAGTTCCAAGAGTGCTAAGGAAAGAAGAAATCGG 1500

Qy   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560
Db   1501 AGGAAGAAAAGAAAACAGAAAGAGCAGTCTGGTGGGGAAGAGAAAGATGAGGATGAATTC 1560

Qy   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620
Db   1561 CAAAAATCTGAATCTGAGGACAGCATCAGGAGGAAAGGTTTTCGCTTCTCCATTGAAGGG 1620

Qy   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680
Db   1621 AACCGATTGACATATGAAAAGAGGTACTCCTCCCCACACCAGTCTTTGTTGAGCATCCGT 1680

Qy   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740
Db   1681 GGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCCTTTTCAGCTTTAGAGGGCGA 1740

Qy   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800
Db   1741 GCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATGAGCACAGCACCTTTGAGGAT 1800

Qy   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860
Db   1801 AACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGACACGGAGAGAGACGCAACAGC 1860

Qy   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920
Db   1861 AACCTGAGTCAGACCAGTAGGTCATCCCGGATGCTGGCAGTGTTTCCAGCGAATGGGAAG 1920

Qy   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980
Db   1921 ATGCACAGCACTGTGGATTGCAATGGTGTGGTTTCCTTGGTTGGTGGACCTTCAGTTCCT 1980

Qy   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGG 2011
Db   1981 ACATCGCCTGTTGGACAGCTTCTGCCAGAGG 2011
```

RESULT 15
AAK02861/c
ID AAK02861 standard; DNA; 1992 BP.
XX
AC AAK02861;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 2852.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 2852; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 1992 BP; 589 A; 399 C; 384 G; 620 T; 0 other;

Query Match 19.6%; Score 1181; DB 22; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   4850 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 4909
Db   1447 TAGGTATGTTTCTTGCCGAGCTGATAGAAAAGTATTTCGTGTCCCCTACCCTGTTCCGAG 1388
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Qy   4910 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 4969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 TGATCCGTCTTGCTAGGATTGGCCGAATCCTACGTCTGATCAAAGGAGCAAAGGGGATCC 1328

Qy   4970 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 5029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 GCACGCTGCTCTTTGCTTTGATGATGTCCCTTCCTGCGTTGTTTAACATCGGCCTCCTAC 1268

Qy   5030 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 5089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 TCTTCCTAGTCATGTTCATCTACGCCATCTTTGGGATGTCCAACTTTGCCTATGTTAAGA 1208

Qy   5090 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 5149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 GGGAAGTTGGGATCGATGACATGTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCC 1148

Qy   5150 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 5209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 TATTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGCTAGCACCCATTCTCAACAGTA 1088

Qy   5210 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 5269
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 AGCCACCCGACTGTGACCCTAATAAAGTTAACCCTGGAAGCTCAGTTAAGGGAGACTGTG 1028

Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 968

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 908

Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 848

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 788

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 728

Qy   5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 668

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 608

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 548

Qy   5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 488

Qy   5810 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 5869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 AAGCTTCCTTTACGTACAATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAG 428

Qy   5870 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 5929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 AAGACATGATAATTGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCA 368

Qy   5930 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 5989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 TGTCCACTGCAGCTTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAAC 308
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Qy   5990 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 6030
          ||||||||||||||||||||||||||||||||||||||||
Db    307 ATGAGCAAGAAGGCAAAGATGAAAAAGCCAAAGGGAAATAA 267
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Search completed: April 22, 2003, 14:24:28
Job time : 798 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2003, 13:39:49 ; Search time 5066 Seconds
(without alignments)
19277.297 Million cell updates/sec

Title: US-09-930-871-11
Perfect score: 6030
Sequence: 1 atggagcaaacagtgcttgt.....aaaaagccaaagggaaataa 6030

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
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23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		559	9.3	579	14	BM718214	BM718214 UI-E-EJ1-
c 2		548	9.1	562	14	BM682680	BM682680 UI-E-EJ1-
3		427	7.1	683	13	BI667397	BI667397 603292178
4		348	5.8	951	9	AL533359	AL533359 AL533359
5		285	4.7	455	9	AA912739	AA912739 ol41c12.s
6		264	4.4	710	9	AL707423	AL707423 DKFZp686K
c 7		213	3.5	717	12	BG724147	BG724147 602697466
c 8		173	2.9	382	12	BG208320	BG208320 RST27812
9		164	2.7	598	14	BM726341	BM726341 UI-E-EJ0-
10		154	2.6	774	13	BI488799	BI488799 603021394
11		148	2.5	482	13	BI032903	BI032903 MR4-NN020
12		146	2.4	735	13	BI488967	BI488967 603021693
c 13		134	2.2	672	17	AG054756	AG054756 Pan trogl
14		115	1.9	450	9	AL120392	AL120392 DKFZp761E
15		107	1.8	225	9	AA214661	AA214661 zq89e09.r
16		98	1.6	343	14	F07776	F07776 HSC2HD061 n
17		98	1.6	873	12	BF527027	BF527027 602039918
18		80	1.3	402	13	BM484672	BM484672 538604 MA
c 19		79	1.3	304	12	BG181807	BG181807 RST660 At
c 20		79	1.3	618	10	BE566126	BE566126 601339238
c 21		79	1.3	892	12	BG215777	BG215777 RST35454
c 22		79	1.3	982	14	BM905527	BM905527 AGENCOURT
c 23		76	1.3	731	9	AI796228	AI796228 wh44d06.x
24		70	1.2	602	9	AL706368	AL706368 DKFZp686H
25		65	1.1	674	12	BG342331	BG342331 602374246
c 26		64	1.1	260	12	BG227970	BG227970 RST41890
27		62	1.0	577	9	AU067361	AU067361 AU067361
28		62	1.0	581	10	BB644560	BB644560 BB644560
29		62	1.0	800	9	AU066802	AU066802 AU066802
30		62	1.0	900	9	AU067321	AU067321 AU067321
c 31		52	0.9	693	17	AG178030	AG178030 Pan trogl
c 32		50	0.8	438	17	AZ495334	AZ495334 1M0331P08
c 33		50	0.8	490	12	BF391260	BF391260 UI-R-CA1-
34		50	0.8	928	14	BQ715936	BQ715936 AGENCOURT
35		48	0.8	561	12	BF076296	BF076296 225823 MA
c 36		47	0.8	325	12	BF471558	BF471558 UI-M-BH3-
37		47	0.8	373	10	AW456773	AW456773 UI-M-BH3-
38		47	0.8	379	12	BE947431	BE947431 UI-M-BH3-
39		47	0.8	386	12	BE944106	BE944106 UI-M-BH3-
c 40		47	0.8	437	10	AW495598	AW495598 UI-M-BH3-
c 41		47	0.8	495	12	BF563427	BF563427 UI-R-BT1-
42		47	0.8	547	12	BF470392	BF470392 UI-M-BH3-
43		47	0.8	618	10	BB622500	BB622500 BB622500
44		47	0.8	721	17	BH035847	BH035847 RPCI-24-3
c 45		45	0.7	293	12	BG183871	BG183871 RST2784 A

ALIGNMENTS

RESULT 1
BM718214
LOCUS BM718214 579 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-EJ1-ajf-a-09-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajf-a-09-0-UI 5', mRNA sequence.
ACCESSION BM718214
VERSION BM718214.1 GI:19036382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 579)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

```
           Clone Distribution: Researchers may obtain clones from Research
           Genetics (www.resgen.com).
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .579
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ1-ajf-a-09-0-UI"
                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      168 a    123 c    125 g    163 t
ORIGIN

  Query Match             9.3%;  Score 559;  DB 14;  Length 579;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-278;
  Matches  559;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5270 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 5329
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGAACCCATCTGTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTG 60

Qy   5330 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 5389
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTG 120

Qy   5390 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 5449
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATC 180

Qy   5450 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 5509
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGATGCAACTCAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAAC 240

Qy   5510 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 5569
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGCCTCTCAATCTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGG 300

Qy   5570 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 5629
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGAGTGGTGACCGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAG 360

Qy   5630 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 5689
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAGAGAGTGGAGAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCA 420

Qy   5690 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 5749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATCCTTCCAAGGTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAG 480

Qy   5750 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 5809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCTGCTGTCATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAAC 540

Qy   5810 AAGCTTCCTTTACGTACAA 5828
           ||||||||||||||||||
Db    541 AAGCTTCCTTTACGTACAA 559


RESULT 2
BM682680/c
LOCUS       BM682680                562 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  UI-E-EJ1-ajf-a-09-0-UI.s1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajf-a-09-0-UI 3', mRNA sequence.
ACCESSION   BM682680
VERSION     BM682680.1  GI:18992576
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .562
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ1-ajf-a-09-0-UI"
                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI).
                     TAG_LIB=UI-E-EJ1
                     TAG_TISSUE=Foveal and Macular Retina
                     TAG_SEQ=GTCC"
BASE COUNT      161 a    121 c    118 g    162 t
ORIGIN
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  Query Match             9.1%;  Score 548;  DB 14;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-273;
  Matches  548;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5281 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 5340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     562 GTTGGAATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATG 503

Qy    5341 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 5400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     502 TACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTG 443

Qy    5401 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 5460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     442 AGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACT 383

Qy    5461 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 5520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     382 CAGTTCATGGAATTTGAAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAAT 323

Qy    5521 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 5580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     322 CTGCCACAACCAAACAAACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGAC 263

Qy    5581 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 5640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     262 CGGATCCACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGA 203

Qy    5641 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 5700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     202 GAGATGGATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAG 143

Qy    5701 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 5760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     142 GTCTCCTATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTC 83

Qy    5761 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 5820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 ATTATTCAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTT 23

Qy    5821 ACGTACAA 5828
           ||||||||
Db      22 ACGTACAA 15


RESULT 3
BI667397
LOCUS       BI667397                683 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603292178F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5311627 5',
            mRNA sequence.
ACCESSION   BI667397
VERSION     BI667397.1  GI:15581630
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11789  row: k  column: 20
            High quality sequence stop: 681.

FEATURES             Location/Qualifiers
     source          1. .683
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5311627"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      236 a    136 c    139 g    172 t
ORIGIN

  Query Match             7.1%;  Score 427;  DB 13;  Length 683;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-210;
  Matches  427;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5587 CACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATG 5646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6 CACTGTCTTGATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATG 65

Qy    5647 GATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCC 5706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      66 GATGCTCTACGAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCC 125

Qy    5707 TATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATT 5766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 TATCAGCCAATCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATT 185

Qy    5767 CAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTAC 5826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 CAGCGTGCTTACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTAC 245

Qy    5827 AATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGAC 5886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 AATAAAAACAAAATCAAAGGTGGGGCTAATCTTCTTATAAAAGAAGACATGATAATTGAC 305

Qy    5887 AGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGT 5946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 AGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGCTTGT 365

Qy    5947 CCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAA 6006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     366 CCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGGCAAA 425

Qy    6007 GATGAAA 6013
           |||||||
Db     426 GATGAAA 432


RESULT 4
AL533359
LOCUS       AL533359                951 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL533359 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN004YF22 5
            prime, mRNA sequence.
ACCESSION   AL533359
VERSION     AL533359.1  GI:12796852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
```

```
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DN004YF22"
                     /clone_lib="LTI_FL015_Brn1"
                     /sex="male"
                     /tissue_type="Adult brain"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was constructed by Life Technologies.
                     Contact : Feng Liang Life Technologies, a division of
                     Invitrogen 9800 Medical Center Drive Rockville, Maryland
                     20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      303 a    189 c    203 g    247 t      9 others
ORIGIN

  Query Match             5.8%;  Score 348;  DB 9;  Length 951;
  Best Local Similarity   99.6%;  Pred. No. 1e-168;
  Matches  448;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   5417 AGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTG 5476
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 AGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGCAACTCAGTTCATGGAATTTG 123

Qy   5477 AAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACA 5536
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AAAAATTATCTCAGTTTGCAGCTGCGCTTGAACCGCCTCTCAATCTGCCACAACCAAACA 183

Qy   5537 AACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTG 5596
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 AACTCCAGCTCATTGCCATGGATTTGCCCATGGTGAGTGGTGACCGGATCCACTGTCTTG 243

Qy   5597 ATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTAC 5656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 ATATCTTATTTGCTTTTACAAAGCGGGTTCTAGGAGAGAGTGGAGAGATGGATGCTCTAC 303

Qy   5657 GAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAA 5716
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 GAATACAGATGGAAGAGCGATTCATGGCTTCCAATCCTTCCAAGGTCTCCTATCAGCCAA 363

Qy   5717 TCACTACTACTTTAAAACGAAAACAAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTT 5776
           ||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db    364 TCACTACTACTTTAAWACGAAAACWAGAGGAAGTATCTGCTGTCATTATTCAGCGTGCTT 423

Qy   5777 ACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAAACA 5836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 ACAGACGCCACCTTTTAAAGCGAACTGTAAAACAAGCTTCCTTTACGTACAATAAAAACA 483

Qy   5837 AAATCAAAGGTGGGGCTAATCTTCTTATAA 5866
           |||||||||||||||||||||||||||||
Db    484 AAATCAAAGGTGGGGCTAATCTTCTTATAA 513


RESULT 5
AA912739
LOCUS       AA912739                455 bp    mRNA    linear   EST 26-AUG-1998
DEFINITION  ol41c12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1526038 3' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN
            II ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AA912739
VERSION     AA912739.1  GI:3052131
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 542   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 376.
FEATURES             Location/Qualifiers
     source          1. .455
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1526038"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      163 a     70 c     89 g    133 t
ORIGIN

  Query Match             4.7%;  Score 285;  DB 9;  Length 455;
  Best Local Similarity   99.7%;  Pred. No. 4.8e-136;
  Matches  335;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   3077 TGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAG 3136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 TGAAAAGAAAAATATATGAATTTATTCAACAGTCCTTCATTAGGAAACAAAAGATTTTAG 62

Qy   3137 ATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATA 3196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 ATGAAATTAAACCACTTGATGATCTAAACAACAAGAAAGACAGTTGTATGTCCAATCATA 122

Qy   3197 CARCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTA 3256
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 CAGCAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTA 182

Qy   3257 TAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCA 3316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 TAGGAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCA 242

Qy   3317 TAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAA 3376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 TAAACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAA 302

Qy   3377 ATTTAAACACGGAAGACTTTAGTAGTGAATCGGATC 3412
           |||||||||||||||||||||||||||||||||||
Db     303 ATTTAAACACGGAAGACTTTAGTAGTGAATCGGATC 338


RESULT 6
AL707423
LOCUS       AL707423                710 bp    mRNA    linear   EST 22-MAR-2002
DEFINITION  DKFZp686K2447_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686K2447 5', mRNA sequence.
ACCESSION   AL707423
VERSION     AL707423.1  GI:19690778
KEYWORDS    EST.
```

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SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
            Wiemann,S.
  TITLE     EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and Wiemann
            ,S.)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Ottenwaelder B
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. No s1 sequence
            available.
            This clone (DKFZp686K2447) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686K2447"
                     /clone_lib="686 (synonym: hlcc3)"
                     /tissue_type="human skeletal muscle"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
BASE COUNT      203 a    137 c    169 g    201 t
ORIGIN

  Query Match             4.4%;  Score 264;  DB 9;  Length 710;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-125;
  Matches  264;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 ATGGAGCAAACAGTGCTTGTACCACCAGGACCTGACAGCTTCAACTTCTTCACCAGAGAA 450

Qy     61 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 TCTCTTGCGGCTATTGAAAGACGCATTGCAGAAGAAAAGGCAAAGAATCCCAAACCAGAC 510

Qy    121 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 AAAAAAGATGACGACGAAAATGGCCCAAAGCCAAATAGTGACTTGGAAGCTGGAAAGAAC 570

Qy    181 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 CTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCAGAGCCCCTGGAGGACCTG 630

Qy    241 GACCCCTACTATATCAATAAGAAA 264
          ||||||||||||||||||||||||
Db    631 GACCCCTACTATATCAATAAGAAA 654


RESULT 7
BG724147/c
LOCUS       BG724147                717 bp    mRNA    linear   EST 08-MAY-2001
DEFINITION  602697466F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4829512 5',
            mRNA sequence.
ACCESSION   BG724147
VERSION     BG724147.1  GI:14003334
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 717)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10749  row: c  column: 17
            High quality sequence stop: 712.
FEATURES             Location/Qualifiers
     source          1. .717
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4829512"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      180 a    182 c    151 g    204 t
ORIGIN

  Query Match             3.5%;  Score 213;  DB 12;  Length 717;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-98;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3200 CAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTATAG 3259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 CAGAAATTGGGAAAGATCTTGACTATCTTAAAGATGTAAATGGAACTACAAGTGGTATAG 553

Qy   3260 GAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAA 3319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    552 GAACTGGCAGCAGTGTTGAAAAATACATTATTGATGAAAGTGATTACATGTCATTCATAA 493

Qy   3320 ACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAAATT 3379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 ACAACCCCAGTCTTACTGTGACTGTACCAATTGCTGTAGGAGAATCTGACTTTGAAAATT 433

Qy   3380 TAAACACGGAAGACTTTAGTAGTGAATCGGATC 3412
          |||||||||||||||||||||||||||||||
Db    432 TAAACACGGAAGACTTTAGTAGTGAATCGGATC 400


RESULT 8
BG208320/c
LOCUS       BG208320                382 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST27812 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG208320
VERSION     BG208320.1  GI:13730007
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
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  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 382.
FEATURES             Location/Qualifiers
     source          1. .382
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      103 a    104 c     82 g     91 t      2 others
ORIGIN

  Query Match             2.9%;  Score 173;  DB 12;  Length 382;
  Best Local Similarity   99.6%;  Pred. No. 7.6e-78;
  Matches  223;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1661 AGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCC 1720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327 AGTCTTTGTTGAGCATCCGTGGCTCCCTATTTTCACCAAGGCGAAATAGCAGAACAAGCC 268

Qy   1721 TTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATG 1780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    267 TTTTCAGCTTTAGAGGGCGAGCAAAGGATGTGGGATCTGAGAACGACTTCGCAGATGATG 208

Qy   1781 AGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCTTGTTTGTGCCCCGACGAC 1840
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    207 AGCACAGCACCTTTGAGGATAACGAGAGCCGTAGAGATTCCATGTTTGTGCCCCGACGAC 148

Qy   1841 ACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCA 1884
           |||||||||||||||||||||||||||||||||||||||||||
Db    147 ACGGAGAGAGACGCAACAGCAACCTGAGTCAGACCAGTAGGTCA 104


RESULT 9
BM726341
LOCUS       BM726341                598 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  UI-E-EJ0-aih-n-09-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
            UI-E-EJ0-aih-n-09-0-UI 5', mRNA sequence.
ACCESSION   BM726341
VERSION     BM726341.1  GI:19047674
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .598
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-EJ0-aih-n-09-0-UI"
                     /clone_lib="UI-E-EJ0"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ0 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
                     optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      160 a    125 c    142 g    170 t      1 others
ORIGIN

  Query Match             2.7%;  Score 164;  DB 14;  Length 598;
  Best Local Similarity   100.0%;  Pred. No. 4e-73;
  Matches  164;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5293 TTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTC 5352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 TTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATCGCGGTC 96

Qy   5353 ATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGAC 5412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 ATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAGGATGAC 156

Qy   5413 TTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGC 5456
           |||||||||||||||||||||||||||||||||||||||||||
Db    157 TTTGAGATGTTCTATGAGGTTTGGGAGAAGTTTGATCCCGATGC 200


RESULT 10
BI488799
LOCUS       BI488799                774 bp    mRNA    linear   EST 28-AUG-2001
DEFINITION  603021394F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192206 5',
            mRNA sequence.
ACCESSION   BI488799
VERSION     BI488799.1  GI:15328027
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
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            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11480  row: k  column: 23
           High quality sequence start: 19
           High quality sequence stop: 763.
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5192206"
                     /clone_lib="NIH_MGC_114"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is  destroyed
                     upon cloning).  Average insert size 1.5 kb, insert size
                     range 1-3 kb.  Library is normalized and enriched for
                     full-length  clones and was constructed by C. Gruber
                     (Invitrogen).  Research  Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      173 a    175 c    203 g    223 t
ORIGIN

  Query Match             2.6%;  Score 154;  DB 13;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-68;
  Matches  154;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5287 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 5346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    392 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 451

Qy   5347 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAG 5406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAG 511

Qy   5407 GATGACTTTGAGATGTTCTATGAGGTTTGGGAGA 5440
          |||||||||||||||||||||||||||||||||
Db    512 GATGACTTTGAGATGTTCTATGAGGTTTGGGAGA 545


RESULT 11
BI032903
LOCUS       BI032903                482 bp    mRNA    linear   EST 14-JUN-2001
DEFINITION  MR4-NN0205-220101-202-a12 NN0205 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI032903
VERSION     BI032903.1  GI:14439529
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 482)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-NN0205-
            220101-202-a12&t3=2001-01-22&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 10
            High quality sequence stop: 482.
FEATURES             Location/Qualifiers
     source          1. .482
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NN0205"
                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      178 a     91 c     99 g    114 t
ORIGIN

  Query Match             2.5%;  Score 148;  DB 13;  Length 482;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-65;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5883 TGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGC 5942
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 TGACAGAATAAATGAAAACTCTATTACAGAAAAAACTGATCTGACCATGTCCACTGCAGC 148

Qy   5943 TTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGG 6002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 TTGTCCACCTTCCTATGACCGGGTGACAAAGCCAATTGTGGAAAAACATGAGCAAGAAGG 208

Qy   6003 CAAAGATGAAAAAGCCAAAGGGAAATAA 6030
          ||||||||||||||||||||||||||||
Db    209 CAAAGATGAAAAAGCCAAAGGGAAATAA 236


RESULT 12
BI488967
LOCUS       BI488967                735 bp    mRNA    linear   EST 28-AUG-2001
DEFINITION  603021693F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192182 5',
            mRNA sequence.
ACCESSION   BI488967
VERSION     BI488967.1  GI:15328195
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM11480  row: j  column: 23
           High quality sequence stop: 728.
FEATURES             Location/Qualifiers
     source          1. .735
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
```

```
                     /clone="IMAGE:5192182"
                     /clone_lib="NIH_MGC_114"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      164 a    173 c    175 g    223 t
ORIGIN

  Query Match             2.4%;  Score 146;  DB 13;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-64;
  Matches  146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5287 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 5346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     393 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 452

Qy    5347 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAG 5406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     453 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCTCTGAGTGAG 512

Qy    5407 GATGACTTTGAGATGTTCTATGAGGT 5432
           |||||||||||||||||||||||||
Db     513 GATGACTTTGAGATGTTCTATGAGGT 538


RESULT 13
AG054756/c
LOCUS       AG054756               672 bp    DNA     linear   GSS 02-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-040I13.R, genomic survey sequence.
ACCESSION   AG054756
VERSION     AG054756.1  GI:16592199
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-040I13.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 672)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-040I13.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      196 a    141 c    117 g    217 t      1 others
ORIGIN

  Query Match             2.2%;  Score 134;  DB 17;  Length 672;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-57;
  Matches  134;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2815 CACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGAC 2874
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 CACTCCTTCCTGATTGTGTTCCGCGTGCTGTGTGGGGAGTGGATAGAGACCATGTGGGAC 586

Qy    2875 TGTATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATT 2934
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 TGTATGGAGGTTGCTGGTCAAGCCATGTGCCTTACTGTCTTCATGATGGTCATGGTGATT 526

Qy    2935 GGAAACCTAGTGGT 2948
           ||||||||||||||
Db     525 GGAAACCTAGTGGT 512


RESULT 14
AL120392
LOCUS       AL120392               450 bp    mRNA    linear   EST 25-FEB-2000
DEFINITION  DKFZp761E108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
            DKFZp761E108 5', mRNA sequence.
ACCESSION   AL120392
VERSION     AL120392.1  GI:5926291
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Koehrer, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Koehrer K
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            No s1 sequence available.
            This clone (DKFZp761E108) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp761E108"
                     /clone_lib="761 (synonym: hamy2)"
                     /tissue_type="amygdala"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT      105 a    103 c    105 g    132 t      5 others
ORIGIN

  Query Match             1.9%;  Score 115;  DB 9;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-47;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    5328 TGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAG 5387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 TGTGGTGAACATGTACATCGCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAG 228

Qy    5388 TGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAG 5442
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                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    229 TGCAGAGCCTCTGAGTGAGGATGACTTTGAGATGTTCTATGAGGTTTGGGAGAAG 283


RESULT 15
AA214661
LOCUS       AA214661                225 bp    mRNA    linear   EST 12-MAR-1998
DEFINITION  zq89e09.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
            IMAGE:649192 5' similar to gb:M94055 SODIUM CHANNEL PROTEIN, BRAIN
            II ALPHA SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AA214661
VERSION     AA214661.1  GI:1813315
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 225)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1023   Std Error: 0.00
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 125.
FEATURES             Location/Qualifiers
     source          1. .225
                     /organism="Homo sapiens"
                     /db_xref="GDB:5278471"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:649192"
                     /clone_lib="Stratagene hNT neuron (#937233)"
                     /dev_stage="hNT neurons"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; Cloned unidirectionally.  Primer: Oligo dT.
                     Differentiated, post mitotic hNT neurons. Average insert
                     size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
                     GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      54 a     39 c     59 g     72 t      1 others
ORIGIN

  Query Match           1.8%;  Score 107;  DB 9;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-43;
  Matches  107;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   5287 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 5346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 ATTTTCTTTTTTGTCAGTTACATCATCATATCCTTCCTGGTTGTGGTGAACATGTACATC 93

Qy   5347 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGA 5393
          |||||||||||||||||||||||||||||||||||||||||||||
Db     94 GCGGTCATCCTGGAGAACTTCAGTGTTGCTACTGAAGAAAGTGCAGA 140


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